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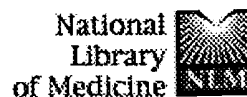
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
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
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
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
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
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
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















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
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
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

















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
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
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
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










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
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=> S L2 AND human  
13 FILES SEARCHED...  
22 FILES SEARCHED...  
37 FILES SEARCHED...  
54 FILES SEARCHED...  
L3 111 L2 AND HUMAN

=> D L3 1-111

L3 ANSWER 1 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:211874 BIOSIS  
DN PREV200400213748  
TI Expression of \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* CHT1 in the \*\*\*human\*\*\* leukemic T cell line  
MOLT-3.  
AU Fujii, Takeshi [Reprint Author]; Okuda, Takashi; Haga, Tatsuya; Kawashima,  
Koichiro [Reprint Author]  
CS Dept. Pharmacol., Kyoritsu Col. Pharmacy, Tokyo, 105-8512, Japan  
SO Journal of Pharmacological Sciences, (2004) Vol. 94, No. Supplement 1, pp.  
202P. print.  
Meeting Info.: 77th Annual Meeting of the Japanese Pharmacological  
Society. Osaka, Japan. March 08-10, 2004. Japanese Pharmacological  
Society.  
ISSN: 1347-8613 (ISSN print).  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 14 Apr 2004  
Last Updated on STN: 14 Apr 2004

L3 ANSWER 2 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:114768 BIOSIS  
DN PREV200400104871  
TI The lymphocytic cholinergic system and its contribution to the regulation  
of immune activity.  
AU Kawashima, Koichiro [Reprint Author]; Fujii, Takeshi  
CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
Shibakoen, Minato, Tokyo, 105-8512, Japan  
kawashima-ki@kyoritsu-ph.ac.jp  
SO Life Sciences, (December 26 2003) Vol. 74, No. 6, pp. 675-696. print.  
ISSN: 0024-3205 (ISSN print).  
DT Article  
General Review; (Literature Review)  
LA English  
ED Entered STN: 25 Feb 2004  
Last Updated on STN: 25 Feb 2004

L3 ANSWER 3 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:79232 BIOSIS  
DN PREV200400080163  
TI Characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
AU Haga, T. [Reprint Author]; Okuda, T.; Kaitsuka, C. [Reprint Author];  
Okamura, M.; Osawa, C. [Reprint Author]; Nishiyama, N. [Reprint Author];  
Yamada, H. [Reprint Author]; Nakamura, T. [Reprint Author]; Kobayashi, Y.  
CS Gakushuin University, Institute of Biomolecular Science, Tokyo, Japan  
SO Journal of Neurochemistry, (December 2003) Vol. 87, No. Supplement 1, pp.  
43. print.  
Meeting Info.: Meeting of the International Society for Neurochemistry  
(ISN). Hong Kong, China. August 03-08, 2003. International Society for  
Neurochemistry.  
CODEN: JONRA9. ISSN: 0022-3042.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 4 Feb 2004  
Last Updated on STN: 4 Feb 2004

L3 ANSWER 4 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2004:65466 BIOSIS  
DN PREV200400066534  
TI Expression of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* CHT1 in rat and \*\*\*human\*\*\* arteries.  
AU Lips, Katrin S. [Reprint Author]; Pfeil, Uwe; Reiners, Katja; Rimasch,

CS Rainer V.; Schmidt, Rupert; Kummer, Wolfgang  
 Inst. for Anatomy and Cell Biology, Justus-Liebig-University, Aulweg 123,  
 D-35385, Giessen, Germany  
 Katrin.S.Lips@anatomie.med.uni-giessen.de  
 SO Journal of Histochemistry & Cytochemistry, (December 2003) Vol. 51, No.  
 12, pp. 1645-1654. print.  
 ISSN: 0022-1554 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 28 Jan 2004  
 Last Updated on STN: 28 Jan 2004

L3 ANSWER 5 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:577555 BIOSIS  
 DN PREV200300581998  
 TI Expression of acetylcholine in lymphocytes and modulation of an  
 independent lymphocytic cholinergic activity by immunological stimulation.  
 AU Fujii, Takeshi; Watanabe, Yoshihiro; Fujimoto, Kazuko; Kawashima, Koichiro  
 [Reprint Author]  
 CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
 Shibakoen, Minato-ku, Tokyo, 105-8512, Japan  
 kawashima-ki@kyoritsu-ph.ac.jp  
 SO Biogenic Amines, (2003) Vol. 17, No. 4-6, pp. 373-386. print.  
 CODEN: BIAME7. ISSN: 0168-8561.  
 DT Article  
 LA English  
 ED Entered STN: 10 Dec 2003  
 Last Updated on STN: 10 Dec 2003

L3 ANSWER 6 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:533308 BIOSIS  
 DN PREV200300536831  
 TI The hemicholinium-3 sensitive \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* is internalized by clathrin-mediate  
 endocytosis and is present in endosomes and synaptic vesicles.  
 AU Ribeiro, F. M.; Alves-Silva, J.; Volknandt, W.; Martins-Silva, C.; Mahmud,  
 H.; Wilhelm, A.; Gomez, M. V.; Rylett, R. J.; Ferguson, S. S. G.; Prado,  
 V. F.; Prado, M. A. M. [Reprint Author]  
 CS Laboratorio de Neurofarmacologia, Departamento de Farmacologia, ICB,  
 Universidade Federal de Minas Gerais, Avenue Antonio Carlos 6627,  
 31270-910, Belo Horizonte, MG, Brazil  
 mprado@icb.ufmg.br  
 SO Journal of Neurochemistry, (October 2003) Vol. 87, No. 1, pp. 136-146.  
 print.  
 CODEN: JONRA9. ISSN: 0022-3042.  
 DT Article  
 LA English  
 ED Entered STN: 12 Nov 2003  
 Last Updated on STN: 12 Nov 2003

L3 ANSWER 7 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:441016 BIOSIS  
 DN PREV200300441016  
 TI Distribution of \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* immunoreactivity in the primate central nervous  
 system.  
 AU Kus, Laura; Borys, Ewa; Chu, Ya Ping; Ferguson, Shawn M.; Blakely, Randy  
 D.; Emborg, Marina E.; Kordower, Jeffrey H.; Levey, Allan I.; Mufson,  
 Elliott J. [Reprint Author]  
 CS Department of Neurological Sciences, 2242 W Harrison Street, Suite 200,  
 Chicago, IL, 60612, USA  
 emufson@rush.edu  
 SO Journal of Comparative Neurology, (August 25 2003) Vol. 463, No. 3, pp.  
 341-357. print.  
 ISSN: 0021-9967 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 24 Sep 2003  
 Last Updated on STN: 24 Sep 2003

L3 ANSWER 8 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:326967 BIOSIS  
 DN PREV200300326967  
 TI \*\*\*HIGH\*\*\* - \*\*\*AFFINITY\*\*\* \*\*\*CHOLINE\*\*\* \*\*\*TRANSPORTER\*\*\*  
 IMMUNOREACTIVE PROFILES IN MONKEY AND \*\*\*HUMAN\*\*\* BRAIN.



[Reprint Author]; Kordower, J. H. [Reprint Author]; Levey, A. I.; Mufson, E. J. [Reprint Author]  
 CS Neurological Sciences, Rush Medical Center, Chicago, IL, USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 785.6. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; (Meeting Poster)  
 Conference; Abstract; (Meeting Abstract)  
 LA English  
 ED Entered STN: 16 Jul 2003  
 Last Updated on STN: 16 Jul 2003

L3 ANSWER 9 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:283258 BIOSIS  
 DN PREV200300283258  
 TI A CHOLINERGIC AUTOCRINE LOOP REGULATES THE GROWTH OF SMALL CELL LUNG  
 CARCINOMA ( SCLC ) CELL LINES.  
 AU Song, P. [Reprint Author]; Sekhon, H. S. [Reprint Author]; Kuryatov, A.;  
 Blusztajn, J. K.; Mark, G. P.; Lindstrom, J.; Spindel, E. R. [Reprint  
 Author]  
 CS Div Neurosci, Dept Path, Dept Behav Neurosci, OHSU/ORPRC, Beaverton, OR,  
 USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 238.2. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; Abstract; (Meeting Abstract)  
 Conference; (Meeting Poster)  
 LA English  
 ED Entered STN: 19 Jun 2003  
 Last Updated on STN: 19 Jun 2003

L3 ANSWER 10 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:282043 BIOSIS  
 DN PREV200300282043  
 TI TARGETED DISRUPTION OF THE MURINE \*\*\*HIGH\*\*\* \*\*\*AFFINITY\*\*\*  
 \*\*\*CHOLINE\*\*\* \*\*\*TRANSPORTER\*\*\* GENE.  
 AU Blakely, R. D. [Reprint Author]; Ferguson, S. M. [Reprint Author]; Wright,  
 J. [Reprint Author]; Bazalakova, M. [Reprint Author]; Apparsundaram, S.  
 CS Dept. of Pharmacology, Ctr. for Mol. Neurosci., Vanderbilt University  
 School of Medicine, Nashville, TN, USA  
 SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002)  
 Vol. 2002, pp. Abstract No. 144.3. <http://sfn.scholarone.com>. cd-rom.  
 Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience.  
 Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.  
 DT Conference; (Meeting)  
 Conference; (Meeting Poster)  
 Conference; Abstract; (Meeting Abstract)  
 LA English  
 ED Entered STN: 19 Jun 2003  
 Last Updated on STN: 19 Jun 2003

L3 ANSWER 11 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:164774 BIOSIS  
 DN PREV200300164774  
 TI Detection of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* in the MOLT-3 \*\*\*human\*\*\* leukemic T-cell line.  
 AU Fujii, Takeshi; Okuda, Takashi; Haga, Tatsuya; Kawashima, Koichiro  
 [Reprint Author]  
 CS Department of Pharmacology, Kyoritsu College of Pharmacy, 1-5-30  
 Shibakoen, Minato-ku, Tokyo, 105-8512, Japan  
 kawashima-ki@kyoritsu-ph.ac.jp  
 SO Life Sciences, (March 28 2003) Vol. 72, No. 18-19, pp. 2131-2134. print.  
 ISSN: 0024-3205 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 2 Apr 2003  
 Last Updated on STN: 2 Apr 2003

L3 ANSWER 12 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:164766 BIOSIS  
 DN PREV200300164766

\*\*\*transporter\*\*\* CHT1 in epithelia.  
 AU Pfeil, Uwe; Haberberger, Rainer V.; Lips, Katrin S.; Eberling, Lars; Grau, Veronika; Kummer, Wolfgang [Reprint Author]  
 CS Institute for Anatomy and Cell Biology, Justus-Liebig-University, Aulweg 123, 35385, Giessen, Germany  
 SO wolfgang.kummer@anatomie.med.uni-giessen.de  
 Life Sciences, (March 28 2003) Vol. 72, No. 18-19, pp. 2087-2090. print.  
 ISSN: 0024-3205 (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 2 Apr 2003  
 Last Updated on STN: 2 Apr 2003

L3 ANSWER 13 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:85974 BIOSIS  
 DN PREV200300085974  
 TI \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 AU Wu, Dong-Hai [Inventor, Reprint Author]; Gu, Yunrong [Inventor]; Millard, William James [Inventor]; He, Yun-Ju [Inventor]  
 CS Gainesville, FL, USA  
 ASSIGNEE: University of Florida  
 PI US 6500643 December 31, 2002  
 SO Official Gazette of the United States Patent and Trademark Office Patents, (Dec 31 2002) Vol. 1265, No. 5. <http://www.uspto.gov/web/menu/patdata.html>  
 . e-file.  
 ISSN: 0098-1133 (ISSN print).  
 DT Patent  
 LA English  
 ED Entered STN: 6 Feb 2003  
 Last Updated on STN: 6 Feb 2003

L3 ANSWER 14 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:55673 BIOSIS  
 DN PREV200300055673  
 TI Single nucleotide polymorphism of the \*\*\*human\*\*\* \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* alters transport rate.  
 AU Okuda, Takashi; Okamura, Michiko; Kaitsuka, China; Haga, Tatsuya [Reprint Author]; Gurwitz, David  
 CS Faculty of Science, Institute for Biomolecular Science, Gakushuin University, 1-5-1 Mejiro, Toshima-ku, Tokyo, 171-8588, Japan  
 SO tatsuya.haga@gakushuin.ac.jp  
 Journal of Biological Chemistry, (November 22 2002) Vol. 277, No. 47, pp. 45315-45322. print.  
 CODEN: JBCHA3. ISSN: 0021-9258.  
 DT Article  
 LA English  
 ED Entered STN: 22 Jan 2003  
 Last Updated on STN: 22 Jan 2003

L3 ANSWER 15 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2003:10758 BIOSIS  
 DN PREV200300010758  
 TI Expression of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*, CHT1, in the neuronal and non-neuronal cholinergic system of \*\*\*human\*\*\* and rat skin.  
 AU Haberberger, Rainer Viktor [Reprint Author]; Pfeil, Uwe; Lips, Katrin  
 CS Susanne; Kummer, Wolfgang  
 Aulweg 123, 35385, Giessen, Germany  
 SO rainer.v.haberberger@anatomie.med.uni-giessen.de  
 Journal of Investigative Dermatology, (October 2002) Vol. 119, No. 4, pp. 943-948. print.  
 ISSN: 0022-202X (ISSN print).  
 DT Article  
 LA English  
 ED Entered STN: 18 Dec 2002  
 Last Updated on STN: 18 Dec 2002

L3 ANSWER 16 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2002:319227 BIOSIS  
 DN PREV200200319227  
 TI Spinal endogenous acetylcholine contributes to the analgesic effect of systemic morphine in rats.  
 AU Chen, Shao-rui; Pan, Hui-lin [Reprint author]

Medicine, 500 University Drive, H187, Hershey, PA, 17033-0850, USA  
hpan@psu.edu

SO Anesthesiology (Hagerstown), (August, 2001) Vol. 95, No. 2, pp. 525-530.  
print.  
CODEN: ANESAV. ISSN: 0003-3022.

DT Article  
LA English  
ED Entered STN: 5 Jun 2002  
Last Updated on STN: 5 Jun 2002

L3 ANSWER 17 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:167549 BIOSIS  
DN PREV200200167549  
TI Distribution of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* in the \*\*\*human\*\*\* and macaque monkey spinal cord  
AU Kobayashi, Yasushi [Reprint author]; Okuda, Takashi; Fujioka, Yasunori;  
Matsumura, George; Nishimura, Yu; Haga, Tatsuya  
CS Department of Anatomy, Kyorin University School of Medicine, Mitaka,  
Tokyo, 181-8611, Japan  
yasushi@kyorin-u.ac.jp  
SO Neuroscience Letters, (January 4, 2002) Vol. 317, No. 1, pp. 25-28. print.  
CODEN: NELED5. ISSN: 0304-3940.  
DT Article  
LA English  
ED Entered STN: 5 Mar 2002  
Last Updated on STN: 5 Mar 2002

L3 ANSWER 18 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:4241 BIOSIS  
DN PREV200200004241  
TI A single nucleotide polymorphism affects the transport rate of the  
\*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
AU Okuda, T. [Reprint author]; Haga, T.  
CS Dept Neurochem, Fac Med, Univ Tokyo, Tokyo, Japan  
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 2433.  
print.  
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San  
Diego, California, USA. November 10-15, 2001.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 28 Dec 2001  
Last Updated on STN: 25 Feb 2002

L3 ANSWER 19 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2002:4240 BIOSIS  
DN PREV200200004240  
TI The use of polyclonal antibodies to partially confirm predicted topology  
of a putative choline cotransporter from Limulus.  
AU Wang, Y. [Reprint author]; Cao, Z.; McAdory, B. [Reprint author]; Newkirk,  
R. F. [Reprint author]; Ivy, M. T. [Reprint author]; Townsel, J. G.  
CS Biol. Sci., Tenn. St. Univ., Nashville, TN, USA  
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 2432.  
print.  
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience. San  
Diego, California, USA. November 10-15, 2001.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 28 Dec 2001  
Last Updated on STN: 25 Feb 2002

L3 ANSWER 20 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:434607 BIOSIS  
DN PREV200100434607  
TI Distribution of the \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* in the central nervous system of the rat.  
AU Misawa, H. [Reprint author]; Nakata, K.; Matsuura, J.; Nagao, M.; Okuda,  
T.; Haga, T.  
CS Department of Neurology, Tokyo Metropolitan Institute for Neuroscience,  
2-6 Musashidai, Fuchu City, Tokyo, 183-8526, Japan  
hmisawa@tmin.ac.jp

CODEN: NRSCDN. ISSN: 0306-4522.

DT Article  
LA English  
ED Entered STN: 12 Sep 2001  
Last Updated on STN: 22 Feb 2002

L3 ANSWER 21 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:252320 BIOSIS  
DN PREV200100252320

TI Spinal cholinergic system mediates the analgesic effect of systemic morphine in rats.

AU Chen, Shao-Rui [Reprint author]; Pan, Hui-Lin [Reprint author]  
CS Penn State College of Medicine, 500 University Drive, Hershey, PA, 17033, USA

SO FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A810. print.  
Meeting Info.: Annual Meeting of the Federation of American Societies for Experimental Biology on Experimental Biology 2001. Orlando, Florida, USA. March 31-April 04, 2001.

CODEN: FAJOEC. ISSN: 0892-6638.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 23 May 2001  
Last Updated on STN: 19 Feb 2002

L3 ANSWER 22 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:125719 BIOSIS  
DN PREV200100125719

TI Molecular cloning and characterization of \*\*\*human\*\*\* affinity choline transporter.

AU Wu, D. [Reprint author]; Gu, Y.; Millard, W.; He, Y.; Lian, W.  
CS University of Florida, Gainesville, FL, USA

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-805.3. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 14 Mar 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 23 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:109007 BIOSIS  
DN PREV200100109007

TI Cloning of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*.

AU Okuda, T. [Reprint author]; Haga, T.  
CS Univ. of Tokyo, Tokyo, Japan

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-625.2. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

LA English  
ED Entered STN: 28 Feb 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 24 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:97086 BIOSIS  
DN PREV200100097086

TI Molecular cloning and characterization of \*\*\*human\*\*\* and murine \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporters\*\*\*

AU Apparsundaram, S. [Reprint author]; Ferguson, S.; Blakely, R. D.  
CS Vanderbilt University, Nashville, TN, USA

SO Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-306.5. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 04-09, 2000. Society for Neuroscience. ISSN: 0190-5295.

DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)

ED Entered STN: 21 Feb 2001  
Last Updated on STN: 15 Feb 2002

L3 ANSWER 25 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:21058 BIOSIS  
DN PREV200100021058  
TI Functional characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* -  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
AU Okuda, Takashi [Reprint author]; Haga, Tatsuya  
CS Department of Neurochemistry, Faculty of Medicine, University of Tokyo,  
7-3-1 Hongo, Bunkyo-ku, Tokyo, 113-0033, Japan  
okuda@m.u-tokyo.ac.jp  
SO FEBS Letters, (3 November, 2000) Vol. 484, No. 2, pp. 92-97. print.  
CODEN: FEBLAL. ISSN: 0014-5793.  
DT Article  
LA English  
ED Entered STN: 3 Jan 2001  
Last Updated on STN: 12 Feb 2002

L3 ANSWER 26 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2000:382237 BIOSIS  
DN PREV200000382237  
TI Modeling adolescent nicotine exposure: Effects on cholinergic systems in  
rat brain regions.  
AU Trauth, Jennifer A.; McCook, Everett C.; Seidler, Frederic J.; Slotkin,  
Theodore A. [Reprint author]  
CS Department of Pharmacology and Cancer Biology, Duke University Medical  
Center, DUMC, Durham, NC, 27710, USA  
SO Brain Research, (4 August, 2000) Vol. 873, No. 1, pp. 18-25. print.  
CODEN: BRREAP. ISSN: 0006-8993.  
DT Article  
LA English  
ED Entered STN: 6 Sep 2000  
Last Updated on STN: 8 Jan 2002

L3 ANSWER 27 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2000:309579 BIOSIS  
DN PREV200000309579  
TI No evidence for cholinergic problems in apolipoprotein E knockout and  
apolipoprotein E4 transgenic mice.  
AU Bronfman, F. C.; Tesseur, I.; Hofker, M. H.; Havekens, L. M.; Van Leuven,  
F. [Reprint author]  
CS Experimental Genetics Group, Center for Human Genetics, Flemish Institute  
for Biotechnology, K. U. Leuven, Campus Gasthuisberg, B-3000, Leuven,  
Belgium  
SO Neuroscience, (16 May, 2000) Vol. 97, No. 3, pp. 411-417. print.  
CODEN: NRSCDN. ISSN: 0306-4522.  
DT Article  
LA English  
ED Entered STN: 19 Jul 2000  
Last Updated on STN: 7 Jan 2002

L3 ANSWER 28 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1996:299739 BIOSIS  
DN PREV199699022095  
TI \*\*\*High\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
status in Alzheimer's disease tissue from rapid autopsy.  
AU Bissette, G.; Seidler, F. J.; Nemeroff, C. B.; Slotkin, T. A. [Reprint  
author]  
CS Duke Univ. Med. Cent., Durham, NC 27710, USA  
SO Wurtman, Richard J. [Editor]; Corkin, Suzanne [Editor]; Crowdon, John H.  
[Editor]; Nitsch, Roger M. [Editor]. Ann. N. Y. Acad. Sci., (1996) pp.  
197-204. Annals of the New York Academy of Sciences; The neurobiology of  
Alzheimer's disease.  
Publisher: New York Academy of Sciences, 2 East 63rd Street, New York, New  
York 10021, USA. Series: Annals of the New York Academy of Sciences.  
Meeting Info.: Eighth Meeting of the International Study Group on the  
Pharmacology of Memory Disorders Associated with Aging. Zurich,  
Switzerland. February 17-19, 1995.  
CODEN: ANYAA9. ISSN: 0077-8923. ISBN: 0-89766-974-6 (paper), 0-89766-973-8  
(cloth).  
DT Book  
Conference; (Meeting)  
Book; (Book Chapter)  
Conference; (Meeting Paper)

ED Entered STN: 2 Jul 1996  
Last Updated on STN: 2 Jul 1996

L3 ANSWER 29 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1994:473136 BIOSIS  
DN PREV199497486136  
TI Cloning and sequencing of a putative \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* cDNA from \*\*\*human\*\*\* brain.  
AU Barnwell, L. F. S.; Gresham, A. M.; Chaudhuri, G.; Townsel, J. G.  
CS Div. Biomedical Sci., Physiol. Dep., Meharry Med. Coll., Nashville, TN  
37208, USA  
SO Society for Neuroscience Abstracts, (1994) Vol. 20, No. 1-2, pp. 533.  
Meeting Info.: 24th Annual Meeting of the Society for Neuroscience. Miami  
Beach, Florida, USA. November 13-18, 1994.  
ISSN: 0190-5295.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
Conference; (Meeting Poster)  
LA English  
ED Entered STN: 31 Oct 1994  
Last Updated on STN: 1 Nov 1994

L3 ANSWER 30 OF 111 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 1993:392990 BIOSIS  
DN PREV199396068290  
TI Pharmacokinetics of two partial benzodiazepine receptor agonistic  
beta-carboline derivatives in healthy volunteers.  
AU Krause, W. [Reprint author]; Dorow, R.  
CS Postfach 65 03 11, W-1000 Berlin 65, Germany  
SO Arzneimittel-Forschung, (1993) Vol. 43, No. 5, pp. 511-515.  
CODEN: ARZNAD. ISSN: 0004-4172.  
DT Article  
LA English  
ED Entered STN: 23 Aug 1993  
Last Updated on STN: 28 Sep 1993

L3 ANSWER 31 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2003-28812 BIOTECHDS  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in a  
cell of a patient suffering from Alzheimer's disease;  
recombinant protein, encoding gene, and monoclonal antibody for use in  
Parkinson disease, Huntington chorea, Alzheimer disease,  
schizophrenia, dysautonomia, myasthenia gravis diagnosis, therapy,  
gene therapy and drug screening  
AU BLAKELY R D; APPARSUNDARAM S; FERGUSON S  
PA BLAKELY R D; APPARSUNDARAM S; FERGUSON S  
PI US 2003114399 19 Jun 2003  
AI US 2001-911077 23 Jul 2001  
PRAI US 2001-911077 23 Jul 2001; US 2001-911077 23 Jul 2001  
DT Patent  
LA English  
OS WPI: 2003-810914 [76]

L3 ANSWER 32 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2003-08295 BIOTECHDS  
TI New transporter array with a non-conserved region of a transporter  
polynucleotide, useful for identifying therapeutic, prophylactic or toxic  
agents in diseases with alteration in the expression profile of  
transporter polypeptides;  
DNA array, RNA array, peptide nucleic acid array, locked nucleic acid  
array, cDNA array, application in drug screening, diagnosis, gene  
therapy, prophylaxis and nucleic acid vaccine  
AU JENSEN J B; MADSEN L S; GETHER U; JENSEN B S  
PA AZIGN BIOSCIENCE AS  
PI WO 2002095064 28 Nov 2002  
AI WO 2002-DK336 21 May 2002  
PRAI DK 2001-803 18 May 2001; DK 2001-803 18 May 2001  
DT Patent  
LA English  
OS WPI: 2003-129438 [12]

L3 ANSWER 33 OF 111 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN  
AN 2001-08236 BIOTECHDS

\*\*\*choline\*\*\*      \*\*\*transporters\*\*\* , useful in diagnosis of  
Alzheimer's disease and screening promoters as drugs for treating  
Alzheimer's disease;  
recombinant protein production via plasmid expression in host cell for  
gene therapy

AU Haga T; Okuda T  
PA Japan-Sci.Technol.  
LO Saitama, Japan.  
PI WO 2001016315 8 Mar 2001  
AI WO 2000-JP5545 18 Aug 2000  
PRAI JP 1999-368991 27 Dec 1999; JP 1999-240642 27 Aug 1999  
DT Patent  
LA Japanese  
OS WPI: 2001-226688 [23]

L3 ANSWER 34 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:361532 CAPLUS  
DN 140:352129  
TI Organic cation transporters  
AU Koepsell, H.; Schmitt, B. M.; Gorboulev, V.  
CS Institut fuer Anatomie und Zellbiologie, Bayerischen Julius-Maximilians-  
Universitaet, Wuerzburg, 97070, Germany  
SO Reviews of Physiology, Biochemistry and Pharmacology (2004), Volume Date  
2003, 150, 36-90  
CODEN: RPBEA5; ISSN: 0303-4240  
PB Springer-Verlag  
DT Journal; General Review  
LA English  
RE.CNT 313 THERE ARE 313 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 35 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:213088 CAPLUS  
TI Localization of cholinergic innervation in guinea pig heart by  
immunohistochemistry for \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporters\*\*\*  
AU Hoover, Donald B.; Ganote, Charles E.; Ferguson, Shawn M.; Blakely, Randy  
D.; Parsons, Rodney L.  
CS James H. Quillen College of Medicine, Department of Pharmacology, East  
Tennessee State University, Johnson City, TN, 37614, USA  
SO Cardiovascular Research (2004), 62(1), 112-121  
CODEN: CVREAU; ISSN: 0008-6363  
PB Elsevier Science B.V.  
DT Journal  
LA English  
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 36 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2004:194824 CAPLUS  
DN 140:319635  
TI An independent, non-neuronal cholinergic system in lymphocytes and its  
roles in regulation of immune function  
AU Fujii, Takeshi  
CS Dep. Pharmacol, Kyoritsu Coll. Pharmacy, Tokyo, 105-8512, Japan  
SO Nippon Yakurigaku Zasshi (2004), 123(3), 179-188  
CODEN: NYKZAU; ISSN: 0015-5691  
PB Nippon Yakuri Gakkai  
DT Journal; General Review  
LA Japanese

L3 ANSWER 37 OF 111 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 2001:635466 CAPLUS  
DN 135:206448  
TI Identification of a gene encoding a \*\*\*human\*\*\* salt-dependent  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* 1  
sequence homology  
IN Bruess, Michael; Boenisch, Heinz  
PA Germany  
SO Ger. Offen., 12 pp.  
CODEN: GWXXBX  
DT Patent  
LA German  
FAN.CNT 1  
PATENT NO.                      KIND      DATE                      APPLICATION NO.      DATE

PI DE 10009055 A1 20010830 DE 2000-10009055 20000228  
PRAI DE 2000-10009055 20000228

L3 ANSWER 38 OF 111 DISSABS COPYRIGHT (C) 2004 ProQuest Information and  
Learning Company; All Rights Reserved on STN  
AN 93:38034 DISSABS Order Number: AAR9318723  
TI ISOLATION AND CHARACTERIZATION OF A SODIUM- AND CHLORIDE-DEPENDENT GABA  
TRANSPORTER CDNA FROM TORPEDO CALIFORNICA (SODIUM DEPENDENT)  
AU SWANSON, GEOFFREY TODD [PH.D.]; CHO, ARTHUR K. [advisor]  
CS UNIVERSITY OF CALIFORNIA, LOS ANGELES (0031)  
SO Dissertation Abstracts International, (1993) Vol. 54, No. 3B, p. 1245.  
Order No.: AAR9318723. 159 pages.  
DT Dissertation  
FS DAI  
LA English  
ED Entered STN: 19930817  
Last Updated on STN: 19930817

L3 ANSWER 39 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50662 peptide DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC C-terminal peptide of \*\*\*human\*\*\* , mouse and rat CHT.

L3 ANSWER 40 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50647 protein DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
(CHT) associated protein sequence #1.

L3 ANSWER 41 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
AN ADD50643 protein DGENE  
TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
\*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
polypeptide, useful in gene therapy to increase cholinergic function in  
a cell of a patient suffering from Alzheimer's disease.  
IN Blakely R D; Apparsundaram S; Ferguson S  
PA (BLAK-I) BLAKELY R D.  
(APPA-I) APPARSUNDARAM S.  
(FERG-I) FERGUSON S.  
PI US 2003114399 A1 20030619 74p  
AI US 2001-911077 20010723  
PRAI US 2001-911077 20010723  
DT Patent  
LA English  
OS 2003-810914 [76]  
CR N-PSDB: ADD50642  
DESC Rat \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* (rCHT).



AN ADD50648 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated protein sequence #2.

L3 ANSWER 43 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50639 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50638  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (hCHT).

L3 ANSWER 44 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50649 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated protein sequence #3.

L3 ANSWER 45 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50645 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC C. elegans CHOI protein.

AN ADD50661 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50660  
 DESC Mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #2.

L3 ANSWER 47 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50641 protein DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR N-PSDB: ADD50640  
 DESC Mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #1.

L3 ANSWER 48 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABU08980 Protein DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR N-PSDB: ABX94339  
 DESC \*\*\*Human\*\*\* choline acetyltransferase.

L3 ANSWER 49 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABU08979 Protein DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR N-PSDB: ABX94338  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*, HACT.

L3 ANSWER 50 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81713  
 DESC Mouse \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 51 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74665 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81712  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 52 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74664 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81711  
 DESC Rat \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 53 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAB74663 Protein DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR N-PSDB: AAF81710  
 DESC C. elegans \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein.

L3 ANSWER 54 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI Identifying genes having altered expression level in presence of non-conventional transmissible agent, e.g. prion, useful for diagnosis and drug screening.  
 IN Mouthon F; Nouvel V; Deslys J P  
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.  
 PI FR 2839081 A1 20031031 100p  
 AI FR 2002-5392 20020429  
 PRAI FR 2002-5392 20020429  
 DT Patent  
 LA French  
 OS 2004-045747 [05]  
 DESC NaCl dependent \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* PCR primer, SEQ ID 125.

L3 ANSWER 55 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADF08397 DNA DGENE  
 TI Identifying genes having altered expression level in presence of non-conventional transmissible agent, e.g. prion, useful for diagnosis and drug screening.  
 IN Mouthon F; Nouvel V; Deslys J P  
 PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.  
 PI FR 2839081 A1 20031031 100p  
 AI FR 2002-5392 20020429  
 PRAI FR 2002-5392 20020429  
 DT Patent  
 LA French  
 OS 2004-045747 [05]  
 DESC NaCl dependent \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* PCR primer, SEQ ID 126.

L3 ANSWER 56 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50653 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #2 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) cDNA.

L3 ANSWER 57 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50650 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC BAC sequence #1 containing hCHT DNA.

L3 ANSWER 58 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50664 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.

(FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #2 for mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) cDNA.

L3 ANSWER 59 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50660 cDNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR P-PSDB: ADD50661  
 DESC cDNA encoding mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #2.

L3 ANSWER 60 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50646 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated DNA sequence #2.

L3 ANSWER 61 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50652 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #1 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) cDNA.

L3 ANSWER 62 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50651 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S

(APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC BAC sequence #2 containing hCHT DNA.

L3 ANSWER 63 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50644 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 (CHT) associated DNA sequence #1.

L3 ANSWER 64 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50657 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*Human\*\*\* chromosome 2 marker D2S340.

L3 ANSWER 65 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50663 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.  
 PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #1 for mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) cDNA.

L3 ANSWER 66 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50638 cDNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR P-PSDB: ADD50639  
 DESC cDNA encoding \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT).

L3 ANSWER 67 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50658 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC \*\*\*Human\*\*\* chromosome 2 marker D2S176.

L3 ANSWER 68 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50656 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC BAC sequence containing hCHT gene.

L3 ANSWER 69 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50655 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p  
 AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 DESC PCR primer #2 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) gene.

L3 ANSWER 70 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50642 cDNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.  
 IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

AI US 2001-911077 20010723  
 PRAI US 2001-911077 20010723  
 DT Patent  
 LA English  
 OS 2003-810914 [76]  
 CR P-PSDB: ADD50643  
 DESC cDNA encoding rat \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (rCHT).

L3 ANSWER 71 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50640 cDNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.

IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p

AI US 2001-911077 20010723

PRAI US 2001-911077 20010723

DT Patent

LA English

OS 2003-810914 [76]

CR P-PSDB: ADD50641

DESC cDNA encoding mouse \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* (mCHT) #1.

L3 ANSWER 72 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50654 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.

IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p

AI US 2001-911077 20010723

PRAI US 2001-911077 20010723

DT Patent

LA English

OS 2003-810914 [76]

DESC PCR primer #1 for \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (hCHT) gene.

L3 ANSWER 73 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ADD50659 DNA DGENE  
 TI Novel isolated polynucleotide encoding \*\*\*human\*\*\* or mouse  
 \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 polypeptide, useful in gene therapy to increase cholinergic function in  
 a cell of a patient suffering from Alzheimer's disease.

IN Blakely R D; Apparsundaram S; Ferguson S  
 PA (BLAK-I) BLAKELY R D.  
 (APPA-I) APPARSUNDARAM S.  
 (FERG-I) FERGUSON S.

PI US 2003114399 A1 20030619 74p

AI US 2001-911077 20010723

PRAI US 2001-911077 20010723

DT Patent

LA English

OS 2003-810914 [76]

DESC \*\*\*Human\*\*\* chromosome 2 marker D2S1893.

L3 ANSWER 74 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94341 DNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -

IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.

PI US 6500643 B1 20021231 20p



PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* , HACT, PCR primer #2.

L3 ANSWER 75 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94340 DNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* , HACT, PCR primer #1.

L3 ANSWER 76 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94339 cDNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR P-PSDB: ABU08980  
 DESC \*\*\*Human\*\*\* cDNA encoding choline acetyltransferase.

L3 ANSWER 77 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN ABX94338 cDNA DGENE  
 TI Novel isolated polynucleotide (I) that encodes \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\* protein, useful  
 for preventing, treating or ameliorating neurological and cognitive  
 disorders such as Alzheimer's or Parkinson's disease -  
 IN Wu D; Gu Y; Millard W J; He Y  
 PA (UYFL) UNIV FLORIDA.  
 PI US 6500643 B1 20021231 20p  
 AI US 2000-657252 20000907  
 PRAI US 2000-657252 20000907  
 DT Patent  
 LA English  
 OS 2003-361535 [34]  
 CR P-PSDB: ABU08979  
 DESC \*\*\*Human\*\*\* cDNA encoding \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* , HACT.

L3 ANSWER 78 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81713 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74666

\*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 79 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81712 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74665  
 DESC \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 80 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81711 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74664  
 DESC Rat \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 81 OF 111 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN AAF81710 cDNA DGENE  
 TI New rat and \*\*\*human\*\*\* spinal cord \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporters\*\*\* , useful in diagnosis of  
 Alzheimer's disease and screening promoters as drugs for treating  
 Alzheimer's disease -  
 IN Haga T; Okuda T  
 PA (NISC-N) JAPAN SCI & TECHNOLOGY CORP.  
 PI WO 2001016315 A1 20010308 90p  
 AI WO 2000-JP5545 20000818  
 PRAI JP 1999-240642 19990827  
 JP 1999-368991 19991227  
 DT Patent  
 LA Japanese  
 OS 2001-226688 [23]  
 CR P-PSDB: AAB74663  
 DESC C. elegans \*\*\*high\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* protein encoding cDNA.

L3 ANSWER 82 OF 111 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS  
 RESERVED. on STN  
 AN 96156006 EMBASE  
 DN 1996156006  
 TI \*\*\*High\*\*\* \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 status in Alzheimer's disease tissue from rapid autopsy.  
 AU Bisette G.; Seidler F.J.; Nemeroff C.B.; Slotkin T.A.  
 CS Duke University Medical Center, Durham, NC 27710, United States  
 SO Annals of the New York Academy of Sciences, (1996) 777/- (197-204).  
 ISSN: 0077-8923 CODEN: ANYAA  
 CY United States  
 DT Journal; Conference Article  
 FS 005 General Pathology and Pathological Anatomy  
 008 Neurology and Neurosurgery  
 LA English  
 SL English

LOCUS (LOC): BX294147 GenBank (R)  
GenBank ACC. NO. (GBN): BX294147 BX119912  
GenBank VERSION (VER): BX294147.1 GI:32445670  
CAS REGISTRY NO. (RN): 543672-06-6  
SEQUENCE LENGTH (SQL): 314450  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Bacteria  
DATE (DATE): 11 Jul 2003  
DEFINITION (DEF): *Pirellula* sp. strain 1 complete genome; segment 15/24.  
KEYWORDS (ST): complete genome  
SOURCE: *Pirellula* sp.  
ORGANISM (ORGN): *Pirellula* sp.  
Bacteria; Planctomycetes; Planctomycetacia;  
Planctomycetales; Planctomycetaceae; *Pirellula*  
NUCLEIC ACID COUNT (NA): 72076 a 92563 c 83065 g 66746 t  
COMMENT:

This project was carried out by  
\*Max Planck Institute for Molecular Genetics, Berlin, Germany; \*Max  
Planck Institute for Marine Microbiology, Bremen, Germany; in the  
framework of the REGX-project, <http://www.regx.de> -----  
Genome Center  
Center: Max Planck Institute for Molecular Genetics  
Center code: MPIMG

----- Summary Statistics  
Sequencing vector: pUC19; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 7142841 bases at least Q40  
Consensus quality: 7145138 bases at least Q30  
Consensus quality: 7145484 bases at least Q20  
Quality coverage: 8.03

-----  
This sequence was finished as follows unless otherwise noted: all  
regions were double stranded, sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid Sequence; assembly was additionally confirmed by long range pcr and cosmid end sequences.

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See <http://www.micro-genomes.mpg.de/pirellula/> for more information including minimal tiling path from a set of 220 cosmids out of 908. See the misc feature tag below for the boundaries of the MTP cosmids.

----- Annotation  
Center: Max Planck Institute for Marine Microbiology  
Celsiusstrasse 1, D-28359 Bremen, Germany.  
Center Code: MPIMM  
Email: [fog@mpi-bremen.de](mailto:fog@mpi-bremen.de)  
Phone: +49 (0)421 2028 938 Fax: +49 (0)421 2028 580

-----  
Three different programs (Glimmer, Critica and Orpheus) were used for ORF-prediction. A nonredundant list of ORFs was generated by suitable parsing of the results.  
Automated annotation was done with the software package Pedant Pro (<http://www.biomax.de>). All ORF predictions and annotations were manually corrected by considering all results of the different tools applied. See <http://www.regx.de> for more information and access to supplementary information.

-----  
REFERENCE: 1 (bases 1 to 314450)  
AUTHOR (AU): Gloeckner, F.O.; Kube, M.; Bauer, M.; Teeling, H.; Lombardot, T.; Ludwig, W.; Gade, D.; Beck, A.; Borzym, K.; Heitmann, K.; Rabus, R.; Schlesner, H.; Amann, R.; Reinhardt, R.  
TITLE (TI): Complete genome sequence of the marine planctomycete *Pirellula* sp. strain 1  
JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 100 (14), 8298-8303 (2003)  
OTHER SOURCE (OS): CA 139:96134  
REFERENCE: 2 (bases 1 to 314450)  
AUTHOR (AU): Kube, M.; Borzym, K.; Heitmann, K.; Klages, S.; Marquardt, I.; Lehrack, S.; Beck, A.; Pawlik, R.; Reinhardt, R.; Gloeckner, F.O.; Bauer, M.; Teeling, H.;

TITLE (TI): Schlesner, H.; Amann, R.  
 JOURNAL (SO): Direct Submission  
 Submitted (21-JAN-2003) Max Planck Institute for  
 Molecular Genetics, proScience Ihnestrasse 73, D-14195  
 Berlin, Germany Max Planck Institute for Marine  
 Microbiology Celsiusstrasse 1, D-28359 Bremen, Germany

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..314450	/organism="Pirellula sp." /mol-type="genomic DNA" /strain="1" /db-xref="taxon:117"
gene	complement(285..4451)	/gene="cycA" /locus-tag="RB7973"
CDS	complement(285..4451)	/gene="cycA" /locus-tag="RB7973" /function="electron transport and membrane-associated energy conservation" /note="PMID: 97428333 PMID: 2986626 PMID: 9281430 PMID: 11152119 best DB hits: BLAST: pir:A83363; probable cytochrome c precursor PA2266 [imported] -; E=5e-09 pir:E83075; probable cytochrome c PA4571 [imported] - Pseudomonas; E=7e-07 pir:CCTW5T; cytochrome c552 [validated] - Thermus aquaticus; E=9e-07 COG: PA2266; COG2010 Cytochrome c, mono- and diheme variants; E=5e-10 PFAM: PF00034; Cytochrome c; E=0.042" /codon-start=1 /transl-table=11 /product="probable cytochrome c precursor" /protein-id="CAD78402.1" /db-xref="GI:32445671" /translation="MNSLRRLMLLSVLVEVTV VRDTPAENVCTFRHSTLGCFCVCSQ FRWPAEQKLKLSKIRQLRKRTMPQRITTVLQWS LFFLCAGVIPGIAQRADAQDAFEF QSNDDVVAIYGNGLADRMQHPWVETFLQHQLKGL DVSFRNMSFSGDRVNQRPRNQGT NDTEYLKHVAPNVVFTFYGFNESAAGPEKAGEHR DELIKLVQRYTQVQKDDGKDLRFV LFSPIAYENTGDASLPDGAELNVNLAAYTEATRE AAEITGAKFVDLFSPTYQLFQSSS ERLTLNGVHLNEAGYKQLAGIISQALLGEKPSD AELQDLYEAIEDKNWHWHNRYPAT DGNDIWGSRSTLTFVDGQSNADV LKHELVM LDM TANRDKVIWAAADGRTLQADDSNV PPPVKVTSNIGGGSASSNAMKEGSVAYLSPEESL AKINVPEGYELNVFASEVQFPDLA NPVQMQVDAHGRLWVASWNTYPKWEPEGKEMNSL MILEDTDNDGKADV RKIFAHVHNP LGFEFWNGGVVVTSGPDLLFLKDTDGDDKADVRY PILQGLGTS DTHHAANNLVYGPDG GIYWQSGIFLVHNHETPWKQNLNIGASGMYRFDP LTFAITPHAGNSPNPHGTSFDYWG YCYASDGTGGRCYQVRPEGNGFKMHKLEKEFRP VAANAILSSEHFPEELQNDILICN TIGFLGVKQYKLDREGDVEEEAAAEKTLKEETGP VKITRNGGLITVDHPALKDAKITG FKLSVNGRQQMNLSEVEVISGGRNIAKTAKLAQS SEYNNGTFPVQRLVDGDKGNFAHT SQQNNPWMRGDFPSPVQISEFKVWNRKGFEDRFN NGKIEFFDGDDEVVAVDIKIVSAD QEEQHREFGEVWGTPGLELLNSDDRNFRPTDAV GEDGALYVSDWHNAIIGHMQHNIR DPNRDHAHGRI FRLTVKNRPLQKPVKIAQSQSIEA LLENLKHVPVNGVRHRTVELTKHD

gene	4473..4817	RNGVKNEALLNQLLES DVRHAVVA
CDS	4473..4817	AKTVRHFVENVDTKGGSEFAAPAELEFVKFDPK HLSGADRKTYELGATIIYQRESHCA TCHMTHGKGT PNVYPPLV GSPWVNGSEDRLIKMA LHGVWGKMTVAGKTYDPARGVPPM TAFRSLLKDDMAAVLTFVRNTWGN EASVVSPEA VSRVREETKGR TTFYKPEEILELH PLEKELMDES VTPETE VFSNEELEKELLAASPAK LAQVALAKGNFQRGKRLFHESSAA CFACHSP PAGTVRMGPDLEKATTKRSREELVDAL LRPSKLIDKDYAQVSVLTADGQIF TGIRVSENDD EIVLRNLAQPEPITISQYDVEDVI ESEVSLMPENLMRQMKNRREFNDL LKYIIEVRKK"
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		/locus-tag="RB7978"
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		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAD78403.1"
		/db-xref="GI:32445672"
		/translation="MRQPTNTLRRLNWGVKHRT TVWTSRGLSFQLGTLPRVFKPWLN LSCNGLVAFRVSGFLSIPYPAVPHNRSRSNAWPS AQGVSSLLPLTLVLRPIVGAKVSS GSEWMAVVGPFLL"
gene	4869..5462	/locus-tag="RB7980"
CDS	4869..5462	/locus-tag="RB7980"
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		/protein-id="CAD78404.1"
		/db-xref="GI:32445673"
		/translation="MDHLKNDLALNQIIESCNSI QTTVHKAQMLPVSRGETGPLRWRE SCDKKIAIAGDILQFQLTEMPQV TDEC DVVQLA LSRSYGP NLMFDQIVSTHIDGKPA RPTNHSMHRS LDFHNAIQSGSTV VIRYQVRVDR TADPSIVALDNIDVRWAFRSQSKR DAARKAHTASPGVSAPHVTGLVPAARAKASALTS SVV"
gene	complement(5520..6023)	/locus-tag="RB7983"
CDS	complement(5520..6023)	/locus-tag="RB7983"
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		/transl-table=11
		/product="hypothetical protein-transmembrane prediction"
		/protein-id="CAD78405.1"
		/db-xref="GI:32445674"
		/translation="MEYTMNFGTNDFGAKDFRRG VLVATATLLSVAFFGGEAFGQCRS RGGGPPSGSPTSFTSGSQY AQN P YGQNALVSSYP QNNLIASQYQQQLLASQRQIASSA YRNTQQQRLALMQSEADVQAYRLARAESKRAARA ERIAARLREQGRSE DAYTLASVNV DKSPPRR"
gene	6183..6290	/locus-tag="RB7984"
CDS	6183..6290	/locus-tag="RB7984"
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		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAD78406.1"
		/db-xref="GI:32445675"
		/translation="MSDVSPFGCSLTGGKWIRCP SPNLSVTLKSSCHEF"
gene	6280..7695	/gene="ansA"
CDS	6280..7695	/locus-tag="RB7985"
		/gene="ansA"
		/locus-tag="RB7985"
		/EC-number="3.5.1.1"
		/function="degradation of amino-acids of the aspartate-group"
		/note="PMID: 1391778 best DB hits: BLAST: swissprot:P30364; ASPG-LUPAN L-ASPARAGINASE"

swissprot:Q9ZSD6; ASPG-LUPLU  
 L-ASPARAGINASE (L-ASPARAGINE;  
 E=3e-62 swissprot:P50288;  
 ASPG-LUPAL L-ASPARAGINASE  
 (L-ASPARAGINE; E=5e-62 COG: ybiK;  
 COG1446 Asparaginase; E=2e-56  
 PFAM: PF02530; Porin subfamily;  
 E=0.047 PF01112; Asparaginase;  
 E=1.9e-57"  
 /codon-start=1  
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 /product="L-asparaginase"  
 /protein-id="CAD78407.1"  
 /db-xref="GI:32445676"  
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 TIQSKEPAMKTKWAIVIHGGAGSS  
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 TNEGRVEMDSSVMDGKTLACGAVAGVTRVKNPIS  
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gene  
CDS

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CDS

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CDS

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gb:AAG60049.1; AF314821-1
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gene product [Drosophila; E=5e-19  
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		CG8646 gene product [Drosophila;
		E=1e-22 COG: ydeN; COG3119
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gene 34792..36138  
CDS 34792..36138

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protein TrkA PA0016 [imported] -;  
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transport systems, NAD-binding  
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gene 35997..37454

CDS 35997..37454

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gene 37294..41439

CDS 37294..41439

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gene

CDS

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misc-feature 41689 416

gene complement(46428..47630)

CDS complement(46428..47630)

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 (AJ003195) membrane spanning  
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 pir:S76812; hypothetical protein -  
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gene	49110..49499	DISDVSIEQGPQIRMFKVGSISIIISTDKSDPKLE
CDS	49110..49499	LVGINNVGEVAGLIDDIRRAERRR RSIHIEQN"
		/locus-tag="RB8054"
		/locus-tag="RB8054"
		/note="PMID: 2509712 best DB hits:
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		PROTEIN XLCOF26; E=0.84"
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		/transl-table=11
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		/db-xref="GI:32445709"
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		TASEVGGLFEAARRPSIEHYCPQCNVRVSQPPTI
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CDS	complement (49613..50851	/locus-tag="RB8055"
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		CGTQCGGACGSAGYGGGMACPTCDPYRYASVEAL
		FMRREGIDNFTVARDFALDDDFE
		WAPRITVGVVPDCVNGFEVGTGVLDWESDVSA
		AVDGLSTLLIEDPLQPGLTGTGF
		DAADEADAQRQIYESRFWSVEMNRTMMAWDVAKL
		LIGGRYIDFEEDFNYSTVNGANTG
		LLRNNAANRMIGLQVGADIYNPMGRFSSSYVRAR
		AGGFLNIAESSVLVRNETDILANG
		SEESTELSGMFEFGTGVRVQVGELMAVRGGFEAW
		YLTGVATSEEQISSATVTPTFGRS
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CDS	complement (50931..52712	/locus-tag="RB8056"
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		APTGVASTVAGKTVSSNVNLIQTQ
		GDAVSGGTTVLYPIRQTSQTMSEIKLSIGTAV
		GLLPIGAPATQQTPLVVEPARTPL
		PRINPHAQPDYDRAESNGIVELTPAQVSTNVEAK
		QSISMDFEVDQTEVQWQPKIASE
		PAPVVEQNVVAEEDIVLAPAVQEPVSPQPAEVEV
		EAVDVAPIETPVVANAIEVSEPIEF
		SLNDATDSLSDADDSISLSFSDSDEPGENLVAD
		LVSMPPEPMKIAVPTKIAPPVEQPT
		DESTLPRLPKPVQIKTPSEMMVQQQRHLPVKIDS
		PTQLERADSERMQNAPVRHRAAVA
		VEAPPMVAVAKRTASVSSESRSVAARIVPAALAS
		HRGEFHRSPATEAERSLRIEDTI
		QCDANDVTSLTVDGVIEAVRVEDDSIARVIGSTS
		RHLRLIGVRPGKTRVLVQQKLAGD
		AESIREIYELHITSPSNVRGGESQQEQSLMELIE
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gene	52654..53058	/locus-tag="RB8059"

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EIIHRTSEHPLYRRRVVPALTILPDRTFGSAGSV
LTQIRLGPATPTPLSGNAQPPARR
YVFTTTRLFQPRRCFTNSIARRSTARRQCHKAN"
gene complement(53080..53925) /gene="spoU"
)

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CDS complement(53080..53925) /locus-tag="RB8060"
) /gene="spoU"

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/function="rRNA processing"
/note="PMID: 7590303 PMID: 2987648
best DB hits: BLAST:
gb:AAF73591.1; (AE002337) spoU
rRNA methylase family protein;
E=2e-27 pir:C72066; rRNA methylase
- Chlamydomophila pneumoniae
(strain; E=5e-27 pir:A75448; rRNA
methylase - Deinococcus
radiodurans (strain R1); E=2e-26
COG: CPn0530; COG0566 rRNA
methylases; E=5e-28 PFAM: PF00588;
SpoU rRNA Methylase family;
E=4.7e-24"

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family protein"
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ARQHAIDSGVHRWVTSEVERKIAAY
TASTDRCVAEFVAPDDSLEQLLERSSSWNDGLILV
LDRVEKPGNLGAVFRSADAAGVSA
VLLSDCPSDRFNPNAIRGSLGAVFTVPSASGSES
QMEAFCLKTHGYRVAAMRVEGSRPL
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PMAGHVDSLNVSVSAAIVAFEAVR QRSNG"

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gene 53897..55168 /locus-tag="RB8061"
CDS 53897..55168 /locus-tag="RB8061"

/note="PMID: 97426617 best DB
hits: BLAST: pir:C65084;
hypothetical protein b2981 -
Escherichia coli (strain; E=9e-35"
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protein"
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/translation="MVSMGQHFCTFASMGEPTRV
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RRGDRVVGRVLAVVNHAHNRYHDETRGFFGFEEC
EDDEEAAIELLDTAGDWLQKRGMT
CVRGPVHPSLNYEVGLLVDGFDTPPTFLIPYNHP
YYERLIQAAGFEKSQDLYSYEASI
DILETLDPKLLFVIEESTRRFNAVCRSIDPKNFN
ADVRFVFLDIYNQSLQRTWGYVPMS
EAEVDDQSNGLKNLLLPKLTSLAEIDGKPVGAGF
GLLDYNPLIKKINGKLLPFGWLKL
LMGRKKLKRRLVLSANVLPYQKWGLGLVTLYKI
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CDS

55165..57267

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repair; DNA synthesis and
replication"
/note="PMID: 92332449 best DB
hits: BLAST: pir:E82133;
ATP-dependent helicase, DinG
family VC1990 [imported] -;
E=4e-87 swissprot:P76257;
YOOA-ECOLI PROBABLE ATP-DEPENDENT
HELICASE YOOA; E=2e-84
gb:AAG56797.1; AE005403-8
(AE005403) putative enzyme
[Escherichia; E=5e-84 COG: VC1990;
COG1199 Rad3-related DNA
helicases; E=4e-88 PFAM: PF00270;
DEAD/DEAH box helicase; E=0.00011
PF00271; Helicase conserved
C-terminal; E=0.5"
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DRPKRVLISTHTISLQEQLIKDIPLNSVIPRE
FSAVLVKGRNNYLSLRMRGRAVEK
SVSLMANDFQMQQLREIRKWSDNTPDGSLSLTP
KPDGQVWDEVRSDTGNCLRNKCPN
FKDCFYFQARRRAQNAQLLIVNHAMLF
TDIAMRR
QGVSLLPDYDAIILDECHTIESVA
SDHLGIRLTSGQFDYLFDRLYNDRQQKGLLV
AHN
LDALQKMVDRCRFAASEMFAGVLD
WMQESRSRNGRVHHPEVVPNPLSEPMEILARR
LR
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LAGGLREWLDQSLKQESVYVWVETSGSRRGM
DRVS
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VIMTSATLATGEQDKFKFFRSRVGLTTGRSL
QVG
SPFDYEQAKLIIIVRGLPDPSAKR
DEFEAALPQQIKRFVGHDTGHAFVLFTSYSL
LRK
CAEAITPWCIERDLHLYSQAGDON
RTQLLDSFRKDPRGVLLGTDSEFWQGVDPGD
ALT
NVVITKLPFSVPDHPLEARLETI
RARGGHPFPDYQLPEAVIKFRQGFGRILIR
TRDDS
GMVVVLDPRIRSKPYGRLFLSALP
PLPCHDVGTVPQKTKKQ"
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complement(57222..57440 /locus-tag="RB8064"

CDS

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complement(57222..57440 /locus-tag="RB8064"

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gene

complement(57424..57540 /locus-tag="RB8065"

CDS

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complement(57424..57540 /locus-tag="RB8065"

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          /db-xref="GI:32445718"
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gene      complement(57645..57842 /locus-tag="RB8067"
CDS      )
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          /db-xref="GI:32445719"
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gene      57894..58541
CDS      57894..58541
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          /db-xref="GI:32445720"
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          RECESARLMVQHELSVTSGSRVNQ
          STKMDDTTFFKLNLEVQPADQGSYTFHVTSSLETL
          APGKDIARRTAIRKVDSAFKLSPG
          TSFVLTGLERSGRERAITQVLVVRQLQGFAEEQTV
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gene      58538..58717
CDS      58538..58717
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          /transl-table=11
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          /db-xref="GI:32445721"
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gene      58838..61033
CDS      58838..61033
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          PMID: 2497103 best DB hits: BLAST:
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          E=0.46 gb:AAF47569.1; (AE003472)
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          E=0.46"
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          RFQSVREQAAAADKVESLQKKVHAQASQRITAA
          KEAHAQNDLSTAVKLLAQVPENLL
          DDESRSIRQSSQVHLDQLKTLHGELQQALAEKSY
          SQVAGLLQQLLELQPDNQKYQQLS
          QQVGDKLLRRAEKLCAEQEYQTARNALNSLPTIC
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gene 61176..62276  
CDS 61176..62276

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GLSKSKAVWGIDVGASGINAIKMRVEKGS DQPIV  
EAAHRVELKNPTCRGGSKSASELI  
PEAITRLMEEIDVSDSKVYANLPACEGIARFCEL  
PPVKDKDAERLIETEVKTRIPIST  
EDLALITWVAPLQKGSTVGRPVVMAAATKLTVSR  
RVDLLGIGGLKLDGLVPSPIALAN  
FAAHEFSELLAPPADKS AKKSKTVEETSDESSE  
DESFSLTSSSKQPTLALIDAGASK  
TTMLLISPISIWFWSHESGGEDITAVVARRTKTT  
AEDAEQSKRNLASIKEPHEVDDDI  
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polyol and carboxylate catabolism"  
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hits: BLAST: ddbj: BAB05586.1;  
(AP001513) BH1867~unknown  
conserved protein; E=1e-23  
pir:B59296;  
alpha-L-arabinofuranosidase II  
[validated] -; E=6e-19  
embl: CAB89837.1; (AJ242516)  
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E=1e-1  
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ase II"  
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ESDDLTKLGGKRLVWKAPDEGPYS  
KEVWAPELHAIGDRYYVYFAASDGDNANHLYVL  
KSKTSDPLGEYTLHGPMATGDGED  
GQSPNVWAIDMTILQHNDNLF AIWSGWDQPGSDN  
QFLYIAPMSSPTKISGPRVLVCDN  
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repair"  
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hits: BLAST: embl: CAB93380.1;  
(AL357523) hypothetical protein  
[Streptomyces; E=1e-12  
swissprot: Q52673; YQGF-RHOCA  
HYPOTHETICAL 17.1 KDA PROTEIN  
-----; E=4e-12 swissprot: Q9ZDJ8;  
Y330-RICPR HYPOTHETICAL PROTEIN  
RP330 -----; E=2e-11 COG: RP330;  
COG0816 Predicted endonuclease  
involved in recombination;  
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gene 62454..62975  
CDS 62454..62975



gene	63046..64737	PTRLFDERFTTVAANAKIROGKTTTRKKTQORVDA
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		transmembrane prediction"
		/protein-id="CAD78456.1"
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		YIVLVGDTDPDYDTPRNQPHQIPTWMIPAPVTSRF
		GSTSTLPTDLPGDRDGDVSDAA
		IGRLPVRSAEQLASVIGRIEAYENSDDFGLWRRS
		FQLTGGVGGFGAMVDTAIESVTRG
		VITTVLPADAKPQIAYASPNHPFCPPGESFTDAV
		LNRYRTGARFWVYAGHGQIDRLEL
		LQTTAADGKPAAREHWSVESLLNNQNATQLERAP
		EGATIAVLLACFAGAYDAPGDCLA
		ERMVLAEGGPIAVIASSRLSMPYGNACMGLGLLQ
		SVYSSGPQNTGCDRIGDAMLHAAR
		SLQSKQQGKQSTMRVMVDTLASMI SPAGTDLKQE
		RLEHAALYQLLGDPTRLRLHPPQPL
		DLSEPSNQTDQOTDGVVARSLSVAVTSPIAGTL
		IVAVERPLTAITKTPTDSTSEHDA
		HGTTITEHQIEVSAGKRILQTLTLPLGESGPLII
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gene	64750..66261	/gene="arsA"
CDS	64750..66261	/locus-tag="RB8078"
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		/note="PMID: 7910580 PMID: 1572648
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		E=1e-56 embl:CAA36398.1; (X52150)
		arylsulphatase a [Homo sapiens];
		E=4e-55 gb:AAB03341.1; (U62317)
		arylsulfatase A [Homo sapiens];
		E=4e-55 COG: aslA; COG3119
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		enzymes; E=2e-31 PFAM: PF00884;
		Sulfatase; E=1.6e-47"
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		LGPQAKIGLAPAETTFAEVCKSAGYRTACHGKWH
		LGHHPKFLPTNQGFQFYGIPYSN
		DMWPLHPDTIRROQKDPNDPGNWPPLPIIESIAG
		QPPRIVNDNVQPADQEQMTVELTR
		RSVEFIKNQSSDKPFLLYLPHPMVHVPLYVSERF
		RGKSGAGLFGDVMMEVDWSVGEIL
		SAIESIDQOKNTLVIFTS DNGPWLSYGNHAGSAA
		PLREGKGTQWEGGVREPTLMWWPE
		TIPAGTTCETFCSTIDVLP TIVELTGGEAPERKI
		DGHSIVDLMLDVP GAKSPHESFVG
		YYGGGQLQ TIRNERFKLVFP HAYRTLGDREPGKD
		GMPDGYAMTKSGLELYDL DADVSE
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gene	complement (66230..66388	/locus-tag="RB8079"

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CDS      complement(66230..66388 /locus-tag="RB8079"
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gene     complement(66385..67146 /gene="hisA"
)

CDS      complement(66385..67146 /gene="hisA"
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histidine"
        /note="PMID: 2664449 best DB hits:
BLAST: swissprot:P74561;
HIS4-SYNY3; E=3e-56 pir:A83003;
phosphoribosylformimino-5-aminoimi
dazole carboxamide; E=5e-49
gb:AAF05093.1; AF150930-2
(AF150930) phosphoribosyl; E=2e-46
COG: slr0652; COG0106
Phosphoribosylformimino-5-aminoimi
dazole; E=3e-57 PA5141; COG0106
Phosphoribosylformimino-5-aminoimi
dazole carboxamide; E=5e-50
NMB0629; COG0106
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dazole; E=6e-44 PFAM: PF00977;
Histidine biosynthesis protein;
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ribotide isomerase"
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SLLNVGVTRLVVGSRALKDPDWFVEMCDKYPGKL
VAGIDARDGKVATQGWLETSDVSA
FEFATKLRSRTENIAAIVYTDIAKDGM MQPNFE
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gene     67116..68816
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repair, base excision repair and
nucleotide excision repair)"
        /note="best DB hits: BLAST:
pir:S75597; hypothetical protein
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(strain; E=6e-94 gb:AAG19190.1;
(AE005016) Vng0705c [Halobacterium
sp. NRC-1]; E=2e-91 pir:G82413;
conserved hypothetical protein
VCA0809 [imported] -; E=2e-83 COG:
slr1343; COG3046
Deoxyribodipyrimidine
photolyase-related proteins;
E=6e-95"
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protein-putative a
deoxyribodipyrimidine

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RHFREELIQRGFDVIYHELTGDRRKARESSFASV
LRKTLAHSVEKILVVAPGDYRVR
EQLKATAEQEDVPLEFLTDNHFYCSPDQFDDWAS
GRKSMVMEQFYRTMRKEHSILLDE
EGAPEGGQWNFDQDNRKTFGKGGPKVPPPTPSFK
PDSITQEVIAMVRDRFEDHPGKVD
QFDLPVCRDDALNSLDDFIEHRLPLFGTYQDAMW
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VVDAAVKAYKDGNAPLNCVEGFVRQILGWREYVR
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VLGLFAQLFGTHPLRFHHWHMAMY
ADAIDWVSLPNALGMSQYGDGGLMATKPYCATGK
YINRMSNHCKNCRYDPAKSTGEDA
CPFTTLYWDFLDRHKQQFQNNNRMTLQLKNIERK
DSSEWTAIRSRARKIRSGTIKLQQ "
gene      complement (68890..69006 /locus-tag="RB8084"
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CDS      complement (68890..69006 /locus-tag="RB8084"
)
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/transl-table=11
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/db-xref="GI:32445730"
/translation="MSRRLAASFSSPHKVVSERR
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gene      69030..70517 /locus-tag="RB8085"
CDS      69030..70517 /locus-tag="RB8085"
/locus-tag="RB8085"
/note="PMID: 11705915 best DB
hits: BLAST: gb:AAG31169.1;
(AF314961) unknown [Salmonella
typhimurium]; E=0.70 PFAM:
PF01011; PQQ enzyme repeat;
E=0.017"
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containing protein"
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IQCHDAQDGAVRWKHSLETDACDFEYSDGPYST
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DTGEEVWRRDLHGEFQVEPELFPSPGATPLLHGEH
LILSLGGANNDAGIIAIHVRDGKT
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CLDPANGEVDWEIPHRSRAPMSYN
SVSPLVWNDHVLMTGPGPGAVCLQILPDRSYEE
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gene      complement (70518..71285 /locus-tag="RB8089"
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CDS      complement (70518..71285 /locus-tag="RB8089"
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protein-signal peptide and
transmembrane prediction"

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gene

complement (71254..73476 )

CDS

complement (71254..73476 )

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QSTSLGSQAAGTGPIQFTLALNAPAPGQTFDMES  
ITLLGYSELSTTIEQTVRVNFTGT  
KIVNGTMSSVTLLSGEFEADELTPLVVTFGDEFH  
GLTSLTWSQGGTARAHQFDNITFS  
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QVV"

/locus-tag="RB8091"

/note="PMID: 20039618 best DB  
hits: BLAST: ddbj:BAA86452.1;  
(AB032964) KIAA1138 protein [Homo  
sapiens]; E=0.74"  
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TSAVQKAAKDRDANSPEETIGDWKPVSDRKPANP  
LGEPERHAKAVENLNRLTEALMAY  
KEDKGHYPPSAQAKAGIKTSLWRVLILPYLGHQD  
LFEKFIDLNPWNRSNPKELIEFIP  
DELVSPERFDSKTNWMLPAHRNYMFGDNRYPRDR  
NIEDGIENTLMLVEVNDDLAVEWT  
RPVDFEPADLGALKGSLGELRSGGTLVAWANGWP  
SYVANSVSTKQWTNAFTYESGDGQ  
RAGAIHKEPDALLAAHKPSRSETKVEAKVSGRVE  
ASKIVENTEVEAESWGENRLPVPP  
SPDLATSNQRIEQLFGEQLVRKQNTQAELSND  
FLKKSLVMSDDAAGAYALQNAID  
LAIDSGDFMLFQAVLDQHASTFEVDLYQVNRDGL  
LEFSRRNDVDEDTASQMAFVRRAL  
VAIQEGLERNDFEGVGRIASALPRVEEERRGFRR  
ANVRGGKRDASAEKLVRLQLTQLS  
SANKQYEQAAEKVAEYRKNPDDELASALGRFYC  
FLKGDWAMGLPLVINGTSEKLSRV  
AKRDLEGANDAEDFLAIGDMWELSEGLPAGIYR  
QGTRDRAGYWYEQSLEVMPESLDR  
LHVQARVKEWQSQDPGSPLATIRTINRQLGLAEN  
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gene

complement (73451..74641 )

CDS

complement (73451..74641 )

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protein-signal peptide and  
transmembrane prediction"  
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/db-xref="GI:32445734"

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FGLVDPHTTASHAFEIWNHGAGPL  
TIDVAETTCKCTVGSAQKGTLPAGEKTSVTLTWN  
TGQKSEQYEQAAARVITNDPTREVI  
DLTVSGVVRTELFVPAKGVFHS GDAGEVVESTLL  
IYSQQHDDIAVVGAESDLVGFDFWE  
SNVVPSSDSQPSLSEQQPTVINQVKLRCAQKPGR  
FQGEVKLHLLVNGESDVIEKSVEL  
TGRVHAPISFHS PMLHSRDGLDLGTLGNDQEHEF  
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DVSIEPTSRFGDYRLTIRIPKGIPSTIFNLDQKR

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CDS       complement(74638..74838 /locus-tag="RB8095"
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                                                /db-xref="GI:32445735"
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gene      complement(74851..76122 /locus-tag="RB8096"
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CDS       complement(74851..76122 /locus-tag="RB8096"
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PF00114; Pilin (bacterial
filament); E=0.86"
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protein-signal peptide and
transmembrane prediction"
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GQCGKADWQGVSGDGSSTTFGGTA
PETAVRAELIARYFLTNGYNTNYAASWHLVRGMV
KTEADPSTGELTTWSGGGFKGLGG
STGPMSVADLERSRISSSNVGFIGCAAPGDVDEA
ILGATLGFDTGTGVWGTALNQTEAV
EYIASGSLLTEAFNDGPAYWNATAGNLDLIGSNE
TLAQIGCERGEPTTAGCAAPTGP
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CDS       complement(76119..76334 /locus-tag="RB8098"
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KKKESVTLDKCLKLAGTSLSSCESN
ATKLTTSHFNTRSKPFGFRQLKSQERL"
misc-feature 76358 763 /note="cosmid pircos-d1d02/ cosmid
pircos-d3d05 joining point"
gene      76464..76715 /locus-tag="RB8100"
CDS       76464..76715 /locus-tag="RB8100"
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TFHNPYSFASHSHSCEGSFLDEFS
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CRFSR"

gene      76684..76875 /locus-tag="RB8101"
CDS       76684..76875 /locus-tag="RB8101"
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CDS      complement(76885..78048 /locus-tag="RB8102"
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                                           systems"
                                           /note="PMID: 1588814 PMID: 1309616
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                                           general secretion pathway protein
                                           G PA3101 [imported]; E=0.063
                                           gb:AAC83358.1; (AF092918) outer
                                           membrane secretion protein T;
                                           E=0.069 gb:AAC79845.1; (AF089753)
                                           cellulose-binding protein CbpC;
                                           E=0.24 COG: PA3101; COG2165
                                           General secretory pathway proteins
                                           G and H and; E=0.006 PFAM:
                                           PF02361; Cobalt transport protein;
                                           E=0.11 PF00114; Pilin (bacterial
                                           filament); E=0.011"
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                                           DLVRRGVLVSEMRICTSTSAQASSAIEHLLSDNEA
                                           DWATNDCVDQLGAEEYTNEMGTVI
                                           KNVARLIEASPADRVEYIERKMLEDGYNTNYAAS
                                           WFLVRSEVILDESGQPQPKDSACT
                                           NDLKSLNVTRGPLTTRLTAKAPSSSTVPLLCDA
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CDS      77942..78313
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CDS      78329..79276
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                                           EMTFDHSIESVAMTQQSGDADEVQWDSTTGEEPP
                                           KIFSVVASQIGTPLATVTINKQGG
                                           EVRREDHAGSKSSLGMGTALALPDKPVKIGESW
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                                           TLKKVKAGVATLSVKSETLTPIEEESLRAQVIQQ
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gene      complement(79324..82143 /locus-tag="RB8108"
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CDS      complement(79324..82143 /locus-tag="RB8108"
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CDS

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VTWWQVLLSKLLIGFAAWVLAVLASVCFALSWL
VLRGGWDWSAIGRISGESIFELM
VYGVGLLICGWIAALIVRNPVGSVMLVIPLIVGL
TLLWNYSVAGLVSTHFHYGVTFLE
ATAAQRVSMCLCLATVYLAALGGVVAGLARHRLAG
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LLSIWTDGNHGFHDLILLVLGWPA
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WGRRPSLAFFGAPVVALLWMLPAF
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LDAELKSSVEGHEVSQSELYGLCVDTPIAAKGY
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RRKALEVAAKWSKLSREQSFVFGALGELLNNAES
NEWIVINGLRQIAYEQNLFSDEAL
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SFLDAPLSEPFYRLEFEQTRFERILDVAVRNTLD
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/note="PMID: 1924314 PMID: 8088782
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probable ABC-type transport system
ATP-binding protein -; E=4e-37
pir:C72303; ABC transporter,
ATP-binding protein - Thermotoga;
E=6e-34 gb:AAF81232.1; (AF263012)
ABC transporter ATP binding
protein; E=9e-33 COG: TM1028;
COG1131 ABC-type multidrug
transport system, ATPase; E=5e-35
PFAM: PF00005; ABC transporter;
E=5e-43"
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protein"
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LESMVDRAAAGRTVLLSSHHINEVERVADMVAMI
HGGQVKLVQSMNDLKQHTRIVTAT
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CDS

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regulator GntR related protein  
ytrA -; E=4e-13 pir:D72336;  
transcription regulator, GntR  
family - Thermotoga; E=9e-13  
gb:AAC62421.1; (AF084104)  
hypothetical protein [Bacillus  
firmus]; E=1e-08 COG: BS-ytrA;  
COG1725 Predicted transcriptional  
regulators; E=4e-14 BH1940;  
COG1167 Transcriptional regulators  
containing a; E=3e-06 BH1164;  
COG1725 Predicted transcriptional  
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Bacterial regulatory proteins,  
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ILKPLRGRGMVRRDAIEACTSAR  
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RLSAAATKSNSDESNLESASSNN EPSHE"

gene  
CDS

83626..85503  
83626..85503

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/function="biogenesis of outer  
membrane"  
/note="best DB hits: BLAST:  
ddbj: BAB06996.1; (AP001518) spore  
cortex protein [Bacillus; E=0.022  
COG: BH3277; COG2244 Membrane  
protein involved in the export of  
O-antigen; E=0.002 PFAM: PF01943;  
Polysaccharide biosynthesis pro;  
E=0.05"  
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protein-putative membrane protein  
involved in the export of  
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TADSATQSTTPRSAFRVDSLAI GMIVMLAMTVLG  
RGIGFIRGMAFCRLMDDTDVGRWS  
MAFGFITLITPVMLLGIPGVLPFTEHFRLKRSL  
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LPDWFGWIVFLQPQDNRLIYGVAGAVVGMIVYNF  
ISDLNGSLRQVRMVSCMQFMQGVG  
FTLLSVAWLLTGGTFTGVVWMFAASCLVASLPGL  
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ADKTLPSDDVPFGLWNMIRRLAPYATALWLMNLI  
GNLFELSDRYMILHFIPATETLSA  
EIAGQAAVGQYHSGRIIPMLLLSLGTMIGGVMLP  
YLSADWEAKRFAAVQTRLRDALLA  
VSIVFTCGSAMAILLGPWIFNVLLQGRYTDGMTL  
MPMALCFCTWAALVTVGQNYLWTV



gene 85427..85855  
CDS 85427..85855

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RPKNGV"

gene 85827..86360  
CDS 85827..86360

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biosynthesis"  
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(AF197933) beta-hydroxyacyl-ACP;  
E=2e-14 gb:AAK04875.1; AE006311-6  
(AE006311); E=3e-14 pir:C82731;  
(3r)-hydroxymyristoyl ACP  
dehydrase XF1044 [imported] -;  
E=6e-14 COG: XF1044; COG0764  
3-hydroxymyristoyl/3-hydroxydecano  
yl-(acyl carrier; E=6e-15 PFAM:  
PF01377; Thioester dehydrase;  
E=2.1e-18 PF01575; MaoC like  
domain; E=0.0056"  
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CDS 86357..87190

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E=6e-31 ddbj: BAB06562.1;  
(AP001516) enoyl-[acyl-carrier  
protein]; E=5e-29 gb:AAD04184.1;  
(L10036) unknown [Nostoc sp. PCC  
7120]; E=2e-28 COG: BH2843;  
COG0623  
Enoyl-[acyl-carrier-protein]  
reductase (NADH); E=5e-30 TM0441;  
COG1028 Dehydrogenases with  
different specificities (related;  
E=1e-09 BS-yfhr; COG1028  
Dehydrogenases with different  
specificities; E=1e-06 PFAM:  
PF00678; Short chain  
dehydrogenase/redu; E=7.1e-05"

gene 87269..88126  
CDS 87269..88126

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DYSDGIRPFHETTRRQFLQAIDISAFSLVAVCNA  
IKDQLANDASVVTIGISTTRMASE  
SYGFMAPIKAALESSLAFLTKSFSRFSQVRFNAV  
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ILVE-METJA PUTATIVE BRANCHED-CHAIN  
AMINO ACID; E=4e-69 gb:AAB90305.1;  
(AE001039) branched-chain amino  
acid; E=4e-65 pir:F69057;  
branched-chain amino-acid  
aminotransferase -; E=2e-46 COG:  
MJ1008; COG0115 Branched-chain  
amino acid; E=4e-70 PFAM: PF01063;  
Aminotransferase class IV;  
E=1.9e-91"

gene 88191..88979  
CDS 88191..88979

/codon-start=1  
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amino acid aminotransferase"  
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NPFSCEDPQVIIIADTISLYPEKFYTEGLELITA  
STIRNHPAALSPRVKSLNYLNNIM  
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GGRLITPPIDAGILEGITRNTVID  
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AAFRARFVAR"  
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gene 88972..89505  
CDS 88972..89505

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FASSKSSNPFEPSSRDVGQYFHLIRTTTDGRGL  
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TRNAGPTNLFDDLQSPSSSGPKQARDRTPDQAVS  
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CDS	89477..90796	HLRVRGGIIPLMIGRPISSPIVDESRTCDNRQ
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		(AL023591) hypothetical protein
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		swissprot:Q50739; YP59-MYCTU
		HYPOTHETICAL 47.5 KDA PROTEIN
		RV2559C; E=2e-91 embl:CAB93386.1;
		(AL357523) conserved ATPGTP
		binding protein; E=2e-90 COG:
		Rv2559c; COG2256 Uncharacterized
		ATPase related to the helicase;
		E=2e-92 ycaJ; COG2256
		Uncharacterized ATPase related to
		the helicase subunit; E=4e-86
		HI1590; COG2256 Uncharacterized
		ATPase related to the helicase;
		E=1e-85 PFAM: PF01057; Parvovirus
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		PF00910; RNA helicase; E=0.0011
		PF00004; ATPase family associated
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		ELITLNAISSGVKDVREVLAKARD
		RVSAGDPRPLLFIIDEIHRFNKSQQDALLADVESG
		IISLIGATTSNPYFAVNAALISRS
		QLFGLEPVSVEDMRSLLKRAITDRECGLGNQNV
		IDEDAIDYLSSASDGDARKALTAL
		EVAVHSHENPKASITRDDVAESMTSRIAGYDATG
		DDHYDLASALIKSIRGSDVDASLY
		WLARMLEGGEDIRFLCRLVILASEDIGNADPQA
		LIIAVSAMQACEMIGLPEAQLTLS
		QTVAYLSLAPKSNATTSAISAARRDVRDRQVIPV
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		LQKIRDQLGRETE"
gene	complement(90882..91109	/locus-tag="RB8137"
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CDS	complement(90882..91109	/locus-tag="RB8137"
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		/transl-table=11
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		/db-xref="GI:32445754"
		/translation="MQFIELTGKSLLDVINEGEI
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		ELRDRHEWVLVGGLGNFEDRLRRITQLDWL"
gene	90960..91187	/locus-tag="RB8138"
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gene	complement(91189..92931	/locus-tag="RB8140"
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/ note="best DB hits: BLAST:
pir:T47011; hypothetical protein
[imported] - Yersinia pestis;
E=0.020 embl:CAB58305.1;
(AL121854) hypothetical protein
SCJ33.06c; E=0.11 pir:E69891;
cytochrome c biogenesis protein
CycX homolog homolog; E=0.28"
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/ transl-table=11
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protein"
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STPESPATSNNTNGEVAAQPVVDD
PAVIDVPQSVASQLDGRRKQLANDLKPEQLRTFL
SEADIEMRMITSGQSGIEDSATAF
SELKRIATWKREASRLIEHADATEKEKAIGRRG
ELQSLSHLASLGLDKAAESLQLLA
ESLQEDSDPEVRSDSQLVLIGFAIEDLRNGKSDA
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VMGQAKDALLQFEHVEEASVRAMILEEFVESGE
AIAGESDAMGGLVDMARQIAGPSF
QISEATARVQNLMEFITEANENTDPSDSAVSIN
DWKAAIESLADEQPDLLTTQFLAG
ASLEAETVGRLLDLSEATYQVLDDKFASMQDDRGS
EARTALQARDNREKIIGKTFDPDL
PSTKGDELSMDDYRGKVVLMPFWSAAFADSLLVV
DNLQKIAHQYPEKVAIVGMNLDVQ
STDVPAFESRNKISFPSFRSVSDPEASVANSVAY
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gene      complement(92961..93179 /locus-tag="RB8143"
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CDS      complement(92961..93179 /locus-tag="RB8143"
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/ translation="MQVRQGVCTEPVLRITRQS
VPDSIGGVYFERLPSRINGRDRKC
LCQISECRSSNPTRIERTVFELARWPVE"
gene      complement(93191..93622 /locus-tag="RB8144"
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CDS      complement(93191..93622 /locus-tag="RB8144"
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/ transl-table=11
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/ protein-id="CAD78489.1"
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TRRVMKIRSSWSVAERLRRRREADDRFADLLDAL
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gene      complement(93667..94122 /locus-tag="RB8146"
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CDS      complement(93667..94122 /locus-tag="RB8146"
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/ transl-table=11
/ product="hypothetical protein"
/ protein-id="CAD78490.1"
/ db-xref="GI:32445759"
/ translation="MLANTKCRVLDPFPTQLAIF
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tRNA	94716..94788	/product="tRNA-Glu" /note="Glu, tRNAscan-SE-score 56.70%" /evidence=not-experimental
gene	complement(95002..96339)	/locus-tag="RB8150"
CDS	complement(95002..96339)	/locus-tag="RB8150" /codon-start=1 /transl-table=11 /product="hypothetical protein-signal peptide and transmembrane prediction" /protein-id="CAD78492.1" /db-xref="GI:32445761" /translation="MVSLHSNGAAPS FHERCVFA VKSRVISGGLFCLVVMASASAQ PDFERPPIDYLNAEVNDPVAKLAKRIEAGEVALN SDPKFGYLPVLEALDVPLSSQTL VFSKTS LQLHRISPRRPRALYFNDDVYVGYCQHG DVLEFASTDAKQGAIFYTLSQSEE KEPEFVRDRGGCLSCHASSRTQNVPGFLIRSVFA DAAGRPKLGSGTFTT DHTSPFDER WGGWYVTGSHGSMRHMGNVICTDEAQELDRESGA NQDDLGEYFR TDSHLTPHSDIVAL MVLEHQ TQMHNAITAANFETRQALHQSYQMNE LL EREP DFISESATRRIESSADRVLK YLLMCDEFTLTDSVAGTSTFAKEFASMGPRDPEQ RSLRDFDLETRLFRYPCSYLIYSD SFMELPAEVKSRVLEKLKHILSGEDQSEAYQH LT GKMRSEILEILRATHPDFQ" /locus-tag="RB8152" /locus-tag="RB8152" /function="transcriptional control" /note="best DB hits: BLAST: pir: C75577; conserved hypothetical protein - Deinococcus radiodurans; E=1e-13 pir: E70324; conserved hypothetical protein aq-268 - Aquifex aeolicus; E=3e-07 swissprot: P44675; YFHP-HAEIN HYPOTHETICAL PROTEIN HI0379 -----;
gene	96496..96870	
CDS	96496..96870	

Predicted transcriptional  
 regulator; E=1e-14 PFAM: PF02082;  
 Uncharacterized protein family  
 UPF00; E=6.3e-10"  
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 protein-putative a transcriptional  
 regulator"  
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gene complement(96932..98392

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CDS complement(96932..98392

)

/note="PMID: 8168477 PMID:  
 10360571 best DB hits: BLAST:  
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 HYPOTHETICAL PROTEIN TM0929 ----;  
 E=1e-09 embl:CAA57668.1; (X82178)  
 orf1 [Thermotoga maritima]; E=0.34  
 gb:AAA65436.1; (U24145) orf1;  
 upstream of ferredoxin; Method:;  
 E=0.34"  
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 VLRFEAMRILLGHPYARRQPKTEL  
 SYSASNLTVQEC LRSKLPMPRPREV LGSETHDQ  
 YFEY YRQLAERE GDQPD SEDST  
 PEPDQSDDSKPGEGTSHPEETLGDDSSDAGDSGN  
 DAVAEQRDETGD ESSVEEDDGSSA  
 ESNEPTPDSPSLEQAADSSVGN DLESYVDPSQTG  
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 AENGWGWTLPGHAQERLLATLRPPLDYRSILRQF  
 RQSVLSVDRRLTRMRPSRRYGFAQ  
 MGSRYDFTTRLLFAVDVSGSM SHRDLQNGFSIIN  
 RFFQYGIRSIDVVWFDTQIRCEPL  
 TFRSARRDVSITGRGGTDLGCVTEFIDEHRGYDG  
 VVFTDGDSPHPKR PANRQTRILW  
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gene complement(98389..99483

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CDS complement(98389..99483

)

/note="PMID: 99287316 best DB  
 hits: BLAST: pir:B72315; conserved  
 hypothetical protein - Thermotoga  
 maritima; E=1e-25 pir:T35221;  
 probable ATPGTP binding protein -  
 Streptomyces; E=5e-15 pir:A75429;  
 conserved hypothetical protein -  
 Deinococcus radiodurans; E=1e-07  
 COG: TM0930; COG0714 MoxR-like  
 ATPases; E=1e-26"  
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gene	complement (99522..10022 3)	/locus-tag="RB8158"
CDS	complement (99522..10022 3)	/locus-tag="RB8158"  /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78496.1" /db-xref="GI:32445765" /translation="MKLPLPSVRKLFREHFSGES PIEIDPGQRAALIKQWRSKLEKIE GVRLTNHPGDRDSRSPTWVRFTIPDPNASQTYR SDELRLENEQGELECVFGKFDRE IAGPISDFGEVESLVAEVLRRYVKRHAGEAKRAK VRSMKSKAIVARVKALAKEEQFDF ATSMDTQKLRLFVKLSSQHMIEIHIPFTRFEKVL PQLQETIRTLRSLYEDGLRFBKMIG FMQADWRTEWIRYEE"
gene	complement (100220..1009 90)	/gene="exoA"  /locus-tag="RB8161" /note="synonym: apeX"
CDS	complement (100220..1009 90)	/gene="exoA"  /locus-tag="RB8161" /EC-number="3.1.11.2" /function="DNA repair (direct repair, base excision repair and nucleotide excision repair)" /note="PMID: 1708495 best DB hits: BLAST: swissprot:P37454; EXO-A-BACSU EXODEOXYRIBONUCLEASE ----- pir:; E=7e-78 pir:F64710; exodeoxyribonuclease - Helicobacter pylori (strain; E=3e-72 pir:C71809; exodeoxyribonuclease - Helicobacter pylori (strain J99); E=2e-71 COG: BS-exoA; COG0708 Exonuclease III; E=7e-79 PFAM: PF01181; Deoxyribonuclease I (DNase I); E=0.25 PF01260; AP endonuclease family 1; E=2e-108" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease" /protein-id="CAD78497.1" /db-xref="GI:32445766" /translation="MIETLKLISWNVNGIRASMD KGFREFVESEQPDVLCLOETKAEP EQVDLSWADELGYHQVWNTATKRGYSGVSTWSRV EPLKVTGKLSIEEHDNEGRVLT FDDFHLVNVYTPNSQRGLARLDYRMQWDEAFLDY VKKLNRKRPVLFCDVNCANKEID LANPKANRKNAGFSDQERAGLDAVTEAGFIDSFR QFHDGPGHYSWWTYRSDARARNIG WRLDYFWVAKNFWDRVADARIRCEIHGSDHCPVE LTLT"
gene	complement (100987..1016 85)	/locus-tag="RB8163"
CDS	complement (100987..1016 85)	/locus-tag="RB8163"  /note="best DB hits: BLAST: pir:F75496; conserved hypothetical protein - Deinococcus radiodurans;

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Vng0533h- [Halobacterium sp.
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GTALT KVSGKGSVFCADSGKKITI
LELQNEAICVNGNDLLAFEMSLN YNIKMMKKMTA
MLAGGLEFNIRLEGTGMVAITSHYD
PITLPVTPHQPVVTDPNATVLWSGQLEPQLKTDV
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CDS      complement(101702..1018 /locus-tag="RB8165"
63)
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SDVVLFLSP"
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CDS      101882..104650 /locus-tag="RB8167"
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pir:G71299; conserved hypothetical
protein TP0648 - syphilis; E=0.027
pir:S49376; hypothetical protein 3
- Pseudomonas aeruginosa ----;
E=0.11 pir:F69210; conserved
hypothetical protein MTH83 -
Methanobacterium; E=0.20 COG:
TP0648; COG0457
TPR-repeat-containing proteins;
E=0.003 PFAM: PF00515; TPR Domain;
E=0.0036"
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VFAASYDDAVQQFCNGQYDAAATT
AASEVERGVWSEWRPRL LIQCQLTQGDYADALQT
YREALQRYPTSIALRYMGLDVLRF
NGLHDEVGTAEADLFAQMORAFAGYITRDNLI AA
GRFLTGRGEDARKVLEMFYDRVRD
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LEEETPDLHLLAKAMESSDGQAA
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SHLRGEYDVEKLMRAAALSTWEQNPNDHLIGRK
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VVAYNLMTLRDR TAKFTVLKQDGI
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 QVAKQRKTTLAMHVAESPAERELL  
 TNGSGPFAESLRTLGLPIEAFFPWTKANPVSHLI  
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gene

complement (127391..1281  
88)

CDS

complement (127391..1281  
88)

/locus-tag="RB8209"

/note="best DB hits: PFAM:  
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 protease family; E=0.1"  
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 LNAWELFAISLCAGVGEELLFRGWLLPWLADGAA  
 SLAPDLEAPSRWWAYGGWLGSLPN  
 SVTEFAWP EEGLLAWWSRVGGWELTAAWLVSSFA  
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gene

complement (128198..1300  
78)

CDS

complement (128198..1300  
78)

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 BLAST: ddbj: BAB04170.1; (AP001508)  
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 transporter; E=5e-21  
 swissprot:P45861; YWJA-BACSU  
 HYPOTHETICAL ABC TRANSPORTER;  
 E=7e-21 ddbj: BAB04845.1;  
 (AP001511) ABC transporter  
 (ATP-binding protein); E=5e-20  
 COG: BH0451; COG2274 ABC-type  
 bacteriocin/lantibiotic exporters,  
 contain; E=5e-22 BS-ywjA; COG1132  
 ABC-type multidrug/protein/lipid  
 transport system,; E=6e-22  
 VCA1084; COG2274 ABC-type  
 bacteriocin/lantibiotic exporters,





		māritima; E=1e-14 pir:A70337; hypothetical protein aq-408 - Aquifex aeolicus -----; E=1e-08" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAD78522.1" /db-xref="GI:32445791" /translation="MSEIRLIEPVVRFCAVISRH QEARQWAKQRLAERWGEKGEKGEK SPFEAGGFYQPEMGDGLTKELIGIAEFADPAGLA DWKNVTNEWSEYASLSDHPEPRP LNLDPGYVSQAKLVLATIKDRDHRIYLRDGIFAE VTLNYVGGRWIIHRWSYPDYRTET VASFAANCRSRLRQHLKATGGFRVGVKKTPGVKP SPKV" /gene="aspC" /locus-tag="RB8219" /gene="aspC" /locus-tag="RB8219" /EC-number="2.6.1.1" /function="degradation of amino-acids of the aspartate-group; amino-acid degradation (catabolism)" /note="PMID: 8907187 PMID: 10029535 best DB hits: BLAST: ddbj:BAB07069.1; (AP001518) aspartate aminotransferase [Bacillus; E=2e-59 embl:CAC11669.1; (AL445064) probable aspartate aminotransferase; E=9e-55 pir:G69119; probable aspartate transaminase (EC 2.6.1.1) MTH1894; E=2e-54 COG: BH3350; COG0436 PLP-dependent aminotransferases; E=2e-60 PFAM: PF01041; DegT/DnrJ/EryC1/StrS family; E=1.5e-05 PF01053; Cys/Met metabolism PLP-depend; E=5.4e-05 PF00222; Aminotransferase class-II; E=0.28" /codon-start=1 /transl-table=11 /product="aspartate aminotransferase" /protein-id="CAD78523.1" /db-xref="GI:32445792" /translation="MPEVSSASNHRFQPSNRQR VNMHPWIADRTASFDSSGIRKVF LAAKLKDPINLSIGQPDFDVPEEIQDATVDAIRS GKNAYSPTQGIAPLREKLLAEINA KYPGQNRDVFVSSGTSGGLVLSLLSMINPGDEVI FLDPIYFVMYPALVSLCGGIPVTVD SYPDFRLDPAKIEAAITPKTKMILVNSPANPTGV TASEQDLRDVGDLAAKHNIALLSD EIYSRFFYDGDGFASPAATNPDTIVIDGFSKSHAM TGWRVGYVHGPPPEIIATMLKIQQY SFVCSPQPAQWGALRAMEISLDGHIDDYRRKRDF MVEQLSPHFELTSPGGAFYLFPA PGTEGGTAFVERAIADGLLIIPGKIFSSRDSHFR VSFAASDDTLRRGAERLIKLAGDN R" /locus-tag="RB8221" /locus-tag="RB8221" /EC-number="4.2.99.10" /function="assimilatory reduction of sulfur and biosynthesis of the serine family" /note="PMID: 7704274 best DB hits: BLAST: ddbj:BAB06322.1; (AP001516) O-acetylhomoserine sulfhydrylase; E=1e-123 pir:D72324; O-acetylhomoserine sulfhydrylase -
gene	132980..134161	
CDS	132980..134161	
gene	134234..135553	
CDS	134234..135553	

gene 135604..137475  
CDS 135604..137475

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pir:T40463; O-acetylhomoserine
(thiol)-lyase (EC 4.2.99.10) -;
E=1e-110 COG: BH2603; COG2873
O-acetylhomoserine sulfhydrylase;
E=1e-124 DR0921; COG0626
Cystathionine
beta-lyases/cystathionine; E=7e-63
PFAM: PF01053; Cys/Met metabolism
PLP-depend; E=6.3e-204"
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HSGQNIVSSTSLYGGTWTLFTQTLKNLGIEVRFF
DPDHPEQIHGLVDENTRLVYMESI
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TPYLLRPIDHGDIDIVIYSTTKFLG
GHGTHIGGCIVDSGNFKWADQPEKWPEFCGPSPS
YHGAVFEEHLRGMGNIAYNVHIRT
HWLRDTGAAMSPFAAFLFLOGIETLHLRMPRHCE
NAMKVAEFLEAHDAVEWVNYPGLK
THSHNKLAEQYLTNGKGAILGFGIKGMEAGKKF
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of sulfur and biosynthesis of the
serine family"
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BLAST: swissprot:P57714;
METX-PSEAE HOMOSERINE
O-ACETYLTRANSFERASE; E=1e-83
swissprot:P94891; METX-LEPME
HOMOSERINE O-ACETYLTRANSFERASE;
E=7e-78 swissprot:Q9JZQ5;
METX-NEIMB HOMOSERINE
O-ACETYLTRANSFERASE; E=1e-77 COG:
PA0390; COG2021 Homoserine
acetyltransferase; E=1e-84 PA0389;
COG0500 SAM-dependent
methyltransferases; E=2e-26
MTH1820; COG2021 Homoserine
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PF00561; alpha/beta hydrolase
fold; E=6.7e-07"
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WDGLIGPGLPIDTDRLFVVCNVLGGCRGSTGPG
DADPTSPDGKPYGANFPRITIGDI
VEAQKLLADHLGIRQWRVVGSLGGHQVLQWIN
RYPDAAKTCVAIATSPRLNSQALG
FDVIARNAIQTDPHYAGGQYYDKDQRPDTGLAIA
RMLGHITYLSVEAMEAKFDPDRHD
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EATCDFLLISFSSDWLFPPAQSRDIVNALTALDK

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CDS	complement (137527..138759)	/locus-tag="RB8223"
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gene	complement (138783..139097)	/locus-tag="RB8226"
CDS	complement (138783..139097)	/locus-tag="RB8226"
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gene	complement (139186..139365)	/locus-tag="RB8227"
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gene	complement (139412..140449)	/locus-tag="RB8228"
CDS	complement (139412..140449)	/locus-tag="RB8228"
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gene 140422..140721  
CDS 140422..140721

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GEDYNESYVSYEDRDEDGTYERSTRYIDSDGDYL  
NDAYVTYDDEDDGDGVYESYDYSEL  
GSTSKNAVPPSRIAQSVKDGLSGKRHEVKGTVRD  
IKTVQORGNEYSLMMQVKSQDGKDV  
WIDLGGHATGVQLFKDDQATFYGPMVKRGEKEVL  
VATAVDLPKHGMYKVERSGSRYTG  
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gene 140779..141291  
CDS 140779..141291

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pyruvate family and D-alanine"  
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hits: BLAST: pir:A69115;  
hypothetical protein MTH1854 -  
Methanobacterium; E=4e-13  
pir:D69083; hypothetical protein  
MTH162 - Methanobacterium; E=4e-09  
gb:AAB89585.1; (AE000988)  
acetolactate synthase, small  
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ADNLPPQDIY"

gene 141467..142522  
CDS 141467..142522

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porphyrins"  
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PMID: 9384565 PMID: 10704318 PMID:  
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swissprot:O50533; HEMZ-STRCO  
PROBABLE FERROCHELATASE  
(PROTOHEME; E=5e-82  
swissprot:P71765; HEMZ-MYCTU  
FERROCHELATASE (PROTOHEME; E=2e-62  
swissprot:P72183; HEMZ-PROFR  
FERROCHELATASE (PROTOHEME; E=3e-42  
COG: Rv1485; COG0276 Protoheme  
ferro-lyase (ferrochelata-  
se); E=2e-63 PFAM: PF00762;  
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se; E=7.2e-89"

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gene	complement(142418..143629)	/locus-tag="RB8234"
CDS	complement(142418..143629)	/locus-tag="RB8234"
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CDS	142595..142942	/locus-tag="RB8236"
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gene	142997..143593	/gene="prdX2"
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		/function="detoxification; stress response"
		/note="PMID: 9115640 best DB hits: BLAST: ref:XP-009063.1; TR00071480-p [Homo sapiens]; E=2e-62 swissprot:Q61171; PDX2-MOUSE PEROXIREDOXIN 2 (THIOREDOXIN; E=3e-62 swissprot:P32119; PDX2-HUMAN PEROXIREDOXIN 2 (THIOREDOXIN; E=4e-62 COG: PA0848; COG0450 Thiol - alkyl hydroperoxide reductases; E=4e-60 PFAM: PF00578; AhpC/TSA family; E=1e-71"
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CDS

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IFDEGDTLGDGSPPISTVQLHGET  
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gene  
CDS

144428..146911  
144428..146911

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systems"  
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60IM-HAEIN 60 KDA INNER-MEMBRANE  
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PROTEIN -----; E=4e-30 COG:  
HI1001; COG0706 Preprotein  
translocase subunit YidC; E=6e-32  
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PF02096; 60Kd inner membrane  
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LVTLSNRGGGIERIELTERKENGRCLKYRRVDVRS  
GYLGYLAADPTATDLGIRVNVVGP  
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 CDS complement (146852..1471 /locus-tag="RB8243"  
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gene complement (147205..1474 /locus-tag="RB8245"  
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gene complement (147441..1482 /locus-tag="RB8246"  
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 CDS complement (147441..1482 /locus-tag="RB8246"  
 41)  
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 Pseudomonas; E=6e-06 pir:T35659;  
 probable transmembrane protein -  
 Streptomyces coelicolor; E=2e-05  
 COG: PA1139; COG2340  
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 NIVAKHITQTGAAVATKDQTTYAVHLFGRPKSA  
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gene complement (148183..1483 /locus-tag="RB8247"  
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 CDS complement (148183..1483 /locus-tag="RB8247"  
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CDS

148395..149156

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embl:CAA98652.1; (Z74134) ORF  
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cerevisiae]; E=2e-36  
gb:AAC69477.1; (AF087482)  
dienelactone hydrolase  
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ddbj:BAA74533.1; (AB019032)  
dienelactone hydrolase [Ralstonia;  
E=1e-08 COG: YDL086w; COG0412  
Dienelactone hydrolase and related  
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E=4.2e-05"  
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149353..151131

CDS

149353..151131

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SYNTHETASE; E=1e-165  
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aspartyl-tRNA synthetase  
[Bacillus; E=1e-161  
swissprot:O67589; SYD-AQUAE  
ASPARTYL-TRNA SYNTHETASE; E=1e-157  
COG: BS-aspS; COG0173  
Aspartyl-tRNA synthetase; E=1e-166  
PFAM: PF01336; OB-fold nucleic  
acid binding dom; E=2.2e-11  
PF00152; tRNA synthetases class II  
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misc-feature 150511 1505

gene 151322..153511  
CDS 151322..153511

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SEAGGGTIRIHDSKVQSQVFELLG  
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(AE005155) cationic amino acid  
transporter; Cat2; E=1e-29  
gb:AAG18789.1; (AE004983) cationic  
amino acid transporter; Cat1;  
E=6e-21 COG: AF1612-1; COG0531  
Amino acid transporters; E=2e-32  
PA5097; COG1113  
Gamma-aminobutyrate and related  
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COG0531 Amino acid transporters;  
E=8e-12 PFAM: PF00324; Amino acid  
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REPTKNIPRAMLLSLVIALLIYLP  
LLFVLTTVGT  
DGSQSIRELAASDPEAVVALAARH  
YLGTSGYWLVLIAAVLSMF  
SALQANLFAASRIAL  
AMSRDNTLPNALSRLAAGSGSPWI  
SVLVTTGLVCLLIQLLPDIAAAGAASSLI  
FLVTF  
AIAHWLAILVRQRSVLT  
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FQGIAPPEAGIIAVMW  
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DVSNI  
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LVPIANPNNARAMIALAD  
TLVPAALGRVLVQTVV  
VAPHDWD  
P  
LVNHRPSAQLH  
SVMNEILHASASL  
GVRCE  
TLTTV  
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QCQSVLLGL  
SEITPEARDTPLEGL  
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SSLSREQQRQVKFL  
RVIPTDTLRADQ  
KRIRKELD  
RTTRVNAGRVCERE  
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gene 153716..154126 /locus-tag="RB8258"  
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gene complement(154068..1543 /locus-tag="RB8260"  
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 94)

/note="PMID: 20150255 best DB  
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 conserved hypothetical protein  
 TC0667 [imported] -; E=4e-10  
 pir:B71520; hypothetical protein  
 CT388 - Chlamydia trachomatis;  
 E=6e-10 COG: CPn0497; COG1872  
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gene complement(154391..1581  
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CDS complement(154391..1581  
 04)

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 /note="PMID: 96062224 best DB  
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 1.5.99.8); E=1e-180 COG:  
 jhp0048-2; COG1012 NAD-dependent  
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 Cj1503c-1; COG0506 Proline  
 dehydrogenase; E=2e-56 sll1561-2;  
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 PF01619; Proline dehydrogenase;  
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HLASRQRHGVAMNVNLLGEALLGDDETRKRMQS  
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FVYLDMEEYSDLYLTADVLRETLE  
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GNIRVGVASHNLFVVALAMIWTQR  
SGASDSVQFEMLEGMANHQRALTERDAAMLLYA  
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function="degradation of  
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conserved hypothetical protein -  
Deinococcus radiodurans; E=4e-10  
pir:I39564; hypothetical protein 6  
gbd-region [imported] -; E=1e-08  
COG: aq-1494; COG0824 Predicted  
thioesterase; E=3e-13"  
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protein-putative a thioesterase"  
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AK  
IIHEYEIRRGDEVLVQATVTLAVIDKTGRLQ  
RVP  
EALLT"  
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locus-tag="RB8266"  
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gb:AAK03329.1; (AE006164) unknown  
[Pasteurella multocida]; E=1e-04  
swissprot:Q58707; YD11-METJA  
HYPOTHETICAL PROTEIN MJ1311 -----;  
E=2e-04 pir:S47803; hypothetical

gene 158178..158603  
CDS 158178..158603

gene 158639..159688  
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CDS	159685..160662	
gene	complement (160746..161867)	
CDS	complement (160746..161867)	

gene	161882..163753	ANKSLAEETLFWIEMRQRDYHNAFDLPPPPEGWL
CDS	161882..163753	ISRGE" /locus-tag="RB8274" /locus-tag="RB8274" /function="two-component signal transduction" /note="PMID: 8346225 PMID: 9097040 best DB hits: BLAST: swissprot:Q06067; ATOS-ECOLI SENSOR PROTEIN ATOS ----- pir;; E=2e-17 gb:AAD47419.1; AF100457-2 (AF100457) histidine kinase [Myxococcus; E=2e-16 ddbj:BAB04255.1; (AP001508) two-component sensor histidine kinase; E=3e-14 COG: atoS-3; COG0642 Sensory transduction histidine kinases; E=2e-18 Rv1827; COG1716 FHA-domain-containing proteins; E=1e-08 PA2882; COG0642 Sensory transduction histidine kinases; E=2e-08 PFAM: PF00498; FHA domain; E=3.2e-19 PF01590; GAF domain; E=4.8e-18 PF00512; His Kinase A (phosphoacceptor) doma; E=6.6e-07" /codon-start=1 /transl-table=11 /product="sensor protein atoS" /protein-id="CAD78553.1" /db-xref="GI:32445822" /translation="MASLFVIRGRDQGKHFQLAP TVTRLGRESSNNVQLLDNEASRSH AEIRGDGTGRRYELVDLGSSNGTLVNNRKITRHV LTSGDRVEIGSTLLIFTGTGNVSA LDAAHGVDIVRQVRGGDASNIVSSLSREGVVSPY TPGGSSSNGPSTDKPATSPTTLPP PIPPPVENPPTPSEDERVDSSASGSDPPGQFHGP PVIGRLDADRSLVEMYLTATIAVGR TDDLDEVLDRLVCLKVFDWVEADRGCIMLRDPESK RLTPAARCDRESATGGTKQNPSSK PQDRIQISHTILDYVLQHKQGVRTNDALDDERFD SAASIVQGGVREALCVPLQGRYEI VGMLYVDITYTTPGELVRKGGATRFHDEHLRLITA VGHQAALAIEDTFYYSALLQGERL AAMGQTIATLSHHIKNIQGVRRGGSYLIESGLQK DDTDAIRGWSIVDRNQERISNLV LDMLTFSKEREPDLQEGNLNEVSDVVELMQSRA GQSEIELVSDLDATLPIATFDSEA IHRAVLNLTNAIDAATKTVLVKTFYDAAQGWIV DVEDDGEGVPEEDREQIFSLFESK KGARGTGLGLPVSAKVLREHGGTLTVDDAASGGA RFRMILPATGTDINELSRSETQA" /locus-tag="RB8275"
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CDS	164318..164707	/locus-tag="RB8280" /note="PMID: 11759840" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78557.1" /db-xref="GI:32445826" /translation="MTGSSGMIEGRIDNNVEAFV DLEIQDDTTHTIAFLVDTGFNGF LSIPFRLVHQLGLPLSDVQQGVADGRSSFFDTV ELTVIWHGNPLTVQAQVLDEPLL GTRLLRGSKIEAAWIQGGMFQIELILDG"
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CDS	complement(165169..166014)	/locus-tag="RB8282" /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78559.1" /db-xref="GI:32445828" /translation="MAGRRIVCPQCKTTLQIPAT MGAGKVKCPKCELMMLAVRAPVTVH VPEENLFDNLPSLGSSAAAPPSSVFRPSGPVTVY QPPKPAKKRGGGSKAAVKIISTIA GLGLLCVLLCAGGIFAVGYLGSRHSGWTSVTYKG YTVSMPAGEDRRDKSQQFPGTTVH ELTGRRKETGSQYSLVVADLPAVIDPNIPIAELL RDMRIRLSNPRPVTRSGVEGMAGT MQSGVGAIEGSDCEIYVHNRNLVVAVYSPYSEIK DLVGGQQRKPRSNESELDKPSEFFD SLEFK"
gene	complement(166175..167167)	/locus-tag="RB8284"
CDS	complement(166175..167167)	/locus-tag="RB8284"  /note="PMID: 98196666 best DB hits: BLAST: pir:F70440; conserved hypothetical protein aq-1630 - Aquifex; E=3e-18 pir:D71323; conserved hypothetical protein TP0436 - syphilis; E=3e-18 pir:F69999; conserved hypothetical protein ytgI - Bacillus subtilis; E=1e-16 COG: aq-1630; COG0618 Exopolyphosphatase-related proteins; E=3e-19 PFAM: PF01368; DHH family; E=2.4e-12 PF02272;

		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative a phopsphoesterase or an exonuclease" /protein-id="CAD78560.1" /db-xref="GI:32445829" /translation="MGVNWKA FVDQIQHYQS FVL VSHIRPDCDALGSELGMAEVLRAV GKDVRIINAHRTPPALSFLDPAGNIEVLGDSVEA EDVKADCIMILDTSAWAQLGDMGD VIRASRADKMVLDDHHVGEDELGARMYKDYQSEAT GHLVVQAADALNVPLTRTMATPLF AAIATDTGWFRFSPVTSPTYRTIARLIDAGVVPS EVYGDLYERDTLGRLLKRLGLILSR TTTEMDGALVYTSVNKEDFELCGAQPNDTEDAIN LTLAIRGTQAGVIFVGQVRGGFKL SFRSRCSLDCNEVARQFGGGGHKAAAGAFLEGTL DEVQDRVLPPIVREALAVALG" /gene="ribF"
gene	complement (167183..168154)	
CDS	complement (167183..168154)	/locus-tag="RB8286" /gene="ribF" /locus-tag="RB8286" /EC-number="2.7.1.26" /function="central metabolism" /note="PMID: 7772835 PMID: 3023344 best DB hits: BLAST: pir:T35984; probable riboflavin kinase (FAD synthetase) -; E=3e-46 pir:C83077; riboflavin kinaseFAD synthase PA4561 [imported] -; E=4e-42 pir:C82293; riboflavin kinaseFMN adenyllyltransferase VC0681; E=2e-41 COG: PA4561; COG0196 FAD synthase; E=4e-43 PFAM: PF01687; Riboflavin kinase / FAD synthetase; E=3.3e-32" /codon-start=1 /transl-table=11 /product="probable riboflavin kinase (FAD synthetase)" /protein-id="CAD78561.1" /db-xref="GI:32445830" /translation="MTSLIHLSDLAGDSDLHL LSL QGGAVSIGNFDGVHLGHRALLERV RWHAQRVGGKAIATVMDPHPASVLRPHGAPPSLT SLSRRAELMSGSGIDHLLVCEATR DFLNQTAEEFFQRLIVEQLSAKAIIEGPNFFFGR DRAGNTTRLKELAAERQIDVEIVV PSVRDERMVSSSRIREAIASGDIVLANQMLGSRY RLTGVVTTGEQRGRTLGFPTANLG GVTLLPEHGVYAALACGDECDGPTNHPAAVHIG PNPTFNERQETKIEAHLDDYDGD YGKSLSLTLVSQVRGVKIFADASALKQQLQIDLO TVRETVSSLQSRP"
gene	complement (168273..169187)	/locus-tag="RB8287"
CDS	complement (168273..169187)	/locus-tag="RB8287" /function="unspecified kinase or ATP dependent regulatory protein" /note="PMID: 20406833 best DB hits: BLAST: pir:H82489; conserved hypothetical protein VCA0191 [imported] -; E=2e-23 pir:G81111; conserved hypothetical protein NMB1197; NMB1159; E=4e-21 pir:C72317; conserved hypothetical protein - Thermotoga maritima; E=9e-21 COG: VCA0191-2; COG0063 Predicted sugar kinase; E=8e-24 PFAM: PF01256; Uncharacterized



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gene	169350..170591	
CDS	169350..170591	
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gene	complement(170605..171453)	
CDS	complement(170605..171453)	

		conserved hypothetical protein; E=4e-29 pir:S76797; hypothetical protein - Synechocystis sp. (strain PCC; E=7e-28 gb:AAD29318.1; AF117208-1 (AF117208) circadian phase modifier; E=2e-24 COG: AF1275; COG1691 NCAIR mutase (PurE)-related proteins; E=4e-30" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein-putative phosphoribosylcarboxyaminoimidazol e mutase (pure)" /protein-id="CAD78564.1" /db-xref="GI:32445833" /translation="MNLPSNQPPSPALLQILQDL ASGQTDVEAAAEISIQASSIGSAAD MQTVPGATVDLGRRLARCGFGEVIYGEKSTDLMT QIVQTOVAVGQGCLITRIDATAAA QLRRVFENTRYNPSARTLRIGCGDENLDPIGVEG HSTHVAVVTAGSTDAHVAEEAAET LAWMGVACERIDDIGVAGPQRLLAAVPRLRAAAA IVVVAGMEGALPAALAGHVATPVI AVPASTGYGANFAGLTPLMGMLTSCAANVAVVNI DAGFKGGYFAGLIASGIANAKSEA ASAEAA" /gene="argG" /locus-tag="RB8293" /gene="argG" /locus-tag="RB8293" /EC-number="6.3.4.5" /function="urea cycle, biosynthesis of polyamines and creatine; assimilation of ammonia, biosynthesis of the glutamate family" /note="PMID: 20158877 PMID: 90046714 PMID: 3174461 best DB hits: BLAST: pir:H72210; argininosuccinate synthase - Thermotoga maritima (strain; E=2e-97 pir:D75490; arginosuccinate synthase - Deinococcus radiodurans; E=3e-96 pir:C83204; argininosuccinate synthase PA3525 [imported] -; E=2e-87 COG: TM1780; COG0137 Argininosuccinate synthase; E=2e-98 PFAM: PF00764; Arginosuccinate synthase; E=2e-190" /codon-start=1 /transl-table=11 /product="argininosuccinate synthase" /protein-id="CAD78565.1" /db-xref="GI:32445834" /translation="MLLDFPARILLTVLACFAPD NLNARPSNIADSPAFGCRSEMKS VLAYSGGLDTSVILGWLQDQGYEVHCVYVDLGQP CEDRDAIMEKARTCGAKSSRLVDV REELCRDFAFPVLAWQAKYEQIYLLGTSIARPLI SKVCLEVAREVGATAYAHGATGKG NDQCRFQLAAEALDPNIEMIAPWRIKSFRDAFPG RTELIEYCDVKRIPVKASTAKPYS SDENVLHISYEAGKLEELDVNGVELVEFGMGVSP QDAPDKPEEVTIGFESGVPKTLNG KAVNALEMVEQLNDIAGRNGVGRIDMVENRFVGM KSRGVYESPGMTVLYDALMYVEQL TMDRDLMHRLRDRMAPEVAEMVYGFWYTPKMDAL MSFIETAQRPVGTGEVTLQLYKGN MVSSRTSPNSLYDEEIATMEGGGSYNQDDAEGFL RIQGLPSRVQGRVSPRKF" /locus-tag="RB8295"
gene	171457..172791	
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gene	complement (172907..1738	

CDS	complement(172907..1738 30)	/locus-tag="RB8295"  /codon-start=1 /transl-table=11 /product="hypothetical protein-transmembrane prediction" /protein-id="CAD78566.1" /db-xref="GI:32445835" /translation="MTFLFTCPHCQSQTEVEDEY SGRTGDCVVCGREITMPEFAGSRR MGNRPGKRKNSAIWFVAAGLALLLIGAGLIAAVQ VGSRTAKKIRTGRQRLSSIKNLEK IASALNAYAADHGVYPAPYTVDAAGRKLHSWRVT ILPYLDEDGLYNQIDKDVWNEGE NQMLLYSQTPAVYRHPESSSWGTGTVYHLVTGAG TLFPSTGPLGPRQVTDGATKTILL AEGQMNTMTESWMEPYDLDIGSVGGLINPPSGNG LGGATDGGVCVATVEGSGYFLPDT TPPLTVQALITPTGGEPLSDDVLDDEWASTQP"
gene	173814..174359	/gene="dtd"
CDS	173814..174359	/locus-tag="RB8300" /gene="dtd" /locus-tag="RB8300" /EC-number="3.1.-.-" /function="other detoxification" /note="PMID: 20459059 PMID: 10383414 PMID: 10918062 PMID: 11568181 best DB hits: BLAST: gb:AAF82117.1; AF276071-1 (AF276071) conserved hypothetical; E=3e-37 ddbj:BAB04962.1; (AP001511) BH1243~unknown conserved protein; E=3e-36 pir:E72338; conserved hypothetical protein - Thermotoga maritima; E=9e-36 COG: BH1243; COG1490 D-Tyr-tRNA <sup>tyr</sup> deacylase; E=3e-37 PFAM: PF02580; Uncharacterized ACR, COG1490; E=3.8e-5 /codon-start=1 /transl-table=11 /product="D-tyrosyl-tRNA (Tyr) deacylase" /protein-id="CAD78567.1" /db-xref="GI:32445836" /translation="MNRNVIRSFHLISDAPRVRP ATNLAHLATTWIANHPMKIVLQRS QHASVSDGKIVGQIERGLVALIGIGHEDTEATA SALADKTAGLRIFSDDNGKMERNV IDAGGDVLAISQFTLLADCRKGRRPAFTDAAPPD RANELYEHYVSELRKTGLSVPCGI FAADMAVSLTNDGPVTIILEL"
gene	complement(174384..1754 12)	/locus-tag="RB8301"
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gene	175602..176399	/locus-tag="RB8306"

		/function="biosynthesis of peptide antibiotics" /note="PMID: 2542219 best DB hits: PFAM: PF02674; Colicin V production protein; E=8.4e-14" /codon-start=1 /transl-table=11 /product="hypothetical protein-putative a gene in the purF operon involved in colicin V biosynthesis" /protein-id="CAD78569.1" /db-xref="GI:32445838" /translation="MQTYDILMTVILVGATLLGA IRGFAWQLASIASIVVSYCVAYHY REPFQNIHAAPPWNQFLAMFILFVGTSFVIWVA LRMVSGMIDRMRLKEFDRQIGALF GLAKGALLCTIITLFAVTLFGERTQRAIVASESG RLIARVLAESNSIMPPELDSVVRP YLDQFSDEELGEPASSEGSWLSQTPIAPNIDPNW SHSNAPTANNFAPQNGFQQAQNDP RSQSPFGGFGGSSTPTPNADFNSAAGSQQPAPTW RQSATPLWQTPRR"
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gene	complement (176695..177654)	/gene="accA"
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/note="PMID: 7774814 best DB hits:  
BLAST: pir:H69878; probable  
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kinase - Streptomyces; E=1e-26  
pir:T36501; probable  
serinethreonine protein kinase -  
Streptomyces; E=2e-26 COG:  
BS-yloP-1; COG0515  
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E=1e-28 PFAM: PF00069; Protein  
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gene

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88)

CDS

complement(178844..1800 /locus-tag="RB8313"  
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homolog yveN -; E=2e-19  
pir:T35514; probable glycosyl  
transferase - Streptomyces  
coelicolor; E=2e-17 COG: BS-yveN;  
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gene	complement (181485..1828 79)	/gene="flhF"
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CDS	complement (182876..184939)	<pre> /locus-tag="RB8323" /gene="flhA"  /locus-tag="RB8323" /function="flagellar organization; type III protein secretion system" /note="PMID: 8097015 best DB hits: BLAST: ddbj:BAB06157.1; (AP001515) flagella-associated protein [Bacillus; E=1e-119 pir:C72319; flagellar biosynthesis protein FlhA - Thermotoga; E=1e-115 swissprot:P35620; FLHA-BACSU FLAGELLAR BIOSYNTHESIS PROTEIN FLHA; E=1e-114 COG: BH2438; COG1298 Flagellar biosynthesis/type III secretory pathway; E=1e-120 PFAM: PF00771; FHIPEP family; E=1.6e-261" /codon-start=1 /transl-table=11 /product="flagella-associated protein" /protein-id="CAD78578.1" /db-xref="GI:32445847" /translation="MQLLMRYRDLVLPIGIIACL VVILVPLPPFLMDLLLATNITVGV IVLLTTVYVSTPLEFSIFPSLLLATTTLARLVNLV ATTRLILTSTESGSGGAAGGVIQG </pre>

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pir:T36501; probable
serinethreonine protein kinase -
Streptomyces; E=2e-34
embl:CAB94054.1; (AL358672)
putative serinethreonine-protein;
E=4e-34 COG: Rv0014c-1; COG0515
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(AP001511) CMP-binding protein
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		E=3e-62 pir:B82628; transcription
		regulator XF1858 [imported] -
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		COG0603 Predicted ATPase (PP-loop
		superfamily), confers; E=6e-64
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		synthase; E=3e-04 PFAM: PF02568;
		Thiamine biosynthesis protein;
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gene	195118..195243	/ locus-tag="RB8344"
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CDS	complement(195240..196583)	/ locus-tag="RB8345" / note="best DB hits: BLAST: gb:AAD19720.1; (AF124349) unknown [Zymomonas mobilis]; E=0.54 PFAM: PF00076; RNA recognition motif. (a.k.a. RRM,; E=0.54" / codon-start=1 / transl-table=11 / product="conserved hypothetical protein" / protein-id="CAD78592.1" / db-xref="GI:32445861" / translation="MKSKRAALWLALGGLVGLGS LNGASAADRFVADASYQGGMPTSQ AEVVPVGHFDASCDSCDTFPMECEGCGELACDG GCGDMGCGDMGGGLFDDGGCGMFD CDLGDPFTLFGGEACGYSVGGWVQMGYHNKALPLF NNRPDEYNLHQAWFYAEKAIDTSN GFDFGGRIDYVYGIDAQDTQAFGIDNGHWDTGWK HGEYGSALPQVYGEVGYGDLVSKF GHFFTIIGYEVVAAPDNFFYSHAYTMYNSEPFTH TGALATYNASDDLTVYGGYTLGWD SGFEDNGDSFLGGVSLAMSDDVTVTYATVAGRFA DEPAGTTSQGYMHSIVTDIALTDQ LQYVLQSDYMDAENGNGGNFKETYGLNNYLIYTV SDCLALGSRFEWYDADAGVFNGNV DVYALTLGANVKPHANVLRPEIRWDWADGADVT GILENDQDDQTTFGIDTIFLF"
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          BH1469~unknown conserved protein;
          E=7e-32 COG: VC1343; COG2195 Di-
          and tripeptidases; E=1e-35 PA5390;
          COG0624 Acetylornithine
          deacetylase/Succinyl-diaminopimela
          te; E=5e-07 HI1348; COG2195 Di-
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          VSAI VIASEA ISSLHRNGWLGLVEKDGRRTANV
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conserved hypothetical protein -
Deinococcus radiodurans; E=2e-67
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gene	228679..229314	/gene="tdk"
CDS	228679..229314	/locus-tag="RB8399" /gene="tdk" /locus-tag="RB8399" /EC-number="2.7.1.21" /function="nucleotide metabolism; pyrimidine-ribonucleotide metabolism" /note="PMID: 2060797 PMID: 2041474 best DB hits: BLAST: gb:AAK03320.1; (AE006163) Tdk [Pasteurella multocida]; E=2e-66 swissprot:P44309; KITH-HAEIN THYMIDINE KINASE ----- pir;; E=3e-65 swissprot:P23331; KITH-ECOLI THYMIDINE KINASE ----- pir;; E=2e-64 COG: HI0529; COG1435 Thymidine kinase; E=3e-66 PFAM: PF00265; Thymidine kinase; E=4.9e-88" /codon-start=1 /transl-table=11 /product="thymidine kinase Tdk" /protein-id="CAD78621.1" /db-xref="GI:32445890" /translation="MAKLYFYSTMNAGKSTVLL QSSYNYRERGMNTLILSPEIDTRF GSGKVASRIGIESESVFNTSDNLLNLVRNETRI NPLHCVLVDEAQFLTRTQVRQLSD VCDDLIPVLAYGLRTDFQGNLFEGSEHLLAWAD TLTELKTICHCGRKATMVLRVSES GQVIRDGEQVQIGGNERYQTVCRLLHFKEAIYQRA EDELPLLDNSNEPRQSER"
gene	229393..231687	/gene="rnr"
CDS	229393..231687	/locus-tag="RB8402" /note="synonym: VvacB" /gene="rnr" /locus-tag="RB8402" /EC-number="3.1.-.-" /function="rRNA processing; mRNA processing (5'-, 3'-end processing, mRNA degradation)" /note="PMID: 9603904 best DB hits: BLAST: ddbj:BAB07272.1; (AP001519) ribonuclease R [Bacillus halodurans]; E=6e-88 swissprot:O32231; RNR-BACSU RIBONUCLEASE R (RNASE R) (VACB PROTEIN; E=8e-84 gb:AAK05040.1; AE006328-8 (AE006328) ribonuclease

BH3553-1; COG0557  
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 PF00773; RNB-like protein; E=2e-87  
 PF00575; S1 RNA binding domain;  
 E=3.2e-08"  
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 VILERLGSSKNPAIDTLTIMRQYALPDEFSEDVL  
 DEAREQADAFDDDDVVPDTRKDLTD  
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 LPDRVIPMIPEIISNHLASLQPERMRLVKTVEIE  
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 TSFVKDLGLGFDNVESRFEIQAVLDKVAGTTLEN  
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 LDKEHYCHFTSPIRRYPDLVHRLVQRLIEQKST  
 PDESFAELVKLGHECSDAERNAAQ  
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 pir:E64856; hypothetical protein  
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 E=2e-60 gb:AAG55866.1; AE005321-9  
 (AE005321) putative nicotinic  
 acid; E=2e-60 gb:AAC78722.1;  
 (U89687) putative nicotinic acid  
 mononucleotide:5;; E=4e-60 COG:  
 ycfY; COG0846 NAD-dependent  
 protein deacetylases, SIR2 family;  
 E=2e-61 PFAM: PF02146; Sir2  
 family; E=3.1e-57"  
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 dazole phosphoribosyltransferase"  
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 CDS 231899..232618

gene complement(232600..2336  
 73)  
 CDS complement(232600..2336  
 73)  
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gene	complement (233700..2345	
	45)	
CDS	complement (233700..2345	/locus-tag="RB8407"
	45)	
		<pre> /note="best DB hits: BLAST: pir:T37061; probable secreted protein - Streptomyces coelicolor; E=2e-27 pir:T35483; hypothetical protein SC6C5.12c SC6C5.12c - Streptomyces; E=2e-16 pir:T35506; hypothetical protein SC6E10.19c - Streptomyces; E=9e-11 COG: DR2293; COG3021 Uncharacterized BCR; E=7e-04 PFAM: PF01260; AP endonuclease family 1; E=0.88" /codon-start=1 /transl-table=11 /product="probable secreted protein" /protein-id="CAD78625.1" /db-xref="GI:32445894" /translation="MHWMLILFVRKMLFLAIAFA SFAFMLRSPLVLAQEQTNSTIRL RVLSYNIHHGRGTDGKIDLDRLANVIRSVDPDLV AVQEVQDQNTTRNGMVNQVETLAVQ TSLHGKFAKQIDYDGGEYGQAVLSKYPIESLEVH WLPGDPIRERRIVGVAEILIHKTR LRFATTHLHHSRADLREKQATELNRLIACGSTPV IIAGDFNAKPASLAMQTLQAKWRI ATTESMHTFPARSPNRQLDYVAMYPANSWRIVES EVLDEPVASDHRPLLVEIELETHS GSLPK" /locus-tag="RB8409" /locus-tag="RB8409" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78626.1" /db-xref="GI:32445895" /translation="MFDSKSKPSETAATVRRPVW THQDFSGGGYFGTIPKSTDRCGVF TAGVLTADVLDRCIGLKRSTNEDDALFSTEQSRC SIQNWRSQKIPHQPENWDR" /locus-tag="RB8410" /locus-tag="RB8410" /note="best DB hits: BLAST: embl:CAB57873.1; (AJ132579) coat protein readthrough [Oat golden; E=0.10 embl:CAB57874.1; (AJ132579) coat protein [Oat golden stripe; E=0.10" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78627.1" /db-xref="GI:32445896" /translation="MTLCSLQSSRDAQSKIGDRR KSRTSPKIGTGERSIGALKTREQL NRLRFAGQPSYTEGSTRRPLPPSAGQLAGSSESQ SLTCETMPRNRIANDDSPMERLA IKR" </pre>
gene	234547..234840	
CDS	234547..234840	
gene	234746..235063	
CDS	234746..235063	

CDS

235092..236180

/locus-tag="RB8411"

/function="transcriptional control"

/note="best DB hits: BLAST: pir:H83475; probable transcription regulator PA1359 [imported] -; E=0.067 embl:CAA64677.1; (X95394) aldehyde dehydrogenase-like protein; E=0.52 COG: PA1359; COG1396 Predicted transcriptional regulators; E=0.006 PFAM: PF01381; Helix-turn-helix; E=7.3e-11"

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/transl-table=11

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gene

complement (236128..237204)

/locus-tag="RB8414"

CDS

complement (236128..237204)

/codon-start=1

/transl-table=11

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/db-xref="GI:32445898"

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gene

complement (237132..237758)

/locus-tag="RB8415"

CDS

complement (237132..237758)

/note="best DB hits: PFAM: PF00583; Acetyltransferase (GNAT) family; E=0.72"

/codon-start=1

/transl-table=11

/product="hypothetical protein"

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/db-xref="GI:32445899"

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CDS

237883..237999

/locus-tag="RB8417"

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CDS	complement (237986..240421)	/locus-tag="RB8418" /gene="priA" /locus-tag="RB8418" /function="DNA synthesis and replication" /note="PMID: 9086272 best DB hits: BLAST: swissprot:P94461; PRIA-BACSU PRIMOSOMAL PROTEIN N' (REPLICATION; E=1e-130 embl:CAA71348.1; (Y10304) priA [Bacillus subtilis]; E=1e-123 swissprot:P74397; PRIA-SYNY3 PRIMOSOMAL PROTEIN N' (REPLICATION; E=1e-112 COG: BS-priA; COG1198 Primosomal protein N' (replication factor Y) -; E=1e-131 PFAM: PF00005; ABC transporter; E=0.66 PF01443; Viral (Superfamily 1) RNA hel; E=0.33 PF00271; Helicase conserved C-terminal; E=7.8e-09" /codon-start=1 /transl-table=11 /product="primosomal protein N" /protein-id="CAD78632.1" /db-xref="GI:32445901" /translation="MGYLAPAGKKRSSHVMLSDS SLSNLGDPDTLNFPPFAAAPVPADS SSSEPTQNELFETDPPPWELTVGEDVQLASIVFA RSPHGPYDYRIPDDLDDVLRPGMR VGVPLGHRKKPTPGWCVSIKTGNAAQKKLRDVSE VIDDEPLCDAALVRLVMFIAHYQ VPAGQVFDTLIPASVRDNAGTRKTTYFRPAPGLT EEQIAKLPSKQQSAMRFLIAQDRP MTAAEIAIMAECTEDPIRRLRKKELLVPEVRREL SQNIRIRAQANDGETRKTHTDLTAQ QENALSRINSAVDSGRGRTLHLHGVTGSGKTEVY IQAIEHVVKQAGSAIVLVPEISLT PQTRGRFEDRFQNVAVLHSQMSASERHFHWQRIR RGEVQVVIGPRSAVFAPLPNLGLI VIDEEDTTSFKQDKQPRYHARKVAHARAMALGIP LVLGSATPSMEAWHATQTGHAEV TMSERVGNRPMPPDVQLVDLRVKEERGKGGAISRP LHAAVLETLKEKGQAILLNRRGY ATTIQCPACGTVCACPDCLTHHRDGGKAMCH YCDYTIPTPPWCPACRFDGMRYGG LGTQRLEMEAKARFPDARIARMDSDTMKRAGSHQ RVLSEFRAGEIDVLLGTQMIAGL DFPNVLLVGVINADSALHFPDFRAAERTFQLVTQ VAGRTGRGDRGGRVIVQTFTEHP AIQAAARHDYLFVEDEMVRKKFNYPPLGSVAR IIRGPLEDKTESVADAIVDRLEK ARDLLKAEVRILGPAPPPIVKISGKYRFHLLLQA TEAAVVGEVIRRLADFKVDPKEE IEFLVDIDPVNLM" /locus-tag="RB8420" /locus-tag="RB8420" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAD78633.1" /db-xref="GI:32445902" /translation="MSSFSSRAQDNPSIIAHPV TRLVTRLNCPALPRPESPSLSRSF HPELLTQTPPEPLVPIRLGRGRLGSHRGAAKDG NRGSRNAHPERRRPHQTAPHRVKE
gene	240382..240843	
CDS	240382..240843	

gene	240840..241310	AIRIPSSSHYTGSLKAMR"
CDS	240840..241310	/locus-tag="RB8421"
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		/protein-id="CAD78634.1"
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		YLPMGYLGGLTARATRPQPT"
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		/db-xref="GI:32445904"
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gene	complement (241421..2433	/gene="atsG"
	76)	
CDS	complement (241421..2433	/locus-tag="RB8423"
	76)	/gene="atsG"
		/locus-tag="RB8423"
		/EC-number="3.1.6.-"
		/function="sulfatase"
		/note="PMID: 9634230 best DB hits:
		BLAST: pir:F70837; probable
		sulfatase (EC 3.1.6.-) atsG -
		Mycobacterium; E=1e-40
		gb:AAF55607.1; (AE003724) CG14291
		gene product [Drosophila; E=1e-20
		gb:AAF29467.1; (AF156255)
		N-sulfoglucosamine sulfohydrolase
		[Mus; E=3e-20 COG: Rv0296c;
		COG3119 Arylsulfatase A and
		related enzymes; E=1e-41 BH1718;
		COG1413 Phycocyanin alpha-subunit
		phycocyanobilin lyase and; E=0.010
		PFAM: PF00884; Sulfatase;
		E=5.2e-22"
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		YQFETPKGSWDQSSSKAHWRDRPD
		QDTPFFSVFNFTGCHESGIENDAKYKSVTKGLSE
		RERQDASKLSTFPPYYPDTPAARE
		DWKRNYELITALDHWVGGLLDQLNADGLDIEDTIV
		FFWSDHGVGLPRAKRWLYDSGTHI
		PLVIRMPAQFRSTDNVAGVVDDRLVSSIDFGPTV
		LNLAGLDVPEPMQGKPFLLTSPLSK
		LAAADRDRYVYGARDRMDERYDIIRMVRDQRYKYI
		RNYEPLKPYFQYMNTPEKGQTMRS
		IREAEQAGTLPEAAMPFFRGTKPTEELYDLEND
		HEIHNLAASSSDHTEVLHRMRAAHE
		QWVTRTKDLGLIPEPILAERASELGSQYAVLRQS
		DDSELANRVAAAALAASEGPRALP
		EMRSALDDIDSAVRYWGATGIGNVFARGEIDKLP
		YLMDLQERLADESVTVRVAAARAL
		CHSGDPEATSKALSVLAELADGAQWERLQAAIV
		LDEIDEKALPVIDSMQDALEPRQE

gene	complement(243479..244753)	/gene="mntH"
CDS	complement(243479..244753)	/locus-tag="RB8430" /gene="mntH" /locus-tag="RB8430" /function="metal ion transporters (Cu(2+), Fe(2+), etc.)" /note="PMID: 10844693 PMID: 10712688 best DB hits: BLAST: pir:T44945; hypothetical protein 6 [imported] - Natronobacterium; E=1e-48 swissprot:Q9RPF3; MNT1-PSEAE MANGANESE TRANSPORT PROTEIN MNTH1; E=1e-18 pir:B83105; probable transport protein PA4334 [imported] -; E=1e-18 COG: PA4334; COG1914 Mn2+ and Fe2+ transporters of the NRAMP family; E=1e-19 PFAM: PF01566; Natural resistance-associated macrop; E=0.00026" /codon-start=1 /transl-table=11 /product="Manganese transport protein mntH1" /protein-id="CAD78637.1" /db-xref="GI:32445906" /translation="MSFATLAGMKLPKFFRRFGP GLLVTAAFIGPGTVTKATTAGANF GHTLLWAIGFSVIATIVFQEMASRLGIVTGRGLG EAIRPTIPNALARGLAIVLVVSAI IVGNAAAYQAGNIAGAAVGVAATGMQHQTLSIV IGLTAWCILMIGHYRSLQRILVAL VVTMSCVFLLTALSVPIDWRSIALGWIQPTIPDG GLKEVLAIIGTTVVPYNLFLHATA SAEKWSSDKKEPVSDENIRDAIQHSRGDTILSVG LGGLVTAAVMATATAAFFQSNTGF TNLADAARQLEPLLGNHARWLFGVGLFAAGLTST ITAPLAAAYAAAGCFGWPIDLDKW RLRTVFTTVIVFGTSFAASGSKPTDIITFAQIAN GLLLPLLAIFLLAVMNNALLGKH RNHWIANTLGVLTVVVVSVLGLRSLVSVSFAG"
gene	244767..245624	/locus-tag="RB8432"
CDS	244767..245624	/locus-tag="RB8432" /note="best DB hits: BLAST: pir:F70844; probable fusion protein - Mycobacterium tuberculosis; E=1e-07 embl:CAC04235.1; (AL391515) conserved hypothetical protein; E=2e-04 pir:E83611; conserved hypothetical protein PA0269 [imported] -; E=0.020 COG: Rv3327-2; COG2128 Uncharacterized ACR; E=1e-08" /codon-start=1 /transl-table=11 /product="probable fusion protein" /protein-id="CAD78638.1" /db-xref="GI:32445907" /translation="MNSHHSSSGYPVMPRSSELV HTSATTIANNDSDNANQRVWNFCA AALILRPPITHPSEVLMTTGLKPLTDAEAREVEL VFRLTKSHLGFVPNSMRTMARQPA ILSSFTLMVGNILGQPSDAKSPIWLGIRLVIKNV IWSLRNMRSKDRPLPLALKNLVAHV TSGAAGCRYCQAHTIGEARDQGVPIEKLEAVWEF DRSDLFDEAEKSALRFALAAGSHP NGVTADHFADLRKHYTEDQIVELGATIALFGFLN RWNDTFATLEPESAAFANQHLSA SGWEIGKHG"
misc-feature	245160 2451	/locus-tag="RB8432" /note="cosmid pircos-a3c02/ cosmid pircos-cle07 joining point"

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gene	245842..248907	/gene="cti"
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38)

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75)

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gene	255833..256477	
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UPTAKE REGULATION PROTEIN; E=8e-13
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ornithine decarboxylase (EC
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Diaminopimelate decarboxylase;
E=8e-44 PFAM: PF02784;
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gene 265206..266162  
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 ligase (EC 6.2.1.-) yhfL  
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		FNL LGS"
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		TATC-HELPH SEC-INDEPENDENT PROTEIN
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		COG0805 Sec-independent protein
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		E=4e-19 VNG2267G; COG0805
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SYA-AQUAE ALANYL-TRNA SYNTHETASE
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- Deinococcus radiodurans (strain;
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gene

300336..300863

CDS

300336..300863

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swissprot:P49786; BCCP-BACSU  
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OF; E=1e-17 COG: BS-accB; COG0511  
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300867..302219

CDS

300867..302219

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BIOTIN CARBOXYLASE (A SUBUNIT OF;  
E=1e-138 pir:S74380; biotin  
carboxylase accC - Synechocystis  
sp. (strain PCC; E=1e-136 COG:  
sll0053; COG0439 Biotin  
carboxylase; E=1e-137 PFAM:  
PF00289; Carbamoyl-phosphate  
synthase L; E=5.1e-48 PF02786;  
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T; E=1e-119 swissprot:P74507;
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T; E=1e-118 COG: PA5131; COG0696
Phosphoglyceromutase; E=1e-123
BH0592; COG1015
Phosphopentomutase/predicted
phosphoglycerate mutase; E=3e-06
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misc-feature

310485 3104

gene

complement(311043..3114  
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CDS

complement(311043..3114  
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hemoglobin major component
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swissprot:P15160; GLB-PARCA
MYOGLOBIN (HEMOGLOBIN) ----- pir::
E=2e-08 COG: Rv1542c; COG2346
Hemoglobin-like proteins; E=2e-19
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1861	aactcgcggt	gttgctcttc	ctgatcagcg	gaaacgattt	tgatgtccac	agcagcgaca
1921	acctcatcgc	cgtcaaagaa	ctcgatcttt	ccgttgttga	aacgatcttc	gaagcctttg
1981	cgattccaga	ccttgaactc	ggagatctgc	acgggcgacg	ggaagtacc	tgcataccaa
2041	gggttgttct	cgtgcagagt	gtgagcaaa	tttcccttgt	ctccatcgac	gagccgttgc
2101	acaggaaagg	ttccgttgtt	gtattcgctc	gactgcgcca	gcttggccgt	tttcgcaata
2161	ttccggcccc	cgctgatgac	ctccacttcc	gaaagggtca	tctgttgccg	accattcaca
2221	ctgagtttga	acccggtgat	tttggcgtcc	ttcagagcag	ggtgggtcaac	agtgatcaac
2281	ccgccatttc	gagtgatctt	aaccggcccc	gtctcctcct	tcagagtctt	ctccgcggca
2341	gcctcctctt	caacgtcacc	ttctcgatcg	agcttgtatt	gcttcacccc	caagaacccg
2401	atcgtgttac	agatcaggat	gtcgttttga	agttcttcag	gaaaatgctc	ggaagataga
2461	attgcattgg	ctgccaccgg	tcgaaattct	ttctccagca	gtttgtgcat	tttaaagcca
2521	ttgccttcgg	gccgaacttg	atagcaacgc	ccaccgggtc	categctggc	atagcaataa
2581	ccccagtagt	cgaactgggt	gccgtgcgga	ttgggggagt	taccgcgatg	tggagtgatc
2641	gcgaacgtca	gcgggtcaaa	tcggtacatc	cccgcgccc	caatgttcag	gttctgcttc
2701	cacggagtct	cgtggttgtg	aacgaggaaa	atcccgcttt	gccaatagat	cccacgctct
2761	ggtccgtaaa	ccaaattggt	ggcggcggtg	tgagtgctcg	aggtaccaag	cccttgcaaa
2821	atgggggtatc	gcacgtccgc	cttgctcatcg	ccatcggtgt	ccttcaagaa	caacaggtca
2881	ggtccggacg	tgacaaccac	accgcccgtt	caaaattcaa	acccgagagg	gttgtgaacg
2941	tgtgcgaaaa	tcttgccggac	atcagctttg	ccatcgttgt	cagtgtcctc	caatatcatc
3001	aaggagtcat	tcattctcct	gccaggttcc	cactttgggt	aagtgttcca	actggccacc
3061	cacaactcgt	catgagcatc	aacttgcatt	tggacggggg	tggctaatac	gggaaactga
3121	acttccgacg	caaagacggt	gagctcgtaa	ccttcgggga	cgttgatctt	cgccagagat
3181	tcctctggac	ttaaagtagg	gacgtgccc	tctttcatag	cattggaact	ggcactccca
3241	ccaccgatat	ttgaggtcac	tttgaccggc	ggtggaacat	tgctgtcgtc	agcctgcaag
3301	gttcgcccac	ctgcggctgc	ccaaatcact	ttgtcgcgat	tggcgggtcat	cacgtcgagc
3361	atcaccaatt	catgcttcag	cacatctgcg	ttgctttgcc	catccacgaa	cgtcaacgtg
3421	gaacgactgc	cccaaagtgc	attgccgtcg	gtcgtctgat	accggttgtg	ccagtgccag
3481	tttttgcct	caatcgcttc	gtacaaatcc	tgaagctctg	catcagacgc	tggcttttcg
3541	cctagcaatg	cctgtgaaat	gataccagcg	agttgcttgt	aaccagcctc	attgaggtga
3601	actccgttga	gcgtgagtcg	ctcggaactc	gactgaaaca	actggtaagt	cggcgagaac
3661	aagtcaacaa	acttcgcgcc	cgtgatttcg	gctgcctcac	gagtcgcctc	ggtgtaagcg
3721	gccaaagtta	cattcagttc	cgccccatcg	ggcagactcg	cgtcgcctgt	gttctcgtag
3781	gcgatcggac	tgaacaggac	gaaacgcaga	tcccttcctg	catctttttg	cacctgcgtg
3841	taacgctgaa	cagctttgat	caattcatcg	cgatgctcgc	cggctttttc	cggctccggca
3901	aacgactcgt	tgaaccata	aaagggtgaaa	acaacatttg	gcgcgacgtg	cttcaaatat
3961	tcggtgtcat	tgggtgaacc	ctggtttctc	gggcgttgat	taacacgatc	ccccgaaaaa
4021	ctcatgtttc	gaaaactgac	gtcgagccct	ttcaactgat	gctgaagaaa	ggtttcgacc
4081	caaggatcat	gctgcatccg	atcggccagg	ccgttgccat	agatggcgac	gacatcgttc
4141	gattggaact	caaaagcgtc	ctgtgcatca	gctcgttgcg	cgatgcccgg	aatgacccc
4201	gcacatagaa	agaaaaggct	ccatttggagg	acagtcgtga	tccttttgcg	cattgttcgc
4261	tttctcagtt	gtcgaatctt	ggagtgcagt	ttcagctttt	gttctgcagg	ccagcgaaac
4321	tggctgcaaa	cgaagcatcc	taacgtggag	tgacggaacg	tgacacagtt	ttccgctggg
4381	gtatcgcgga	ctggtactgt	aacttcgtaa	agaacagaca	acagcatcaa	agaacgacgt
4441	aagctgttca	cgaagcgaa	tcccttgcgc	atatcgacga	gccaacgaac	actttgcgac
4501	gttctactgaa	ctggggcggt	aaacaccgta	ccaccgtctg	gacaagtctc	gattaaagct
4561	ttcagctcgg	aacgctcccc	cgagtcttca	agccgtggct	caatttatca	tgcaacggat
4621	tggctcgttt	tcgtgtctct	ggtttcctca	gcattcccta	tcggcggttc	cctcataacc
4681	gttctaggtc	gaacgcgtgg	ccttcggcac	aaggagtttc	ttcgcttctc	ccattgacgc
4741	tcgtgctccg	tccgatttgt	ggtgcaaaa	tctcttcagg	cagcgaatgg	atggcggtcg
4801	tcggaccggt	tctttgaaaa	ccagcgccga	gcagtggcac	aggagcggaa	cgatggaaga
4861	cgaccaactg	ggaccatttg	aagaatgatt	tggcactgaa	ccagatcatc	aatcgtgca
4921	actcgattca	gacaaccgtc	cacaaggctc	aaatgcttcc	agtctcgcgt	ggagaaaccg
4981	gacctctccg	atggcgtgaa	tctgttgaca	agaaaatcgc	gatcgcgtga	gacatccttc
5041	agttccaact	cacgtttggag	atgccacagg	tcactgacga	gtgcgacgtt	gtgcaactag
5101	cactttcgcg	aagctacggt	cccaacttga	tgttcgatca	aattgtatcg	accacatcg

5221	atg̃cgat̃cca	aāgtgg̃t̃tcg̃	accgtt̃gtca	ttcg̃gt̃accā	āg̃t̃ccg̃c̃g̃tc	gaccgcaccg
5281	cggatccatc	aatcg̃tcg̃ct	ctcgacaaca	tcgat̃gt̃ccg	ctgg̃gc̃gt̃tc	cgctcaca
5341	gcaaacgcga	tg̃ctg̃cccgc	aaggcacaca	cgg̃ct̃tcacc	agg̃cg̃t̃ctcc	gccccacacg
5401	tcaccgg̃cct	cg̃tt̃ccgg̃ct	gccc̃gt̃gcaa	aag̃cg̃tcgg̃c	tt̃tg̃act̃tca	agc̃gt̃t̃gt̃t̃t
5461	gaaacg̃t̃ct̃t	c̃cgaacagaa	acgaaagatc	tgg̃caat̃cgg	cgt̃gt̃ctccat	gccagat̃gct
5521	cagc̃gt̃ct̃cg	gg̃gg̃g̃ct̃t̃t̃t	at̃cgac̃gt̃tg	act̃gac̃gcga	gag̃t̃gt̃acgc	at̃cct̃ct̃gaa
5581	cg̃t̃c̃ct̃t̃gt̃t	cac̃gaag̃tcg	gg̃cg̃g̃caat̃g	cg̃tt̃ct̃gccc	gag̃cc̃gc̃gcg	tt̃tag̃att̃cg
5641	g̃ct̃cg̃tg̃cga	gt̃cg̃atac̃gc	ct̃gaac̃at̃cc	gc̃ct̃c̃act̃t̃t	gc̃at̃caat̃gc	tag̃cc̃g̃ct̃gc
5701	tg̃ct̃gag̃tg̃t	t̃cc̃g̃atac̃gc	cg̃ag̃ct̃cg̃cg	att̃tg̃ac̃gct	gg̃ct̃tg̃ccaa	cag̃tt̃gt̃t̃gc
5761	tg̃atact̃gcg	ac̃gc̃gat̃cag	gt̃t̃gt̃t̃t̃t̃gt	gg̃at̃ag̃ct̃gc	tg̃accaat̃gc	gt̃t̃ct̃g̃ccca
5821	tat̃gg̃att̃t̃t̃t	gg̃gc̃atact̃g	cg̃ag̃cc̃g̃ct̃c	gt̃gaat̃gaag	tgg̃g̃act̃gcc	tgat̃gg̃cg̃gt
5881	c̃ct̃cc̃ac̃ct̃c	gagaac̃gaca	ct̃gg̃ccaaat	g̃ct̃t̃c̃acc̃gc	caãagaac̃gc	aac̃gg̃ataac
5941	aaag̃tc̃g̃ct̃g	tag̃c̃g̃act̃aa	aac̃gcc̃ac̃gt̃	cgg̃aaat̃ct̃t	t̃cg̃cac̃caaa	at̃catt̃t̃gt̃a
6001	cc̃gaaat̃t̃ca	tt̃gt̃gt̃act̃c	cat̃cg̃cg̃tcg	t̃cgaagaat̃c	aaag̃g̃caacc	gac̃gc̃cg̃cca
6061	ac̃gc̃g̃ac̃g̃ac	t̃cg̃t̃c̃ct̃cta	c̃ctaacc̃aag	gac̃act̃t̃t̃cg	cg̃aaaaãac̃g	t̃cac̃gt̃gaag
6121	t̃cg̃at̃ccaac	gc̃gg̃g̃c̃ag̃ag	ct̃t̃att̃t̃gaac	cg̃ag̃cc̃gg̃aa	at̃cgaat̃gag	att̃gaac̃cg̃g
6181	gg̃at̃g̃ac̃g̃ca	cg̃t̃ct̃cc̃c̃ct̃	tt̃cg̃g̃ct̃gt̃t	cc̃ct̃c̃acc̃cg̃	tgg̃aaaat̃gg	att̃c̃gat̃gt̃c
6241	c̃ct̃ct̃c̃ct̃aa	tt̃gt̃tc̃ag̃t̃	ac̃g̃ct̃gaaga	g̃ct̃c̃gt̃g̃cca	tgaat̃t̃t̃taa	gacaac̃gat̃c
6301	ct̃t̃g̃ct̃g̃c̃g̃g	cc̃gt̃t̃g̃c̃gt̃t	t̃g̃c̃gt̃t̃t̃gt̃c	g̃cc̃cc̃cg̃aa	caat̃ccaag̃	t̃aaag̃ag̃c̃ct̃
6361	g̃cc̃at̃gaaga	cc̃aaat̃gg̃gc	cat̃t̃gt̃g̃att	cat̃g̃gt̃gg̃ag	cc̃gg̃c̃ag̃ct̃c	acc̃gg̃ct̃caa
6421	ct̃t̃gg̃cg̃ac̃g	cat̃cg̃ag̃taa	g̃caac̃gc̃acc	aaag̃gt̃ct̃gc	aac̃ac̃gc̃gt̃t	g̃caaacc̃gg̃t
6481	cg̃cg̃at̃at̃gc	t̃gg̃cg̃g̃ac̃g̃g	cg̃cg̃ac̃gg̃cc	at̃gg̃ac̃ac̃g̃g	tt̃gaag̃c̃cg̃t	gatt̃c̃gaacc
6541	tt̃g̃gaag̃ac̃g	at̃ccaat̃ct̃t	caac̃g̃ct̃g̃ga	cg̃ag̃gt̃t̃cag	tt̃gt̃g̃ac̃gaa	cg̃ag̃gg̃ac̃gc
6601	gt̃cg̃ag̃at̃gg	att̃cat̃cg̃gt	gat̃gg̃at̃gg̃c	aag̃ac̃act̃cg	cgt̃gt̃gg̃c̃gc	ag̃t̃t̃gt̃gg̃g̃
6661	gt̃g̃ac̃ac̃gg̃g	t̃caagaac̃cc	gat̃ct̃c̃act̃c	gc̃ac̃gc̃cg̃gg̃	tg̃at̃g̃ac̃aga	gac̃g̃aaac̃ac
6721	gt̃g̃ct̃g̃ct̃gg	tt̃gg̃t̃cc̃cg̃g	t̃g̃cc̃g̃ac̃g̃ag	tt̃cg̃cg̃g̃aaa	ct̃cag̃caag̃t	gc̃ct̃ct̃cg̃t̃c
6781	gat̃cc̃g̃aaat̃	act̃t̃t̃ct̃gt̃c	cc̃aac̃gc̃gat̃	gg̃cg̃at̃g̃ac̃g	cat̃cc̃ag̃cat̃	t̃g̃ct̃t̃cg̃g̃ca
6841	act̃c̃ag̃gat̃g	aag̃ac̃gaat̃c	gc̃at̃ct̃t̃g̃ga	acc̃gt̃c̃gg̃ct̃	gc̃gt̃c̃gt̃g̃ct̃	gg̃att̃cc̃cac
6901	gg̃caac̃ct̃cg	cg̃g̃ct̃g̃gaac	cag̃cacc̃g̃ga	gg̃cac̃ag̃caa	ac̃aaact̃gcc	agg̃t̃cg̃agt̃c
6961	gg̃tg̃att̃t̃cac	cc̃at̃cg̃t̃t̃gg̃	gg̃cg̃gg̃c̃acc	t̃ac̃gc̃gg̃cca	at̃gg̃att̃gt̃g	c̃gc̃cg̃t̃t̃t̃ca
7021	ggaac̃cg̃g̃cg̃	tt̃gg̃cg̃aaga	gt̃ac̃at̃cc̃gc̃	aac̃ag̃t̃gt̃cg̃	c̃gt̃at̃g̃ac̃at̃	c̃gc̃cg̃cg̃caa
7081	at̃g̃cg̃gt̃ac̃g	c̃gaat̃c̃ag̃t̃c	g̃ct̃cg̃ag̃t̃ca	gc̃ag̃t̃c̃acc̃g̃	ac̃at̃cat̃g̃ct̃	gaat̃cg̃act̃c
7141	gat̃cc̃g̃gg̃tg̃	tt̃gg̃cg̃g̃att̃	gatt̃g̃ct̃gt̃c	t̃ct̃c̃ag̃caag̃	gc̃g̃ag̃at̃c̃gt̃	gat̃gc̃ag̃cac̃
7201	aac̃acc̃c̃ct̃g̃	gc̃at̃g̃ag̃ct̃g̃	cg̃c̃ag̃c̃ag̃cc̃	gac̃ag̃c̃acc̃g̃	gac̃gt̃t̃t̃c̃ga	aac̃gc̃act̃t̃g̃
7261	att̃ct̃cg̃aca	ac̃g̃gt̃gg̃ag̃c	acc̃gg̃cg̃g̃aa	gc̃g̃acaac̃ca	aat̃caaacc̃c̃	at̃c̃cg̃cat̃cc̃
7321	gac̃gaat̃caa	ag̃at̃c̃ag̃g̃ga	ac̃cg̃at̃t̃cag̃	cc̃ac̃ag̃g̃cca	gc̃g̃at̃t̃gg̃aa	t̃cg̃cg̃g̃caac̃
7381	att̃g̃ac̃g̃ct̃t̃	t̃cat̃gaag̃gt̃	ct̃att̃t̃g̃gaag̃	ag̃cg̃at̃caac̃	t̃cac̃gt̃t̃ct̃c̃	ct̃cc̃gg̃t̃gg̃t̃
7441	gac̃gt̃g̃ac̃ac̃	gc̃gg̃att̃t̃c̃ga	cg̃cg̃ac̃att̃g̃	cag̃cg̃at̃aca	aagaac̃g̃ct̃a	cc̃cc̃act̃t̃cg̃
7501	gaaaag̃at̃gg̃	gaaag̃ct̃cac̃	tt̃t̃cac̃ag̃ac̃	ct̃g̃gaat̃t̃cc̃	tt̃cc̃g̃ct̃gg̃g̃	t̃aact̃cc̃g̃cc̃
7561	at̃g̃caag̃t̃cc̃	t̃cg̃gc̃gt̃t̃t̃g̃	gaaact̃t̃gat̃	c̃gaat̃gg̃ag̃c	c̃gat̃gg̃ag̃gg̃	caag̃tt̃c̃ac̃g̃
7621	ct̃cg̃t̃t̃t̃t̃cc̃	gac̃gt̃t̃t̃cc̃c̃	c̃gaag̃gt̃t̃gg̃	aag̃at̃cg̃t̃cc̃	ac̃g̃acc̃ac̃ac̃	ct̃caaag̃t̃cc̃
7681	cc̃cg̃act̃c̃gc̃	aat̃agg̃ag̃tg̃	aac̃g̃ac̃cg̃cc̃	gat̃ct̃t̃t̃caã	gc̃c̃ag̃aaag̃gg̃	aact̃cg̃ct̃ga
7741	tt̃cg̃t̃t̃t̃t̃cca	cc̃cg̃g̃ct̃cg̃g̃	gt̃gg̃t̃ag̃act̃	ct̃t̃cc̃g̃t̃cac̃	gg̃at̃c̃ag̃t̃gc̃	cact̃t̃caatt̃
7801	cc̃c̃ct̃t̃cg̃at̃	c̃gt̃g̃ac̃g̃ag̃c̃	at̃gg̃t̃t̃t̃t̃ct̃	g̃ct̃t̃t̃g̃g̃aaã	gg̃g̃ct̃t̃cc̃ca	ac̃gc̃gc̃gt̃cg̃
7861	gact̃g̃ct̃g̃ac̃	g̃ct̃gg̃cat̃gg̃	gt̃g̃at̃gt̃c̃ga	t̃ct̃caac̃caã	cg̃cat̃t̃cg̃ct̃	at̃cg̃att̃t̃t̃ca
7921	at̃cg̃ag̃ac̃gt̃	gc̃gg̃cc̃c̃att̃	ct̃ct̃c̃ag̃aga	act̃g̃ct̃t̃ccã	tt̃gt̃c̃ac̃gg̃g̃	cc̃gaat̃g̃c̃gg̃
7981	aat̃c̃ac̃gc̃ga	gg̃cc̃g̃ac̃ct̃g̃	cg̃act̃gg̃aca	ct̃caaacc̃gg̃	ct̃cc̃cg̃cc̃aã	gag̃ct̃ct̃cg̃g̃
8041	gaag̃cc̃c̃cg̃c̃	gg̃t̃cg̃t̃g̃ccã	aat̃g̃ag̃cc̃gg̃	acc̃aaag̃t̃gg̃	act̃gat̃c̃g̃ag̃	cg̃g̃att̃t̃t̃t̃t̃t̃
8101	cc̃g̃ac̃g̃ac̃cc̃	t̃gat̃ag̃t̃t̃t̃g̃	at̃g̃cc̃g̃cc̃gc̃	cc̃g̃ag̃t̃c̃g̃aã	ac̃g̃caag̃ct̃g̃	t̃cg̃g̃ct̃cat̃c̃
8161	aaaag̃t̃t̃cat̃	t̃ct̃caãat̃cã	t̃gg̃at̃c̃g̃cc̃g̃	aag̃gc̃gg̃t̃gã	tt̃ac̃gaac̃aã	cact̃gg̃g̃c̃ct̃
8221	t̃cat̃cg̃c̃acc̃	gact̃c̃ag̃ccã	ag̃c̃gt̃t̃c̃ct̃g̃	ag̃at̃t̃gat̃cã	ag̃cc̃cg̃c̃g̃ag̃t̃	t̃ct̃t̃ct̃cat̃c̃
8281	cg̃gt̃gg̃ac̃cg̃	ct̃t̃cat̃t̃t̃gg̃	aacc̃g̃att̃t̃gc̃	at̃gaac̃g̃ag̃g̃	t̃ct̃t̃g̃ag̃c̃ct̃	t̃cc̃aaaacc̃g̃
8341	ct̃gat̃cg̃ac̃g̃	cãact̃g̃att̃t̃	cg̃cc̃ag̃t̃ct̃	cact̃t̃g̃ac̃ct̃	gac̃gg̃g̃act̃c̃	cg̃cg̃cg̃ac̃gc̃
8401	cg̃gaac̃aag̃t̃	caatt̃c̃ct̃t̃c̃	tc̃caat̃g̃ag̃t̃	ct̃g̃ct̃ct̃g̃aã	t̃gc̃ct̃at̃g̃ag̃	cg̃gt̃t̃gg̃t̃cg̃
8461	at̃cg̃g̃ct̃g̃ct̃	t̃g̃ct̃t̃cc̃g̃aã	cag̃t̃t̃c̃gg̃cg̃	aac̃gt̃t̃gg̃gc̃	gag̃ac̃ct̃t̃gg̃	tt̃gg̃act̃t̃gg̃
8521	ct̃cg̃ct̃at̃gc̃	gg̃act̃cc̃aat̃	gg̃gt̃t̃t̃caag̃	ct̃g̃accaat̃t̃	gc̃g̃ag̃ac̃ag̃t̃	t̃gg̃g̃c̃ct̃at̃c̃
8581	gg̃g̃att̃t̃gg̃gt̃	cat̃caac̃gc̃g̃	tt̃gaat̃gat̃g̃	ac̃at̃g̃cc̃g̃tt̃	t̃gat̃c̃ag̃t̃t̃c̃	ac̃g̃att̃g̃aac̃
8641	aact̃cg̃cc̃gg̃	t̃g̃act̃t̃gt̃t̃g̃	cc̃gaat̃g̃c̃gã	cg̃at̃cg̃at̃cã	aaaat̃c̃g̃caã	cag̃g̃ct̃t̃ccã
8701	t̃cg̃c̃acc̃gt̃g̃	cc̃gt̃g̃caat̃g̃	t̃cgaag̃cc̃gg̃	c̃gt̃ac̃ac̃ccã	gaag̃aaaacc̃	gg̃gt̃gaac̃cã
8761	ag̃t̃cat̃cg̃ac̃	cg̃cg̃t̃caat̃g̃	cg̃ac̃gg̃cg̃ac̃	ag̃cat̃gg̃t̃t̃g̃	ggaat̃g̃accã	t̃cgaat̃g̃c̃gc̃
8821	gc̃ag̃t̃g̃cc̃ac̃	gat̃c̃ac̃aaat̃	ac̃g̃acc̃cg̃gt̃	cag̃cc̃aaaag̃	gaat̃att̃acã	ag̃ct̃ct̃t̃cg̃c̃
8881	gt̃t̃ct̃t̃caac̃	aac̃ac̃ac̃caã	t̃g̃gaag̃t̃c̃gã	aaac̃cc̃aag̃c̃	gg̃caaag̃gc̃g̃	t̃gt̃cg̃t̃t̃t̃gã
8941	ct̃t̃ct̃g̃gg̃gt̃	cc̃caaaat̃gg̃	ac̃ct̃g̃cc̃act̃	ac̃ct̃cc̃ag̃at̃	caag̃cg̃ag̃cã	at̃c̃gaag̃cc̃g̃
9001	c̃ct̃g̃caag̃cc̃	gaaat̃cg̃ct̃t̃	cg̃ct̃c̃gaag̃c̃	caaaag̃aaãc̃	gc̃gg̃t̃gt̃t̃ag̃	aag̃c̃ag̃gt̃gã
9061	tt̃t̃cg̃agaac̃	t̃gg̃ac̃ac̃ag̃c̃	aact̃ct̃caat̃	c̃gc̃gt̃c̃g̃ac̃	aac̃caac̃ct̃g̃	aatt̃c̃aaaac̃
9121	gc̃t̃t̃t̃caat̃c̃	gc̃ct̃cg̃gt̃cã	gt̃t̃cg̃ac̃cg̃g̃	t̃g̃ac̃gaag̃ag̃	at̃gaag̃att̃c̃	t̃cg̃at̃g̃accã
9181	gt̃cg̃gt̃ct̃t̃g̃	tt̃cac̃ag̃g̃cã	ag̃ct̃t̃cc̃cg̃ã	caag̃act̃gt̃c̃	t̃ac̃g̃ag̃at̃cc̃	act̃gt̃gat̃gã
9241	gatt̃cc̃cg̃cã	gat̃gt̃cat̃cg̃	gat̃gg̃aaaat̃	c̃gaag̃cg̃t̃t̃g̃	act̃cat̃cc̃gã	gt̃ct̃t̃cc̃cg̃g̃
9301	aac̃ag̃g̃cc̃cg̃	gg̃cc̃gc̃gg̃cg̃	at̃g̃cc̃gt̃cc̃g̃	gt̃cc̃aact̃t̃c̃	at̃ct̃t̃g̃ag̃t̃g̃	aatt̃c̃g̃ag̃gt̃
9361	ag̃ag̃att̃gt̃t̃	t̃cgaag̃gaag̃	gc̃ag̃cc̃cc̃ac̃	cc̃aac̃gt̃ct̃g̃	gac̃ct̃g̃c̃att̃	cag̃cat̃cc̃gc̃
9421	cg̃act̃att̃cc̃	cag̃cc̃cg̃cat̃	gg̃aac̃gt̃cg̃c̃	caac̃gc̃cc̃at̃c̃	gac̃gg̃gt̃gat̃c̃	t̃caaaac̃gg̃g̃
9481	t̃t̃gg̃gc̃g̃att̃	gc̃at̃cg̃aaat̃	t̃ccaac̃aat̃c̃	gc̃act̃gg̃gg̃cã	cag̃t̃t̃t̃ct̃ac̃	tt̃caaac̃gc̃cc̃
9541	act̃t̃cg̃cc̃aã	ag̃t̃gaag̃act̃	caac̃gt̃t̃t̃cg̃	att̃cc̃g̃ct̃t̃g̃	gaac̃aac̃g̃ct̃	ac̃g̃gaag̃ag̃g̃
9601	cc̃gaac̃g̃att̃	gg̃t̃cg̃cg̃t̃gc̃	gt̃ct̃t̃t̃c̃ag̃c̃	g̃ct̃gt̃g̃cg̃gc̃	aat̃cc̃act̃cg̃	caat̃caac̃gt̃
9661	cccc̃gaac̃aã	gt̃cg̃cg̃aaag̃	c̃gg̃ccaag̃aã	ac̃ct̃g̃c̃g̃aaã	gat̃cg̃at̃ccc̃	cc̃ag̃t̃g̃act̃t̃

9781	gāttcaāaaa	ċtgaċgaagc	aaċtġgaatc	aacccaġccċ	ġcċaċċācgc	ttgtcatġgt
9841	ggagatggaa	gagccacgcg	aaacċtttgt	gatgcaacgt	ggcaactact	tgtcacctgg
9901	ggaccgagtt	tcaccgggga	cgccgatggc	tċttcatcaa	atgaacgagg	acċttccaaa
9961	gaatcgċctg	gggċtagcac	gttggttggg	cgatcccgcg	aatccgttga	ccgcccgtgt
10021	gacggċcaat	cgċtggtggg	ċtcaattgtt	tggċcagggg	atcgtagaca	cggtggaaga
10081	ċtttggaaacg	cagċcatcgc	caccgacgca	cccċgatttg	ċtcgactggc	tggċċċttga
10141	attggċcgaa	tcaggċttgg	cgatgaaaca	tgtċċtgaaa	acgatċgtga	tgtcggaaac
10201	ċtatcaacag	gactċċaaag	ttcgggcaga	tċtgatcgag	gċcgacccgg	cgaataaatg
10261	gtacgcgagg	ggaccgtgtt	ttcgcatgtc	agcggagatg	attcgċgaca	atgċtttggc
10321	ggċcagcgga	ttgċtċtċcg	caaaaatgca	cggtċċtċca	atcatgċċgc	atcagccgac
10381	gggaatttgg	cgċtaagtag	ggcggaacga	accgaagtgg	atcgċggcaa	cggatcaaga
10441	ċcgataccga	cgċggċgttt	acgttggttg	gċgacgċċc	gċacċttacc	ccagċtttgt
10501	gaatttċgat	ggċċċċgatc	gaagtċċttg	cgċtggċggg	cgċċċgagaa	ċcaacacgċċ
10561	gċtgċaggca	ċtgacattgc	tcaacgatċċ	ggċttacgtc	gaaatggċtċ	tċgċtċtggc
10621	aaatċgċatc	ttatgtgaac	accċtgacgg	gagċgactċċ	gatċgacttt	cgċcgċcatt
10681	cgaaatċgtt	ttgtċgagac	gaccagċċċċ	ċcaagaatċċ	gċtċggċttga	tgacgttċċt
10741	tgatgagcga	aagcagcacc	ttċattċċaa	tċċċgagċtt	gċċaagtċgc	ċgtttċgaga
10801	gċaatċgttt	ċcgaaċaaca	ċtgtttatċċ	atċċacagaa	gaattgggċg	catggttċta
10861	cgċċgċgaac	gtċċgttga	atttggacga	gacaatċacg	aaggactgaa	acċtċċċċgċ
10921	aaatċċċtċg	actċattgag	atgatċgtċg	aagatgaaaa	ċċtatċgatc	ċaaacaacga
10981	atċaatgtgt	ċcgċtċgċgg	agċaatgtċa	gċgaaccaga	cgċgtċgaca	actċtttċag
11041	cgċgċċggca	tgggċċtċgg	aggattċgċt	ċtgacatċgc	tgttċċagċt	tgaacaaaaċ
11101	gċagċgttċg	gacaggagaa	aatggatċċ	gċggċttggaa	ċacacċatċċ	agċtċgċgċċ
11161	aaaagtgtga	tċtatatċċa	ċatggċgggċ	gċċċċċtċgċ	atċtggatċt	gttċgatċac
11221	aaacċggċttt	tċgacggagċg	ttċgggacaa	ċtatgċċċgċ	atgagtċċtt	ċaacggaaag
11281	ċaattggċat	tċattċgtga	acaacċgaag	ttgtttggċa	ċċċċaacgga	ċcaagċtttċ
11341	ċaattċċaac	gttgtggaga	atcaggagċa	ċaaatttċga	acċtgatgċċ	ċaacċtacag
11401	acggtċgċċg	acgaattgtg	ċttċatċaaa	acgċtċgċata	cgċgacċaatt	ċaatċacgċa
11461	ċċċgċċċaaa	tgtgtttgtċ	cagtgttttċ	gagċgattċg	gċċggċċċag	catċggttċg
11521	tgggtċagtt	atgggatagg	aagtaaaaċ	aagaacċtac	cgċactttgt	ċacggtċatċ
11581	acgggtċaag	ttttgggagċ	gggċaacagt	gċatggggaa	gċggċtttċt	gċċaacċgtt
11641	catċagggaa	ttgaattċċg	ċagċċaggg	gacċċggċċċ	ttttċċtatċ	taatċċċgag
11701	ggċatgċggċ	cgċċggacċg	tċgaaagggt	gtċgatgċċg	tċaaggatċt	ċaatgċtttg
11761	cggttggatg	atgttgggtga	ċċċtgaatċ	tċgacċċgċa	tċagċċaata	cgagatggċċ
11821	tatċggatgċ	aaacċċċċg	tċċċgagtċg	atgaacatċg	ataatgaac	ggċċgacgtt
11881	catċagatgt	atggċacċg	acċgggaaaa	acgagċttċg	ċcaacaattg	ċċtċgċċċ
11941	cgċċgttttg	tċgaacgtgg	agtċgċttt	gtacaactgt	tċgacċaagg	atgggacċac
12001	catggaacaa	tċgagaatċg	ċttggċggċa	aagacgaaag	aagtggatċa	acċgatċgċt
12061	gċgttgatċa	aagatċtċaa	acagċgaggċ	atgċtggacg	atacgċtċgt	ggtċtgggċċ
12121	gċtgagtttg	gtċgċactċċ	gatggċacag	gċgagċaacg	gtggċggċac	gċċgacgaaa
12181	gtċggacgag	atċacċacaa	agaagċttċ	acgatċtggg	tggċgggċgg	cggaacċaaa
12241	gċtggtċaca	ċċċatggċg	gacċgatgaa	ċċggċtċacg	ggattgtaga	aaatggċgtg
12301	ċacatċċatg	acttgaatgċ	ċacċattċċt	catċtċgċtag	ggatċgatċa	ċcaaagactċ
12361	acċttċċgċt	acċaaggacg	ċcagttċċga	ċtċacċgacg	tacacggaaa	cgċċgtċaac
12421	gacatċatċa	gttgatgċċt	ttgaaacggg	ċattċċggag	agtċċatċat	tagggċaact
12481	gċċgagtgat	cgtaagtċċg	ttċaattċaa	tċatggċacċ	ggċttggċtċg	gttċgċtċga
12541	aagċgatċgt	tċgagacċċg	gċggċaagg	ċaacgactċċ	gagtgaatgċ	tgttgaatgċ
12601	tċagċattċg	ċcgaggagċt	gċċttggaat	ċcaaatċag	acggacaaċg	ċtċttċatċg
12661	tgaatċgċgg	ċagċgttgtg	gtggċċtċċt	ggċtċgċċgg	ċttċagċaca	atċtċgċċċg
12721	aatċċgaatċ	gċaaacgtag	tgaatċacga	ċttċgtatċg	accactċtċt	ttċacċtċaa
12781	taggċċaagt	gattċgggtċt	cgċgtċgttg	tċċagċgatċ	agċċċaactg	tgtgċċċacg
12841	aaattċċatċ	cgċaaacċċg	acgċċgċċt	ċcagċttċgċ	atċċacagċg	ggċaagtaaa
12901	cgċacċgċat	cgaaatċaatg	ggċacċggċċ	gaatċgċgtg	gataċtgggt	gtaattċċċt
12961	gaacatattt	ttggatċgtċ	gatċgċaact	gċttċgċtag	ttċċggatga	ċtċgacċgċa
13021	tatċgggtgg	ttggċċggċg	tċggċtċgtċa	tgtċgaacaa	agacċċttċ	gacttċtċaa
13081	tċgtċaatċg	gtgagtattg	gttċgċacċg	ċċgċċttgċċ	aaacttċtċg	aatgtċatċg
13141	gattggggċg	gtaggtċag	atċgaacgat	cgċgaagtgt	gggatċggċċ	ċċatċgċgtā
13201	tċaattċċag	ċagċtċċtċg	ċċgtċċagċg	gċacċtttgt	cggtāaaggā	atatċacacċ
13261	actċgatċag	cgċċggċaac	agatċgatgt	gagċċgċaac	ttgċgaaatg	tttċgċgċt
13321	gaatgtttċċ	tgtċċaacgċg	atgaaacaa	gċacgċggċa	acċtċċttċg	tgaacċgtċg
13381	ċtttgggttċċ	tċgċatgċċa	ċċgttgaaac	gċttċċċatt	gggċċċgttg	tċggċtagaa
13441	acacgacgat	ggċtċċċtċa	tċċaacgaat	ggċtċċgaa	acactttagċ	aatċgagaca
13501	ċattgggtgċt	gatgttċtċg	accatċgċgt	agacċgċtċg	tgttttċtċg	tċgatċgaac
13561	cgċċgttċga	tċgatċgaat	aaatċtċgċt	tċacċtgaaa	cgċacċatgċ	ggċgċgttga
13621	acgggacċga	gċaaaagaat	ggacggċtċg	gatggtttċg	aatgaactċċ	acċgċgċat
13681	cggtċaacac	gtċċgtgatg	tatċċċttg	tttċgactgg	cgċgċgttt	cgċtċċaaca
13741	acċgatċgċt	gtacagattg	aaatggċċgċ	cgċgaaacċ	aaagaactċa	ttāaacċċtt
13801	gtċċgttċgg	gtċgacċggċ	atttgggċac	ċattgtgċċa	ċttċċċaaag	ċagċċċgtċg
13861	ċatatċgċgċ	ggāacgataċ	aatċċggċga	gċgttċgtċt	ttċċgtċtċt	atċactċċac
13921	gċċttċċggt	gacacċggċg	actċċċgagċ	gttċgggata	acgtċċċgtċ	agċāaagċċg
13981	ċċgtgtggg	agċgċāaaca	ggagagacat	aaaagċgtċ	ċaacċtċgċa	ċtttċattċg
14041	ċcagagċatċ	gagċgtċggā	gttgagatċt	ttggattċċg	gtċgċċgċċ	aaatċacċċċ
14101	aaċċttgggtċ	gtċċgtċāaa	atċāaaagċa	ċattgggacg	atċggaagċċ	tċtċgttggā
14161	tċgaagtċċċ	tċgacċgatċ	acgaagagaa	ċċatċacgac	ggtagċāaa	atċttċtttg
14221	ċāāāāāāat	cgċtċtttċgċ	attċtċgattċ	tċagtgtċtċ	ċaggattggg	ggggċggggg

14341	gċgaġcācag	tgttāgactt	tcaāccāctt	cċtttggttc	ācacaāaage	aaċcāaccāġ
14401	ggctctcgaa	tttcccagat	tgatcgaatc	cgaagcccaa	cttgacgcac	tgctcgcccg
14461	gccatcgga	gagttggtga	agttcatgca	acaactcgat	ggcgacctga	tcatcttggg
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14581	agggctgcaa	aagaacgttc	tcggggtggc	tcgcttttct	gatgcggacg	ctcgcgctcg
14641	cctggaatct	gctggcatca	agacgatcca	gtgcgatttg	ctcaaccgag	aagcgggtggc
14701	caacccttct	tcctgtgcca	atgtcctggt	catggccggg	cgtaaatttg	gcaccgaggg
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14821	tcgcgattcc	aacatcgttg	cgttttccac	cgggtgtggt	taccgcgtgg	ctcgtttgga
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15421	cgacggatcg	tattgaaccg	atgcagatca	gtgacttata	accaccatt	cgcgaaaatg
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15901	acttgcaacc	ggcgcgtcgt	ggttgtgtgt	tgccgtatga	attctggcgg	gagttcgctg
15961	agattgagaa	cgtcatcgca	atcaaactgg	ctcccttcaa	ccgctacca	actttggatg
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16441	gtgtgatcgc	cgcctaccct	cacctccatg	acaacgcatt	cgtacgcgaa	aatctgagcc
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16561	tttactgga	acagcgagat	gcaaccgatc	cgatcctgga	cgaaccacct	tttgatgacg
16621	cttgtgatgc	tgctggttgc	caccgcgggt	tcggcgggcg	atcgcccaaa	catcttgctg
16681	atcgtttcgg	atgaccaggg	gtacaacgac	ttgggtcaac	tcggcaacgg	aatcatcaca
16741	cccgcctcgg	atcgacttgc	caagggaaggc	acacgactga	caaatttcta	tgtcgtttgg
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17041	cagcgaatgc	tgccaacatc	gcgcggcttt	gatgatttct	atgggttcgt	gaacactggc
17101	attgattact	tcacgcagca	cgatcacggc	gtgccctgca	tggttcgtaa	cctcgaaccg
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29041	caatccccct	ccatcgaaatc	ggcḡgtgacc	gaggacattt	cacccgacga	acgggacggt
29101	ttḡctggctg	aattgattgt	cttggatgtc	gactatcggc	ggcgacgatc	cgagagcccc
29161	aacgagcaag	actacctgga	tcḡctttccc	gacaacḡtct	cagtcactccg	cgacḡctttc
29221	cgcgggaacg	accaacccaa	gcgagccttc	ctgcccḡctt	cggttgaaca	actgagtḡag
29281	caattccccct	cḡttgcagat	caccgaacta	ctcggcgacg	gcggaatggg	tgcḡgtctac
29341	aaagcacgcg	aggaaggḡct	cḡatcgcḡtc	gttḡctctca	aaatccttcc	cgaagaattt
29401	ggtcacgacg	tcaagtttgc	gttgcḡtttc	actcḡtgaag	ctcgcacḡct	cgcgaatttg
29461	aaccatccca	acatcḡtctc	ggtctatgag	ttcggacacg	tcgatgacac	gtactatttc
29521	ttgatggaat	acḡtggacgg	gtcḡacḡctg	cgḡgatgtḡḡ	tcgḡḡccḡḡ	tcagctcḡct
29581	cccḡctcatg	cactggcgat	cḡtgccḡcat	ctttḡcḡacg	cacttcagta	cḡctcatḡac
29641	aacggcḡtta	tccaccḡgag	catcaaaccḡ	gaaaacattc	tgatggcḡgt	cgacḡḡttcḡ
29701	gtaaaaattḡ	ccḡacttccḡ	acttttcḡga	atcctttḡḡḡ	atcaagacca	accttcḡḡḡḡ
29761	ctcaactḡga	cccaccagat	catgggcacc	cgcḡḡgtaca	tggcaccḡga	acaactcḡaa
29821	ggtgcccḡtg	gagtcḡacca	tcḡcḡccḡac	atttattcḡc	tcḡḡcḡtḡḡt	cttctacḡag
29881	atḡctḡactḡ	gtḡaacttcc	aatcḡḡtḡct	ttcḡcḡḡttc	catcḡaagaa	ggtccagatc
29941	gatḡttcḡat	tḡḡatḡatḡt	tḡttttḡaga	acḡctcḡaga	aggaaccḡca	acḡtcḡḡtat
30001	cagcḡagcca	gccaaatcaa	atcḡḡacḡtg	caatccattḡ	cctcḡḡḡtḡa	ccḡtgccḡca
30061	ttḡḡcaccca	ctcaagtcat	gccatcḡḡat	ccccacḡtg	atcatgcccc	ctcḡtctcḡ
30121	ggcḡcccacg	accaggaaat	cgcḡḡḡccḡa	ttḡttḡttḡa	cccḡccḡcca	actcatḡḡag
30181	cgḡḡtcḡaat	catcḡctḡcḡ	acctctḡttc	gccḡḡacagḡ	tḡcttcagat	tttcḡtcḡḡc
30241	ḡtḡḡcactḡa	tcḡccctḡḡḡ	agcctactḡc	tḡḡḡḡccca	acacḡcatḡt	gccacatcḡa
30301	ttḡttcagcḡ	gcḡtḡatcḡt	gcacḡtctat	ḡḡtttḡctḡc	tḡatcattḡt	ḡḡctḡccaac
30361	ḡttttḡḡttc	ḡaatcaaacḡ	cḡtcḡacacc	tcccaaccḡa	tcaacḡaaat	ccḡtḡaaagḡ
30421	ctḡaatḡcag	tcagaagctt	ctcacttccḡ	ḡtcḡḡtcḡga	tcatcḡḡaat	tcactḡḡtḡḡ
30481	ttḡatttḡga	tcccḡtḡct	cḡtcḡccḡca	ḡḡattcḡatt	ccatcctcca	tcccaactca
30541	ctttatccat	cḡctḡatcct	ḡḡḡtḡtḡatc	ḡḡactcḡttḡ	ḡctcḡtḡcḡḡ	ḡttḡtacḡcḡ
30601	atḡḡcḡatḡa	aatcagaacc	ctḡḡcḡtcaa	aaactcḡḡcḡ	ḡḡcḡaagḡtḡ	caccaatḡcc
30661	ḡagcḡagagc	tcḡccḡaaat	cḡagcaaacc	aacatccḡct	ḡatttctagc	ttctagcttc
30721	tagcttctag	cttctagctt	ctagctactḡ	ḡctactḡḡct	actḡḡctact	ḡḡctactḡḡc
30781	tactḡḡctag	tḡḡctactḡḡ	ctactḡḡcta	ctḡḡctactḡ	ḡctactḡḡct	actḡḡctact
30841	ḡḡctactḡtg	ḡctctḡtḡḡc	tctḡtḡḡctc	tḡtḡḡctctt	tccactctca	aacaacccca
30901	ccatttgccc	gcagcḡtttḡ	accattcacc	caagaccat	ccḡḡaccḡḡc	caaaaaggac
30961	accacḡḡatḡ	cḡatḡtcatc	ḡḡḡttḡtccc	agacḡttcca	gcḡḡcḡacat	ḡttcḡttaac
31021	cḡatcḡatca	actcatctḡa	cttḡtḡctcc	agḡaaaagct	tḡḡtcḡcḡḡt	tḡḡḡccagga
31081	ḡcaacagagt	tḡaccḡtḡat	ctḡtcḡtcc	ctcaattcat	tcḡccagcac	agatḡcatḡ
31141	gcctccacag	cgcḡctttḡt	tḡcḡḡḡtaa	acaccḡtaat	tcḡḡcattcḡ	caatccḡatḡ
31201	acḡctḡḡacḡ	acagattḡat	caccḡḡacca	ccatcḡcḡaa	ḡtcḡḡcagḡc	cḡcttctcḡc
31261	atcḡtḡtḡḡa	aacacccctt	cagḡttḡaca	tcḡaccagcc	ḡagcaaaatc	ctcḡtcḡḡag
31321	ḡtctcagcaa	gcḡḡttḡcat	cttcagaacḡ	ccagcḡttḡt	tḡaccaacac	ḡtccaccccg
31381	ccaaacḡact	ccḡtcḡcḡaa	atcaaagagt	ttctcḡaccḡ	cḡtccḡagtc	actcacatcḡ
31441	ḡcttḡaaatḡ	actḡtḡccḡa	accacctḡct	tctḡtḡatḡc	ḡttḡḡḡtcḡ	ttcatcḡḡcc
31501	gccttḡḡaac	tḡtttḡcḡta	ḡttḡatcaca	accḡaaaatc	cḡtcḡctcḡc	caatcḡttcḡ
31561	ḡcaattḡccḡ	caccḡatccc	gcḡtḡaccḡa	ccḡḡtḡacaa	tḡḡcaacccḡ	ḡttḡtḡttḡ
31621	ttcatttḡaa	aatḡctttct	tcḡctagtḡa	aatḡttḡaaa	tḡatcctcaa	ḡtaatḡacct
31681	tḡcacccḡaa	ḡagtacḡccḡ	gccttttaca	ctatttcaac	aaaccaccc	ccḡttttcat
31741	ḡḡcacḡcḡtt	tctcctḡḡtc	aatctcttca	tḡtcccḡagt	cttacctctc	ctttctacat
31801	tḡctactcac	ttattttttḡ	cctttcḡcḡt	catccaatḡc	cactḡagccc	tccḡḡcḡtca
31861	cḡactcacc	aaacatcttḡ	atḡatctacḡ	ccagacḡct	cḡḡctatḡaa	ḡcactḡcḡḡt
31921	ḡttatḡacḡḡ	cctcḡatttc	gccacḡccaa	aactḡḡatḡc	ḡatḡḡcagcḡ	ḡaagḡtḡtḡc
31981	ḡḡttcḡatcḡ	ḡḡcctacḡcḡ	agccctḡtct	ḡcacaccctc	acḡḡḡtcagc	ctactḡacag
32041	ḡḡctḡtatcc	ḡtttcḡacat	tcḡcatcttḡ	ḡagtccatcc	ḡḡtacacaag	ḡḡaacacḡcc
32101	aaaaagtḡḡa	ctttḡḡaaaa	atḡccḡacct	tcccḡcaatt	aatḡcḡḡḡaa	ḡḡtḡḡḡtaca
32161	cḡaccagcḡt	caccḡḡcaaa	tḡḡcaactḡḡ	cḡactcttḡa	agtctḡḡcca	aaacatattc
32221	ḡcaacḡcḡḡ	ctttḡattcc	tḡḡtḡcḡtct	ḡḡcaaatttḡ	gcḡḡagacḡḡc	gaaaagacḡt
32281	cacḡtcatḡḡ	ḡaacccḡacḡ	tttcaacḡaag	acḡḡccatat	ccḡḡḡaagac	atccagcaac
32341	ḡatttḡḡtcc	cḡatḡttttḡ	ḡtcḡaccatḡ	tḡattḡatca	ḡatḡḡccḡag	gcḡcaagcḡt
32401	cḡcaacaacc	tttcttḡatc	atccacaatḡ	aattḡcttcc	ḡcacḡatcca	atcḡttḡaaa
32461	ccccḡagga	tcḡaagḡctḡ	aagcḡḡcaac	ctcḡtcttḡc	ḡcacatḡatc	ḡaatacatḡḡ

32581	acgtggtātt	cātgggēt̄gac	aatḡgcāct̄c	acgaggēt̄tga	cēt̄tgacaāt	ccgaaattt̄g
32641	gacaaccggg	ggaacaaaa	cacactcgtc	atācgcḡtgc	cggaaatḡtc	aacggcḡgca
32701	agttc̄gac̄ct	gaatgatḡcg	ggcactcatg	ttc̄cḡct̄gat	cgt̄ct̄gḡgga	ccḡccat̄c̄ḡg
32761	tacc̄cḡc̄cḡg	ccagḡtt̄t̄gt	gac̄gact̄t̄gg	t̄ggat̄gt̄c̄gt	ggat̄ct̄gt̄tc	cccac̄ct̄att
32821	gcgaatt̄gac	c̄ggt̄ac̄gaca	at̄cc̄ct̄gaat	cact̄gagḡgt	c̄gat̄gḡc̄cḡc	agc̄at̄cḡcḡc
32881	c̄gc̄gaatt̄ca	c̄gḡccaaacc	gggaaḡcatc	gt̄c̄cḡt̄gḡgt	gcacc̄ac̄ḡcḡ	att̄aḡc̄gḡaa
32941	aagḡaḡac̄ag	t̄ct̄gt̄tc̄gac	gḡtt̄cat̄gḡc	gact̄at̄cc̄ag	tcagāagḡac	caatt̄gt̄gḡg
33001	ac̄ḡcc̄cḡc̄ga	act̄ḡcc̄gḡcc	gaat̄cacc̄ag	c̄gḡc̄aḡc̄gaa	t̄gat̄gaac̄ac	ḡcc̄gaat̄c̄ag
33061	ct̄cḡc̄gt̄cc̄g	act̄cḡaḡaaa	gt̄tt̄tt̄tc̄gaa	c̄ḡct̄t̄cat̄ca	aaac̄gc̄ct̄cc	caḡtḡatt̄ga
33121	gaaac̄aact̄t	cc̄gḡḡac̄c̄ga	gat̄gaat̄c̄ga	caḡct̄c̄gḡtc	ḡc̄gḡatt̄acc	act̄cḡatt̄tc
33181	ac̄ct̄act̄t̄gc	t̄gaac̄aḡcac	gc̄agat̄c̄gḡt	gt̄gḡgḡact̄t	gt̄t̄gḡgt̄ct̄g	gc̄gt̄gt̄aaaa
33241	gt̄c̄aḡct̄c̄gc	c̄ggt̄gt̄cc̄gc	gt̄c̄gatt̄t̄ca	aac̄acc̄gt̄c̄g	c̄ggt̄at̄gḡct	gt̄ct̄ct̄ḡcca
33301	ḡc̄gḡcaat̄ca	acc̄aḡc̄gacc	ḡct̄gḡgat̄ca	agḡtt̄gaaḡt	t̄gc̄ḡaḡḡcca	acc̄acc̄cḡcḡ
33361	at̄gḡct̄tc̄ga	c̄ct̄cḡacc̄ag	tt̄cc̄att̄t̄gc	cc̄cḡct̄t̄cat	caat̄gc̄gaaa	aac̄gḡaḡat̄g
33421	ct̄gt̄c̄gt̄gḡc	c̄gc̄ḡatt̄gḡc	gḡaḡtac̄aca	aact̄t̄ḡcc̄cḡ	ac̄gḡgt̄gaac	gc̄gaatt̄t̄ca
33481	gac̄gc̄act̄gt	t̄gaac̄cḡtc	tt̄tc̄ḡct̄t̄t̄g	att̄t̄ct̄t̄cc̄ḡ	at̄agḡgc̄aḡg	gac̄gḡtt̄t̄gc
33541	cc̄gḡcc̄gt̄ca	t̄c̄gt̄cc̄cc̄gc	ct̄tc̄ḡct̄t̄cḡ	taat̄caāaca	c̄ggt̄ḡacc̄ga	aaḡaḡccaac
33601	t̄c̄gt̄tḡaḡca	gataāat̄gḡ	tt̄t̄acc̄gt̄ct̄	gḡḡct̄gaact	t̄cat̄gt̄gḡcḡ	tḡcc̄cḡcca
33661	cc̄gḡgḡat̄cc	ct̄tc̄ḡcc̄aaa	acc̄at̄gat̄gḡ	gt̄ḡaḡt̄gat̄g	gac̄cḡtt̄t̄gḡ	at̄ccaatt̄tc
33721	caāat̄cac̄ga	ct̄tt̄at̄cc̄at	ḡcc̄caāat̄ca	gḡc̄gt̄gāāaḡ	c̄gaat̄c̄ḡgt̄t	at̄c̄gḡgc̄gat̄
33781	gt̄cc̄cḡacc̄c	aḡtḡaḡc̄gt̄g	c̄ggt̄gc̄gt̄cc	t̄gḡc̄ḡgt̄t̄tc	caacc̄ac̄ḡcc̄	t̄gat̄cc̄cḡct̄
33841	gḡtḡacāaca	gḡgc̄at̄c̄gt̄g	tt̄cat̄aḡacc	t̄gc̄ac̄ac̄gḡc	gt̄tt̄ḡacc̄ga	acc̄gt̄ct̄t̄cḡ
33901	ḡcc̄aḡtt̄cat̄	acāac̄cḡt̄c̄gt̄	c̄gaḡcc̄acc̄ḡ	cc̄gat̄att̄gt̄g	ct̄ḡaḡaḡc̄aḡ	cac̄ḡct̄t̄cc̄c̄
33961	gt̄c̄ḡat̄c̄gḡ	tt̄ḡccāaḡt̄g	t̄gc̄c̄cāt̄cca	cc̄at̄c̄acc̄gc̄	t̄ct̄cḡacc̄ga	ccc̄ct̄tt̄t̄ca
34021	accaatt̄tt̄g	c̄ḡcc̄cḡt̄ḡga	at̄c̄gḡct̄t̄gc	ac̄ac̄ḡatāaḡ	cc̄gt̄ḡac̄ḡcc̄	gt̄t̄cc̄cḡct̄ḡ
34081	gaḡgc̄gt̄ata	gc̄ac̄gḡḡct̄t̄	gt̄tt̄ḡgat̄gc	at̄c̄ḡccāaga	acc̄cḡgḡtt̄ḡ	ct̄gt̄gc̄ct̄t̄ḡ
34141	ḡcc̄ḡccāaḡḡ	t̄cḡcc̄ḡḡact̄	caḡtt̄t̄ḡcc̄c̄	gat̄t̄c̄ḡgt̄gt̄	c̄gāāaḡt̄gḡc̄	gt̄gḡtaḡat̄c̄
34201	c̄ct̄t̄c̄gt̄c̄gḡ	cac̄cḡc̄ct̄cḡ	gḡgc̄gt̄t̄gt̄g	gt̄t̄cc̄aāacc̄	aaac̄gt̄t̄c̄aḡ	t̄gt̄tt̄cc̄cḡcc̄
34261	at̄cac̄cḡḡac̄	t̄cc̄ct̄t̄ḡcaa	aac̄gḡcc̄aaa	acāacc̄at̄gḡ	cc̄at̄c̄agḡcc̄	aaatt̄t̄cat̄c̄
34321	cc̄aāaḡt̄ac̄ḡ	ct̄cḡc̄gt̄t̄gt̄	t̄gt̄tt̄ḡct̄gḡ	t̄cḡc̄ḡct̄ca	att̄c̄ḡct̄ḡct̄	cat̄ct̄cḡtc̄
34381	t̄ct̄cc̄gat̄ca	t̄gḡtt̄ḡc̄gat̄	t̄ct̄t̄ḡc̄gt̄gt̄	ct̄gḡtḡaḡaa	aaact̄c̄gt̄t̄ḡ	aaḡgḡgḡcat̄
34441	catacc̄cc̄c̄aḡ	taḡgc̄gt̄ḡga	gḡḡaḡaḡaga	gḡaāaḡt̄gḡc̄	t̄caḡgḡcc̄ac̄	agḡgḡcc̄ac̄aḡ
34501	gaḡcac̄ḡaḡc̄	taḡḡaḡct̄t̄c̄	t̄c̄ct̄cc̄cḡtḡ	ac̄att̄ḡcc̄ga	t̄cḡgc̄ḡgt̄gḡ	t̄t̄gat̄ct̄aḡ
34561	gat̄ḡct̄c̄gt̄t̄	ct̄tc̄gāac̄ct̄	t̄t̄c̄ct̄ḡgaat̄	cc̄ḡct̄gt̄ḡct̄	t̄t̄caatt̄t̄tc̄ḡ	ccc̄ac̄ct̄att̄
34621	t̄ḡct̄gt̄act̄a	c̄ct̄ḡcc̄att̄ḡ	at̄c̄at̄t̄gc̄ga	t̄ct̄cḡt̄t̄gḡt̄	att̄t̄gḡtḡca	ac̄ac̄gḡc̄ac̄ḡ
34681	agḡat̄tt̄gt̄c̄	gt̄gat̄c̄ct̄t̄	c̄gḡc̄ac̄ḡc̄ct̄	t̄cc̄ac̄ac̄gḡc̄	c̄cḡct̄gḡat̄c̄	acc̄gḡct̄t̄ca
34741	t̄gḡc̄ḡgt̄c̄gt̄	t̄tt̄c̄ḡcc̄ct̄ḡ	gt̄t̄ct̄ct̄t̄ct̄	t̄gḡact̄gḡat̄	gḡt̄ct̄ḡaḡcc̄	gat̄ḡagḡatt̄
34801	t̄t̄ḡacc̄ct̄cḡ	gt̄gḡc̄gḡcac̄	gḡtt̄gḡac̄gc̄	t̄gḡat̄c̄ḡct̄ḡ	ac̄at̄ḡct̄gt̄ḡ	caḡac̄gc̄cḡḡ
34861	cac̄aḡt̄gt̄ca	c̄gt̄t̄ḡatt̄ga	caḡc̄ḡacc̄ct̄	gaḡat̄c̄gt̄t̄c̄	gat̄cc̄at̄caa	taḡc̄gaat̄t̄ḡ
34921	gat̄gt̄cc̄gḡḡ	caat̄c̄ḡagḡḡ	caac̄gc̄ct̄cḡ	caḡaḡc̄acc̄ḡ	t̄gt̄t̄gt̄t̄ct̄c̄	gḡcc̄ḡac̄gt̄t̄
34981	ct̄ḡaḡt̄gc̄cḡ	act̄t̄gt̄gc̄ct̄	c̄gc̄c̄gt̄c̄acc̄	gḡaḡac̄ḡac̄ḡ	aaḡt̄caac̄at̄	t̄gt̄c̄gc̄cḡcḡ
35041	aḡcat̄gḡcca	aaḡc̄act̄gḡḡ	gḡct̄cḡcc̄gc̄	c̄gc̄gat̄c̄ḡct̄c̄	c̄gc̄gt̄tt̄ac̄gc̄	ccc̄cḡc̄gt̄t̄t̄
35101	c̄gt̄ḡac̄ct̄gt̄	c̄ḡac̄gt̄tt̄t̄ga	ct̄accāac̄gt̄	cact̄t̄cc̄aaa	t̄cḡac̄aḡt̄t̄t̄	ḡct̄gt̄c̄act̄c̄
35161	gaacāact̄ct̄	cc̄ḡct̄tc̄ḡga	ḡct̄c̄ḡct̄c̄ga	gcc̄at̄cc̄ḡca	ac̄cc̄cḡat̄gc̄	gat̄t̄cc̄ḡct̄ḡ
35221	gaac̄act̄t̄cḡ	ct̄c̄gc̄ḡḡaca	act̄gc̄aḡgt̄c̄	t̄at̄gāaat̄gḡ	at̄gt̄c̄ḡcḡḡc̄	gḡḡct̄cc̄cḡḡ
35281	ḡc̄gḡc̄aḡḡca	agāaḡt̄t̄gat̄	ḡgaatt̄ḡcaa	ct̄t̄cc̄ḡcc̄ga	ḡc̄gt̄t̄c̄gt̄gt̄	t̄gḡat̄c̄ḡct̄c̄
35341	gc̄ac̄gc̄gāaḡ	taḡc̄gat̄gt̄ḡ	gat̄c̄ḡcc̄aḡc̄	gḡt̄gc̄cḡac̄ḡ	aaac̄ac̄ḡaḡc̄	c̄ggt̄ḡacc̄ga
35401	gt̄c̄aḡc̄ct̄gḡ	t̄t̄gḡgat̄ḡcc̄	gḡat̄gc̄cḡtc̄	aḡc̄gt̄t̄ḡct̄c̄	ḡcc̄aāat̄att̄	t̄gḡt̄gḡt̄ḡaḡ
35461	aaac̄gc̄cḡtc̄	ḡcaāacāat̄c̄	caaḡgt̄cat̄ḡ	at̄c̄gc̄cḡḡcḡ	ḡc̄gḡc̄ḡaāac̄	gḡgt̄tat̄cac̄
35521	t̄t̄gḡct̄gḡac̄	t̄ḡct̄c̄ḡgt̄cḡ	ḡgāaḡact̄t̄t̄	c̄gc̄acc̄gt̄gc̄	t̄gt̄t̄ḡgāaca	aḡac̄gc̄ḡaaa
35581	c̄gt̄t̄ḡc̄ḡaḡc̄	aatt̄t̄ḡcc̄aa	gt̄t̄ḡct̄gc̄ct̄	gac̄gt̄c̄acc̄ḡ	t̄gḡt̄ḡcat̄gc̄	caac̄gc̄ccaac̄
35641	c̄gḡc̄gc̄aḡcḡ	t̄tt̄t̄ḡgāaga	cḡaaḡgt̄gḡc̄	gḡc̄ac̄ḡgt̄cḡ	act̄act̄t̄c̄gt̄	t̄gḡtt̄gc̄acc̄
35701	gḡcaac̄gat̄c̄	aaāacāac̄at̄	cat̄gḡc̄gḡgc̄	gt̄t̄ḡaḡgt̄c̄	gc̄ḡaḡt̄t̄gḡḡ	c̄gc̄at̄c̄ḡc̄gt̄
35761	gt̄gat̄gt̄ḡcḡ	t̄gḡt̄c̄ḡac̄ḡ	t̄cc̄cḡatt̄ac̄	ḡcc̄aāc̄gt̄gḡ	t̄cḡḡaāaḡt̄	c̄gḡcat̄c̄gat̄
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35881	gcc̄at̄cat̄ca	ḡcc̄aāaḡcaa	att̄ḡcc̄aāac̄	gḡtt̄cc̄at̄cḡ	gt̄gt̄ct̄ac̄ga	att̄gḡaāat̄c̄
35941	ct̄ḡgāagḡat̄	cc̄ḡcc̄gt̄cac̄	ac̄agḡc̄gt̄cḡ	ct̄gḡcc̄aācc̄	t̄gc̄ct̄t̄t̄gḡc̄	gḡgḡc̄gat̄gc̄
36001	ct̄gat̄c̄ḡcc̄ḡ	c̄gatācāac̄ḡ	c̄gac̄gḡatt̄t̄	gt̄t̄c̄ḡc̄gt̄cc̄	caacc̄cḡcc̄aḡ	c̄gac̄gt̄ḡct̄ḡ
36061	gaaḡt̄caac̄ḡ	ac̄at̄c̄att̄gt̄	c̄gc̄ct̄t̄gat̄c̄	gat̄tt̄at̄cc̄ḡ	at̄gc̄cḡac̄ga	aḡt̄c̄ct̄t̄t̄ca
36121	ct̄ct̄tt̄tc̄aca	c̄gc̄ḡatt̄gat̄t̄	gt̄gc̄ct̄gt̄ca	cc̄ac̄gāac̄gc̄	t̄c̄ctāaḡcca	ac̄cc̄cc̄aācḡ
36181	ct̄gt̄tt̄gt̄gaa	c̄gatt̄t̄cc̄att̄	t̄t̄ḡcc̄ct̄cca	ct̄ct̄t̄gḡḡaa	t̄t̄cac̄ct̄at̄c̄	gc̄gc̄cḡaḡtc̄
36241	c̄ḡcc̄ḡacāat̄	c̄gt̄c̄ct̄ḡct̄ḡ	c̄gt̄tt̄t̄t̄acc̄ḡ	gc̄ḡac̄gat̄t̄ḡ	ccc̄gḡgt̄tt̄ḡ	acc̄gc̄gt̄cca
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36361	at̄c̄gat̄c̄ḡct̄	ḡct̄gt̄t̄aḡga	at̄ḡct̄t̄gt̄t̄cc̄	aḡatt̄t̄cc̄gḡḡ	caḡc̄gāaḡac̄	ccc̄gāac̄gc̄cc̄
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36661	gt̄ḡac̄gāact̄	gac̄gc̄gt̄ḡcḡ	t̄gc̄gt̄gḡaḡt̄	t̄ct̄c̄ct̄t̄ḡcḡ	agḡaḡat̄cc̄ḡ	ac̄gḡat̄gt̄ca
36721	ac̄ḡct̄ct̄caa	aḡcc̄aḡc̄ct̄ḡ	t̄t̄ḡgāatt̄at̄	ccaat̄c̄ḡct̄t̄	gaatt̄t̄gḡat̄	ct̄gḡcat̄gḡc̄
36781	aac̄gt̄gat̄ga	c̄gc̄att̄t̄c̄ga	c̄gc̄aāacc̄ḡac̄	gc̄at̄c̄gt̄c̄gc̄	ḡct̄c̄gat̄at̄ḡ	gat̄t̄c̄ḡact̄t̄
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36901	gt̄gc̄gat̄cac̄	c̄gaḡgc̄aḡca	at̄gc̄ḡaḡgḡc̄ḡ	aḡat̄c̄ḡact̄t̄	t̄gac̄ḡaḡt̄cḡ	ct̄t̄c̄gt̄c̄aḡc̄
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37021	aḡtt̄ḡacc̄ga	agḡt̄ḡcc̄ḡaa	c̄gatt̄t̄ḡct̄t̄t̄	c̄gaac̄ct̄ḡcḡ	t̄c̄gt̄tt̄t̄gḡc̄	t̄ac̄ac̄ḡacc̄ḡ

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45061	aaaccatggg	tattgccaga	cgcgttttcc	ggttcggaaa	tcaacaccca	acaaacgctg
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45181	ttgaccggtg	gcttttcagct	gctgtgtctt	ctcctgaatc	atccgttctt	ggcgagggtc
45241	ggtggacgac	tcacacatcc	atcgcggtt	gctcagtggc	atgtgaccgg	agcctgaact
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46561	agcgattcga	gcattcgaāa	caacaacaaa	cgatcaaga	cgcggggaat	gaatcccaga
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51481	tġġaagaga	ccġaagcggt	tġġttggcc	accġaaacca	ttggtgggtg	ttcġacggcg
51541	accġcġcġc	gatġtġġaāc	gggagcattc	tġcatġcggt	cġġaatcagc	tġgttccaac
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51661	ggagtcttġa	tttġcaccġġ	ctttġġcagc	cġcġġcāaag	tġgattcġtc	agtġġgttġt
51721	tccacġġġġġ	gagcġatctt	cġtcġġcacc	gcaattttca	ttġġctcagġ	catcġagacc
51781	aattcatcag	cġaccaagtġt	ctcġcccggt	tcatctġaat	cagāġaaact	cagcġāaact
51841	ġaatcġtctġ	catcactcaa	cġaatcġġtc	gġctcattġa	gġġāaaactc	aatcġġttct
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51961	tġġacttcġġ	ctġġctġcġġ	tġagactġġt	tcttġcacag	cġġġtġctag	aacġatġtct
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52141	acgttġġtġc	agacttġagc	aggcġtcagc	tcaacġatġc	cġtttġattc	agctcġatcġ
52201	taattġġtġt	gagcġtġcġġ	attġattctc	ġġcāaagġag	tccġġġctġġ	ctccacġacc
52261	aacġġtġtct	gctġcġtġcġ	gggagcacca	atcġġaagca	aaccġacagc	ġġtġccaatc
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52441	gtcttaccġġ	cġacġġtġca	tġctacġcca	gtcġġtġcag	cagġtġctc	cācāaacġġġ
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52561	tccġccaaca	ccġtġtttcc	ggcġacttġġ	ctcġcġġcā	tġcāaccacc	ccaaccāaaa
52621	ġcttġġġtca	accaacġagc	cagccttġcġ	cġtttġcġġc	agctġctcat	tġgattcġag
52681	cccġtġġġt	tcatġtġctt	ġccaatcagc	atġġcġġatc	cttacġctca	cġatctttta
52741	ġġatcatġta	ccccccġġc	acattttccġ	cġtcġttġġc	cġagtġāaat	tatccaccġġ
52801	acctccġāac	accctctġta	tġgtcġtcġġ	gtġġttccġġ	cattāacġat	ttġccagat
52861	cġāacġtttġ	gttctġctġġ	atcġġtcttġ	acacagatāc	ġġcttġġacc	agctcġccc
52921	actcġttġa	ġcġġāaacġc	tġagccacca	ġcġagġcġat	acġtġttcac	aactcġġctġ
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53221	cġcttġcġtġ	cctāacacca	ccġccactt	tctcġcāaa	tctġaatcġa	aagġġġccġ
53281	cġagccttcc	actcġcattġ	ctġccacġcġ	ġtagccatġt	gttttcagġa	atġcctccat
53341	ctġcġattcġ	ctccccġacġ	ccġacġġaac	ġġtġaacacġ	ġctcccaatġ	atccacġaat
53401	cġcġttġġġā	ttġaatcġat	ctġagġġaca	atccġacāac	aggaccġctġ	atācġcctġc
53461	cġcatcġġcc	ġaacġāaaca	ctġccccā	attġccagġt	ttctcāactc	gatccagcac
53521	cāagatcāac	ccġtcatctc	atġāāaagc	ctccāāaagc	tġctccagcġ	aatcġtccġġ
53581	agccācāaac	tctġctācac	agcġatccġt	cġāagccġtġ	taagcġattt	tġcġāaacac
53641	ttctġacġtġ	accacġcġat	ġcactcġġā	atcāatcġcġ	tġctġccttġ	cġacġġcctġ
53701	ctcġġġcātā	tccġġcġġcc	ccġccġattc	ġġatagtttġ	ġġttcġatct	cġtagāacġc
53761	cġtcagtttġ	aaccġcġcct	cġatcġctcġ	cagġġactct	cġtġġġccat	cġaccāāaac
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53881	attttġcagā	cttcġtatġġ	tttccatġġġ	ġcāacacttġ	tġcacattcġ	cttcġatġġġ
53941	āġāacāacc	cġagtctġct	atcttctāac	gtttġccāaa	cagcttctct	ġctaccaacc
54001	cctġaacġct	cġaatġtccġ	āāaatġtġtt	ġtġccāacc	gtttccġġac	ġccaagacca
54061	āaagġcattt	ctcġatctcġ	āāaagcġtct	ctacagcġac	gatccġaact	ġġġtġccġcc
54121	ġctatġġagc	ġaacġġġtca	aattġġtġcġġ	attcāagcac	caccatttt	acġatāacġc
54181	cġāagġccā	acctttctġġ	ttcġtġtġġ	cġatcġtġtc	ġtcġġccġġġ	ttttġġcġġt
54241	cġtcaatcac	ġccācāacc	ġctaccacġa	cġagactcġc	ġġġttcttġc	ġcttcttġcā
54301	atġcġagġac	ġatġāagagġ	ccġccatcġa	acttctcġac	accġccġġcġ	actġġttġā
54361	ġcāacġcġġġ	atġacctġġġ	tācġcġġcc	ġġttcaccc	agcctġāact	acġāagtġġġ
54421	actġttġġtt	ġatġġcttġc	acacġccġcc	ġactttcttġ	atccctācā	accatccġtā
54481	ctacġāacġc	ctġattcāag	ctġctġġatt	tġāāagtġcġ	cagġatctct	acagttacġa
54541	agcttcġatc	ġacatcctcġ	āaacġctcġa	cccġāaactā	ctġtttġtca	tġāāāatc
54601	ġacġcġacġt	ttcāatġcġt	tġtġccġttc	ġatcġacccġ	āāāacttā	acġcġġacġt
54661	ccġagtġttc	ctġġacatct	acaaccaatc	actġcagcġa	acttġġġġct	acġtccġġat
54721	ġagcġāagcġ	ġāagtġatġ	accāāagcā	cġġtctġāā	aacctġcġtġc	ttccāaact
54781	caccagcatc	ġccġāaatcġ	atġġcāaac	cġtcġġtġcc	ġġttttġġtc	tġctġġactā
54841	caaccctttġ	atcāāāāāā	tcaacġġġā	ġctġcttcca	ttcġġttġġt	tāāāactttt
54901	ġatġġġacġc	āāāāactcā	agcġtcttġc	tttġġtġcagc	ġccaatġtġc	taccġagatā
54961	ccaāāaatġġ	ġġtctġġġtt	tġġtġcagct	ctcāāāaat	ttġccġġāag	cġatcāaat
55021	tġġaatcġā	atġġġtġagt	tctcttġġġt	ġctcġāāagc	aatcāacttt	cacġagġtac
55081	ġatcġagcġc	ġġtġġtġcā	cccġāagcā	aacġcacġcġ	atttatġatc	ġatcġtġac
55141	accġġaatcā	ġāacagġcat	ccacġtġagc	ġāaccactct	cġatcġattc	ġatattġġġc
55201	cccġġcġġcā	ġcatcagccġ	acġactacca	cġctacġāac	ctcġcġāaca	ġcagctcġag
55261	atġġctcġtt	cġġtctcttc	ġġcattġacc	ġaccġcġagc	atttġġtġcġt	cġāagcagġc

55381	caāācagaaġ	ċgggġtċgca	aāaacccaag	ċgtġcgtċg	acgatgtcġa	tgatcgtātt
55441	ggccccgctg	gtgatcggga	caaagaatcc	gatcggccaa	aacgcgtcct	gatctcaaca
55501	cacacgatca	gcctgcaaga	acaactgatt	ggcaaagaca	tcccgtgctg	caatagcgtc
55561	atccccacgag	agttttctgc	ggtgctggtg	aagggccgca	acaactactt	gtcgctacga
55621	aggatgggac	gāgcggtcga	gaaatcagtg	tcattgatgg	ccaatgattt	ccaaatgcag
55681	cagcttcgcg	aaattcġcaa	gtggtccgac	aacactcctg	acggctcgct	ctcaacattg
55741	ccgatcaaac	ccgacggtca	ggtttgggac	gaggtccgca	gtgacacggg	caattgcctt
55801	cgcaataaat	gcccgaactt	caaggactgc	ttttacttcc	aagcccgcag	ccgtgccag
55861	aacgcacaac	tgttgatcgt	caatcacgcg	atgctgttca	ccgacatcgc	aatgcgcagg
55921	caggggtgtt	cactgctgcc	tgactacgac	gcgatcatcc	tcgacgaatg	ccacaccatt
55981	gaatccgtcg	ccagtġacca	cctcggcatt	cgattġacca	gcggccaatt	tgattacctg
56041	ttcgaccgtc	tctacaacga	ccgccaacaa	aaggggttgc	tcgtcgcgca	caacctggat
56101	gcgttgcaga	agatggtcga	ccgatgcġgg	tttgcgġcca	gcgaaatgtt	tgccgggtgtg
56161	ctggactgga	tgcaagaatc	acgctctcgc	aacggccggg	tgcatcatcc	cgaagtgggtg
56221	cccaaccġgc	tcagcġaacc	gatggagatt	ctcgtcġggc	ggctgġgtgc	tcacgġcġac
56281	gcacaagaca	acgactcġga	tcgġcaagac	ttccaatcġg	ctcacgatcġ	acttctcġcc
56341	ttggccgggtg	gccttcġcġga	atggctcġac	caatcġctca	aacaagaatc	ggtctattgg
56401	gttġaaacct	ccggcagcġg	tcgġcġaatg	gaccġagtct	ctttgtcġgc	ctccccaatc
56461	gatattggcc	aaacġcttġg	cġaġaagtg	tttcġaagtg	aacaaattgg	ctccgtcatc
56521	atgaccagtġ	ccacġttggc	gaccġġcġaa	caagacaagt	tcaaattctt	ccgcagtġgc
56581	gttġgcctġa	cġactġgġcġ	ctcactcġaa	gtcġġcagcc	cġtttgatta	tgagaagġaa
56641	gccaagctġa	tcatcġttcġ	tggactccct	gatccatcag	cġaaacġaga	cġaattcġaa
56701	gcggcġcttc	cccaacaaat	caagcġattc	gttggacaca	ccgatġġcca	cġcġtttġtg
56761	ctgttġacġa	gttactcġtt	gcttcġcaaa	tgtgtġagg	cgatcacacc	gtggtġcatc
56821	gaacġtgacc	tġcacttġta	cagccaagcġ	ggcġatcaaa	accġaacġca	actġctcġat
56881	tcattcġcġa	aagatccacġ	tggcġtgctġ	cttggcaccġ	acagcttctġ	gcagggagtġ
56941	gacġttcctġ	gcġacġctct	caccaacġtc	gtgattacġa	agctġccġtt	ctctġttccc
57001	gaccatcġcġ	tactġġaagc	acġġctagaa	accatccġcġ	cccġcġġcġg	cccccattc
57061	cctġactacc	aatġġcccġa	agccġtgatc	aaattcġġgc	aagggtttġg	acġcġgatc
57121	cġcacccġcġ	atġactcġġg	aatġġtcġtg	gttctġġatc	cacġaatccġ	atccaaacc
57181	tacġġccġac	ttttcctcag	cġcacttccġ	cctttġccat	gtcacġatgt	cġġcacġġtc
57241	ccacġacaaa	agacaaagaa	ġcaatġagca	agcġcagttc	ġcttattġġa	tgtġtġcagġ
57301	aaccġttġcġ	aatġcġatġc	agtcaaagcġ	ttġatccġcc	aaggggtġaa	gttttcġcaa
57361	ġctttatccc	ġaagġġattġ	cagacġġtag	ccġgtġġtt	ġaacġcagtg	aacaccaccġ
57421	gattcatġcc	ccttġġġcaa	tttcġcacc	tġaagġġġtc	ġtagaġactt	cġcaccttct
57481	agggtcagat	cġagtttttc	gtttccġggg	gtġcġgtġct	acġcġġcacc	ctccġcccac
57541	aatctġtgat	cccttccġag	atġcagaaaa	ġctġaagtcġ	ġaatcaaaaa	aaagtġagcc
57601	atacagaaġt	cġtġtcccac	ġagcġaacġc	cacaatġatc	caaatcatġt	ttcġcġatġt
57661	ġgattġġttt	cġaacagġtc	catcġatcġc	tġcaccttca	tcġagtcaag	ccġtġcatt
57721	cġaccaagġt	catccġccat	cataccġġca	tcġatġġaca	cagġtġcġt	cġġaaatatt
57781	ggcġcttġġ	cġttagccac	ggtttccġcġ	cctaacġġgc	tcacatcġtt	atġccġatc
57841	atttctġacc	ctatttġagcġ	ggcġacatca	atttcccacc	accaaatttc	ġatttġġtat
57901	ccaatġggġt	cctccatcġc	tcttcttġtc	ccġtttġġtt	tttcctaatġ	cġtctcatcġ
57961	ctctaccġct	ġatcġtgctt	ggctcġcġtg	ctccctġtct	atctġccġaa	cagaaatcġt
58021	tġacġattca	gtġġttcġaa	cttġactcġa	cġġagcagcc	cġaactġacġ	aġaagctġġ
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58201	cġaccaaaat	ġġacġacacc	acattcaaāt	tġaacttġġa	ġġtccaacct	gcagatcagġ
58261	ġaagctacac	ġttccatġtc	acctcctcġc	tagaaactct	cġcacccġġġa	aagġacatcġ
58321	cccġacġaac	cġcġataaga	aagġtcġact	cġġcattcaa	actġtctcca	ġġcacġagct
58381	tcġtactġac	aggcctġġag	cġaagcġġac	gtġaaagagc	aatcacacaa	gtġctġġtcġ
58441	ttcġcttġca	agġttttġcc	ġaagaacaaa	ctġtagaaac	ġġttcaaaat	ġġġctġġaac
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58681	tcġcġacġac	tġcġattacc	cccaagcccc	aaagtġaaga	aacaataaac	gtttagcġtg
58741	agattcatġa	accġġcġtac	caaagccttc	ccġcġaagca	ġagcatcact	aagctcagġc
58801	ġattġacttc	tccagtgctc	ġacttġġatc	ctġaacġatġ	tccġtcactt	cttctġcttc
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58921	cġġatġcġġġ	ġctttcctġc	atġagaaatġ	tġttcagtgġ	ġġcġactcġġ	taagcctġac
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59041	ġġaacaagag	accaaactct	ccġatġcġġt	ġġccġccġtg	aaatġccacġ	agtacġaacġ
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87001	gtacgcagaa	aaagtcaccc	cacgcgggga	agcagtttcc	acgaacgagg	tcgcgtcaac
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87121	tgccggcatg	tccatcaact	attttgatgc	cgacgtagtc	ggagcgggtca	ccaacgcate
87181	ggctcgactga	aaccgggttc	ccaagctgag	ttcgccact	caccgacaac	acacatccat



87301	c̄t̄t̄c̄t̄c̄āc̄ḡc̄	gaagac̄ḡc̄c̄a	agatc̄ā̄ḡt̄ḡt̄	c̄t̄ac̄gat̄c̄ac	ggact̄ḡc̄t̄ḡt̄	ac̄ḡḡc̄ḡac̄ḡḡ
87361	c̄ḡt̄ḡt̄t̄c̄ḡaa	gḡgat̄ḡc̄ḡḡa	t̄c̄t̄ac̄t̄c̄ḡḡḡ	caāaḡt̄ḡt̄t̄c̄	gc̄act̄c̄ḡaāḡ	acc̄ac̄at̄ḡac̄
87421	ac̄ḡḡc̄t̄c̄t̄ac̄	gaāaḡc̄ḡc̄t̄c̄	ḡt̄ḡc̄ḡat̄c̄at̄	ḡc̄t̄ḡḡac̄at̄t̄	ccc̄at̄c̄ḡcaa	t̄c̄ḡat̄ḡc̄t̄t̄t̄
87481	ḡac̄ḡact̄ḡc̄a	ḡt̄ḡaāc̄ḡaāa	cc̄ḡt̄t̄ḡcaāa	aāat̄ḡḡt̄t̄t̄ḡ	ac̄agāaḡḡc̄t̄	ac̄at̄t̄c̄ḡc̄t̄t̄
87541	ḡḡt̄c̄ḡt̄c̄ac̄c̄	c̄ḡt̄ḡḡt̄ḡḡc̄a	ac̄caāt̄t̄ḡḡḡ	ḡc̄t̄caāacc̄c̄ḡ	t̄t̄c̄t̄c̄ḡt̄ḡt̄ḡ	aaḡat̄cccc̄a
87601	aḡt̄gat̄c̄at̄c̄	at̄c̄ḡc̄ḡḡata	c̄ḡat̄c̄t̄c̄ḡt̄	ḡt̄acc̄c̄t̄ḡaḡ	aaḡt̄t̄c̄t̄aca	cc̄ḡaaḡḡt̄t̄t̄
87661	ḡḡaāc̄t̄gat̄c̄	acc̄ḡc̄ḡt̄c̄ḡa	c̄ḡat̄cc̄ḡcaa	cc̄at̄cc̄c̄ḡcc̄	ḡc̄ḡc̄t̄c̄aḡcc̄	ccc̄ḡc̄ḡt̄ḡaa
87721	ḡt̄c̄ḡt̄t̄ḡaāc̄	t̄ac̄c̄t̄caāca	ac̄at̄c̄at̄ḡḡc̄	gāaḡat̄c̄ḡaa	ḡcc̄at̄t̄c̄ḡc̄ḡ	cc̄ḡḡḡt̄ḡc̄at̄
87781	t̄ḡaāḡc̄ḡḡt̄ḡ	at̄ḡc̄t̄ḡaāca	cc̄aāaḡḡc̄ḡa	aḡt̄t̄ḡcc̄ḡaḡ	t̄ḡc̄acc̄ḡḡc̄ḡ	ac̄aāc̄at̄t̄t̄t̄
87841	cat̄c̄ḡt̄c̄c̄ḡt̄	gḡc̄ḡḡc̄c̄ḡḡt̄	t̄ḡat̄c̄ac̄cc̄cc̄	ac̄caāt̄c̄ḡat̄	gc̄aḡgāat̄cc̄	t̄t̄ḡaāḡḡḡat̄
87901	c̄ac̄ḡc̄ḡtāac̄	acc̄ḡt̄ḡat̄t̄ḡ	at̄c̄t̄c̄ḡc̄t̄c̄ḡ	c̄ḡaaāat̄ḡḡḡ	at̄c̄ḡaāḡt̄ḡḡ	cc̄ḡaḡgāaḡc̄
87961	cat̄ḡac̄cc̄c̄ḡt̄	c̄ac̄ḡac̄at̄c̄t̄	t̄t̄ḡt̄c̄ḡc̄c̄ḡa	t̄ḡaāt̄ḡc̄t̄t̄c̄	c̄tāacc̄ḡḡc̄ḡa	ḡt̄ḡcc̄ḡc̄c̄ḡa
88021	aḡt̄cat̄cc̄cc̄cc̄	ḡc̄ḡḡt̄caāac̄	t̄c̄ḡat̄ḡḡḡc̄ḡ	aḡt̄c̄at̄t̄ḡḡc̄	gat̄ḡḡcaāac̄	cc̄ḡḡcc̄caāt̄
88081	ḡact̄caāaāḡ	c̄t̄caāc̄ḡc̄ḡḡ	cc̄t̄t̄c̄c̄ḡt̄ḡc̄	at̄t̄t̄ḡt̄ḡḡc̄t̄	c̄ḡt̄taḡtaḡt̄	t̄c̄ḡc̄caāḡac̄
88141	c̄ḡtaḡc̄ḡḡaā	ḡt̄c̄ḡc̄caāḡa	c̄t̄t̄t̄c̄ḡḡc̄t̄ḡ	ḡaḡcc̄caāt̄c̄	ḡcc̄ḡaāact̄c̄	t̄t̄ḡḡc̄ḡaḡt̄t̄
88201	cc̄ḡc̄t̄ac̄at̄t̄	t̄t̄c̄t̄ḡt̄ḡc̄ḡt̄	ac̄t̄t̄t̄ḡḡḡt̄c̄	at̄t̄ḡc̄ḡac̄ḡḡ	aāac̄act̄c̄ḡḡ	t̄t̄c̄ḡt̄t̄t̄taā
88261	gāac̄c̄aḡaḡa	ḡt̄t̄c̄ḡc̄caāa	gāac̄c̄t̄cc̄c̄c̄a	ac̄tāc̄t̄ḡḡc̄	t̄caāac̄aāt̄c̄	gḡaḡḡt̄t̄ḡḡḡ
88321	atāac̄c̄aḡḡḡ	at̄c̄aḡḡc̄at̄c̄	c̄ḡḡtat̄aḡat̄	atāac̄at̄ḡc̄a	aat̄cc̄at̄c̄ḡa	cc̄ḡḡc̄acāaḡ
88381	cc̄c̄t̄t̄t̄c̄c̄ḡt̄	t̄c̄ḡḡḡt̄t̄ḡc̄	ḡaḡc̄ḡat̄ḡta	c̄t̄cc̄ḡcaāca	t̄c̄t̄t̄c̄ḡat̄t̄ḡ	cc̄ḡaāc̄act̄c̄
88441	gc̄at̄t̄c̄t̄ḡat̄	t̄c̄ḡc̄ḡc̄aḡc̄a	cat̄ḡat̄c̄ḡta	aḡḡc̄t̄ḡcc̄ḡc̄	t̄ḡaāact̄ḡḡa	aācc̄ḡat̄t̄c̄ḡ
88501	c̄t̄t̄caāḡcaā	ḡaḡt̄t̄c̄caāt̄	cc̄t̄t̄t̄c̄ḡaāc̄	c̄ḡc̄c̄t̄t̄c̄at̄c̄	ḡc̄ḡaḡac̄ḡt̄t̄	gḡt̄c̄aḡt̄act̄
88561	t̄t̄c̄act̄t̄tāat̄	cc̄ḡc̄acc̄c̄aca	ac̄aḡat̄ḡḡḡc̄	ḡt̄ḡḡt̄c̄t̄ḡḡc̄	at̄caāḡc̄ḡa	aāat̄ḡḡḡḡc̄a
88621	c̄ḡc̄caāc̄t̄ḡḡ	tāac̄ḡaāaca	t̄t̄ḡc̄at̄ḡḡḡc̄	ḡaḡḡac̄t̄t̄ca	c̄ḡḡaāc̄t̄t̄ḡt̄	ac̄aāḡaāac̄ḡ
88681	c̄ḡḡḡt̄c̄caāc̄	caāc̄c̄t̄ḡt̄t̄c̄	ḡac̄ḡat̄ḡt̄t̄c̄	aāt̄c̄ḡcc̄at̄c̄	ḡt̄cc̄aḡt̄ḡḡa	cc̄c̄c̄aaḡcaāḡ
88741	cc̄c̄ḡc̄ḡat̄aḡ	ḡact̄c̄c̄ḡḡat̄	caāḡcc̄ḡt̄t̄t̄	c̄ḡat̄c̄ḡc̄t̄ḡt̄	t̄t̄c̄t̄ḡt̄c̄t̄c̄ḡ	c̄ḡt̄cc̄at̄c̄c̄a
88801	aaāat̄c̄c̄t̄at̄	c̄ac̄cc̄cc̄c̄aḡc̄	c̄ḡtaḡḡḡaāc̄	ḡt̄c̄ḡt̄t̄c̄ḡcc̄	c̄ḡc̄aḡḡaāaḡ	ḡtaḡc̄ḡḡaāḡ
88861	t̄c̄ḡc̄caāḡac̄	t̄t̄t̄c̄ḡḡcc̄ḡḡ	cc̄cc̄c̄caāc̄ḡc̄	c̄ḡaāact̄c̄t̄t̄	gḡc̄ḡaḡt̄t̄cc̄	ḡc̄t̄ac̄ḡac̄ḡḡ
88921	c̄ḡaḡt̄t̄c̄c̄c̄ḡ	t̄ac̄ḡḡcc̄c̄caā	t̄cc̄c̄t̄c̄ac̄ḡc̄	t̄ḡc̄t̄ḡaaāac̄	ḡc̄ḡt̄c̄ḡc̄ḡḡa	gat̄ḡc̄t̄t̄ḡaḡ
88981	ḡt̄t̄ḡc̄ḡḡḡḡḡ	t̄t̄t̄t̄ḡacc̄ḡa	gat̄cc̄cc̄c̄t̄t̄t̄	ḡcc̄ḡac̄cc̄c̄ḡa	ḡact̄ḡact̄t̄t̄	cc̄ḡc̄at̄c̄ḡac̄
89041	ḡc̄ḡaḡt̄ḡaaā	ac̄ḡt̄c̄acc̄ḡḡ	aḡḡac̄ḡaāac̄	ḡt̄c̄c̄t̄c̄c̄ḡt̄c̄	aāac̄ḡc̄ac̄ḡt̄	gḡaḡc̄ḡt̄c̄at̄c̄
89101	ḡac̄aāac̄cc̄ḡc̄	aḡcc̄act̄t̄c̄ḡ	t̄cc̄ḡḡc̄ḡḡḡt̄	caāḡt̄ḡaāt̄c̄	ḡat̄t̄ḡc̄ḡt̄t̄t̄	gat̄c̄ḡḡt̄c̄ḡc̄
89161	caāt̄ḡt̄ḡt̄cc̄	at̄t̄ḡḡḡt̄c̄aḡ	c̄ḡḡt̄c̄at̄c̄ḡa	c̄t̄caāt̄t̄t̄ḡc̄	caāat̄ḡḡat̄t̄	c̄ḡḡt̄c̄t̄cc̄ac̄
89221	cc̄at̄c̄ḡc̄t̄cc̄	aāat̄c̄ḡḡccc̄	ḡt̄ac̄ḡt̄c̄aḡc̄	ḡatāc̄ḡt̄t̄ḡa	t̄ḡcaāt̄c̄ḡc̄a	t̄c̄ḡḡt̄c̄t̄c̄at̄
89281	t̄t̄ḡc̄ḡḡḡt̄cc̄	ḡt̄ḡḡc̄ḡḡaāt̄	cat̄cc̄c̄c̄act̄t̄	gḡc̄at̄ḡat̄t̄ḡ	ḡt̄c̄ḡt̄cc̄aāt̄	c̄t̄c̄ḡt̄cc̄c̄c̄c̄a
89341	at̄c̄ḡt̄c̄ḡac̄ḡ	aḡaḡt̄c̄ḡc̄c̄a	c̄ac̄ḡt̄c̄ḡc̄ac̄	aāt̄c̄ḡc̄c̄aāc̄	ḡt̄t̄acc̄ac̄cc̄c̄	c̄aḡc̄ḡat̄t̄ḡc̄
89401	c̄ḡc̄t̄c̄c̄t̄ḡt̄c̄	at̄t̄ḡc̄t̄c̄t̄t̄c̄	c̄ḡt̄t̄t̄t̄ḡt̄t̄	t̄c̄ḡc̄ḡac̄ḡc̄ḡ	t̄c̄at̄cc̄c̄c̄ḡc̄t̄	ḡc̄t̄t̄act̄t̄t̄t̄ḡ
89461	aāt̄t̄ḡt̄c̄ac̄ḡ	t̄c̄ḡacc̄at̄ḡḡ	at̄c̄t̄at̄t̄t̄t̄ḡc̄	c̄ḡat̄caāḡaā	ḡc̄t̄ḡacc̄at̄t̄	t̄ḡt̄t̄t̄ḡc̄t̄ḡc̄
89521	cc̄aḡcc̄c̄c̄t̄t̄ḡ	ḡcc̄ḡc̄ḡc̄ḡaā	t̄ḡc̄ḡt̄cc̄c̄aā	gāaḡc̄t̄at̄c̄ḡ	ḡaḡt̄t̄c̄ḡt̄c̄ḡ	ḡcc̄aāc̄aācā
89581	cat̄c̄c̄taḡḡc̄	gāaḡḡḡaāac̄	t̄ḡc̄t̄t̄c̄ḡḡc̄ḡ	at̄t̄gat̄c̄ḡcc̄	aḡt̄ḡḡt̄c̄ḡc̄ḡ	t̄t̄ḡḡc̄t̄c̄ḡat̄
89641	c̄c̄t̄ḡc̄t̄ḡc̄ac̄	gḡcc̄cc̄acc̄c̄ḡḡ	gāacc̄ḡḡcaā	ḡacc̄ac̄ḡc̄t̄ḡ	ḡc̄t̄c̄ac̄c̄t̄ḡa	t̄c̄ḡc̄ḡt̄c̄ḡa
89701	gc̄agāac̄ac̄aḡc̄	ḡaḡc̄t̄gat̄c̄a	c̄t̄c̄t̄caāt̄ḡc̄	cat̄c̄aḡc̄aḡc̄	gḡt̄ḡt̄ḡaāaḡ	ac̄ḡt̄t̄c̄ḡc̄ḡa
89761	aḡt̄ḡat̄ḡḡcc̄	aāaḡc̄ac̄ḡc̄ḡ	ac̄c̄ḡc̄ḡt̄ḡt̄c̄	gḡc̄ḡḡḡc̄ḡac̄	cc̄aāḡḡcc̄ac̄	t̄ḡc̄t̄t̄t̄t̄c̄at̄
89821	t̄ḡat̄ḡaḡat̄t̄	cat̄c̄ḡat̄t̄c̄a	ac̄aāat̄c̄t̄c̄a	ḡcaāḡac̄ḡc̄a	c̄t̄ḡc̄t̄c̄ḡcc̄ḡ	at̄ḡt̄ḡḡaāt̄c̄
89881	gḡḡcat̄c̄at̄c̄	t̄c̄t̄c̄t̄ḡat̄c̄ḡ	ḡt̄ḡcc̄acāac̄	c̄aḡcaāt̄c̄c̄a	t̄act̄t̄c̄ḡcc̄ḡ	t̄caāt̄ḡcc̄ḡc̄
89941	ḡc̄t̄cat̄c̄aḡt̄	c̄ḡaāḡcc̄aāt̄	t̄ḡt̄t̄c̄ḡḡc̄t̄t̄	agāac̄c̄t̄ḡt̄t̄	t̄c̄ḡḡt̄c̄ḡaāḡ	ac̄at̄ḡc̄ḡc̄aḡ
90001	c̄c̄t̄ḡc̄t̄ḡaaā	c̄ḡḡḡc̄ḡat̄c̄a	cc̄ḡac̄c̄ḡaḡa	at̄ḡt̄ḡḡc̄c̄t̄ḡ	gḡaāat̄c̄ḡa	at̄ḡt̄ḡacc̄at̄
90061	c̄ḡac̄ḡaāḡac̄	ḡc̄ḡat̄c̄ḡact̄	at̄c̄t̄c̄t̄c̄at̄c̄	t̄c̄t̄c̄ḡḡat̄	gḡaḡac̄ḡc̄t̄c̄	ḡtaāaḡc̄t̄c̄t̄
90121	c̄ac̄ḡḡc̄act̄ḡ	gāaḡt̄ḡḡc̄aḡ	t̄ḡc̄ac̄aḡc̄c̄a	t̄ḡagāat̄c̄c̄a	aāaḡc̄at̄c̄ḡa	t̄c̄ac̄ḡc̄ḡaḡa
90181	c̄ḡat̄ḡt̄t̄ḡcc̄	gāat̄cc̄at̄ḡa	cc̄aḡt̄c̄ḡc̄at̄	c̄ḡc̄t̄ḡḡt̄t̄ac̄	gat̄ḡcc̄acc̄ḡ	ḡc̄ḡat̄gat̄c̄a
90241	c̄t̄at̄ḡat̄t̄t̄ḡ	ḡcc̄aḡc̄ḡc̄ac̄	t̄ḡat̄caāaāḡ	cat̄t̄c̄ḡaḡḡc̄	aḡc̄ḡat̄ḡt̄ḡḡ	ac̄ḡc̄ḡt̄c̄c̄t̄t̄
90301	ḡt̄act̄ḡḡc̄t̄c̄	ḡcc̄c̄ḡḡat̄ḡc̄	t̄ḡḡaḡḡḡc̄ḡḡ	t̄ḡaāḡac̄at̄t̄	c̄ḡc̄t̄t̄c̄c̄t̄t̄t̄	ḡc̄aḡḡc̄ḡat̄t̄
90361	ḡḡt̄ḡat̄t̄t̄t̄ḡ	ḡcc̄aḡc̄ḡaḡḡ	ac̄at̄t̄ḡḡcaā	c̄ḡc̄ḡḡac̄cc̄c̄ḡ	c̄aḡḡc̄ḡt̄t̄ḡa	t̄c̄at̄c̄ḡc̄ḡḡt̄
90421	c̄aḡc̄ḡcc̄at̄ḡ	caāḡc̄t̄t̄ḡc̄ḡ	aḡat̄gat̄c̄c̄ḡḡ	act̄t̄cc̄c̄ḡaā	ḡc̄t̄caāc̄t̄c̄a	ḡc̄t̄taāḡc̄c̄a
90481	aāc̄ḡḡt̄ḡḡcc̄	t̄ac̄c̄t̄c̄aḡc̄c̄	t̄t̄ḡc̄t̄cc̄c̄aā	ḡaḡcaāc̄ḡc̄ḡ	ac̄ḡact̄t̄cc̄ḡ	c̄ḡat̄c̄aḡc̄ḡc̄
90541	c̄ḡcc̄c̄ḡt̄c̄ḡḡ	ḡac̄ḡt̄t̄c̄ḡaḡ	at̄c̄ḡcc̄aḡḡt̄	cat̄t̄cc̄c̄ḡt̄t̄	cc̄caāḡat̄ḡc̄	t̄t̄c̄ḡt̄t̄ḡc̄ḡḡ
90601	ac̄act̄ac̄ac̄c̄	gḡc̄ḡcc̄c̄ḡaāḡ	aāc̄t̄t̄ḡḡt̄c̄a	t̄gḡc̄ḡac̄ḡḡt̄	t̄acāaḡt̄cc̄ḡ	c̄ḡc̄acāac̄ac̄
90661	c̄ḡaḡḡaḡḡḡc̄	ḡt̄ḡḡcc̄aāḡc̄	t̄ḡḡat̄t̄act̄t̄	gḡḡc̄ḡt̄c̄ḡac̄	c̄ḡcc̄ḡc̄t̄act̄	ac̄aāac̄c̄ḡḡt̄
90721	c̄ḡaḡc̄ḡaḡḡa	t̄t̄c̄ḡaāt̄c̄aḡ	aāc̄t̄c̄ḡc̄c̄t̄c̄	ḡc̄ḡḡc̄t̄ḡcaā	aaāat̄t̄c̄ḡc̄ḡ	at̄c̄aḡt̄taḡḡ
90781	c̄aḡaḡaḡac̄c̄	ḡaḡt̄ḡaāt̄c̄a	cat̄c̄c̄ḡt̄ḡac̄	t̄c̄t̄c̄ḡḡac̄ḡḡ	gḡaāaḡc̄aḡc̄	ḡtaāc̄ḡaāt̄t̄
90841	ḡt̄t̄c̄t̄at̄t̄c̄ḡ	at̄c̄ḡt̄t̄ḡc̄t̄t̄	caācāac̄at̄t̄ḡ	t̄ḡaḡḡḡat̄t̄c̄	act̄ac̄aḡc̄c̄a	at̄cc̄aḡc̄t̄ḡa
90901	ḡt̄ḡat̄c̄c̄t̄t̄c̄	ḡc̄aḡt̄c̄ḡḡt̄c̄	c̄t̄c̄ḡaāat̄t̄c̄	cc̄ḡaḡc̄aḡac̄	c̄ḡcc̄ḡact̄aā	aācc̄c̄at̄t̄c̄ḡ
90961	t̄ḡac̄ḡat̄c̄c̄c̄	t̄c̄aḡc̄t̄c̄ḡat̄	t̄t̄c̄ḡcc̄ḡaāc̄	t̄t̄ḡt̄t̄ḡat̄t̄c̄	ḡcaāaāat̄aḡa	ḡt̄c̄acc̄at̄t̄ḡ
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101461	aaccċċcttċ	ttcagcaaāt	tċcccaatcċ	ttgċgacaga	atċċċtċċċ	gttċgaactt
101521	cacattgccc	gtgtaagcga	tcattgaacc	catttttċgtc	cacacċtċċ	cgttgaggtt
101581	gatgtccaac	attċċgtċċġ	attċċagttċ	aaacaggccc	tgattgaggt	cċttċtċċċġ
101641	cgġtttċtċċ	aagaagcġgt	cgagggaata	gċgtċtttċa	ċtċatċgtga	gatċċtċcag
101701	gtcatggtga	taaaaagaga	acaacċtċċġ	actċċacċċ	cacaacċċa	ttgaacċċgt
101761	cgggċċġgtg	ccacaccaac	cċgagtgtag	ċgattċċatċ	ggaacċċgtċ	gtċċtċċġċ
101821	gggtttċatċ	cgtċċgagċġ	gggtċċtgag	agċgtagaat	ċatċċtaccġ	atgatttċga
101881	aatċċċatċt	ċtċċċċċtġ	cġttċccaaċ	ċacċċaccaa	agċatgagac	ċtġtċċtagt
101941	gaatċċatċt	cġttċċtċtġ	ttgacaacca	atacċagċat	ċagttċtċċġ	aaġtgatċga
102001	cċtġġġċċat	cġttċtċgtā	cġtċċatġġ	tċaattċġġċ	ċaaacċatga	ċacċagċġċ
102061	taattġtċtġ	ċtċċtċċttt	cġgttttġċt	tġtċtċġttġ	ċtċacċċċġ	ċċċċċgtttt
102121	cġċġġċċagċ	tacċagċagċ	cġgtċċagċā	atċttġċaaċ	ġġċċagtagċ	acġċċċġġċ
102181	aacċagċċċċ	ġċttċċġgaag	tċgagċgagġ	tġtttġġagċ	gaacċttġġċ	cġċġttġġt
102241	gataċagtgċ	ċaactċactċ	agġgtġactā	cġtġgatġt	ċtġċaaactt	atċċċgaagċ
102301	cċtġċagċga	tatċċaaċċā	ġċatċċactċ	cġgttċatġ	ġġtċtġgatġ	tattġċġatt
102361	ċaacġġċttġ	ċatġatgaag	tċġċċagċċ	agaagċagac	ttġttċċċac	aaatġċagċġ
102421	tġċċttċċġġ	ġgataċatċā	ċtċċċċāċā	ċċtġatċċċ	ġċagġċċġt	ttċtġactġġ
102481	tċġtġġċgaā	gatġtċċċā	agġtatġġā	aatġttċċat	ġacċġġġtġċ	gtġatċċċga
102541	ċċċġġattac	ċtċċatġċċt	atċttġġċċac	agċċgaactġ	ġċġattċċgaā	aaġgtġattt
102601	ċċaagġċċċċ	ġċgaacacġċ	ttċaaċaaġċ	ċttġaaactġ	ġagġaaġaaā	ċtċċċċacċt
102661	ġċatċacttġ	ttġġċċaaġġ	cġatġġaaċtċ	ċagċġatġġġ	ċagġċtġċċġ	ċċagċaaat
102721	ċġċaatċċċā	ċtċċtċtatċā	acċċċaaċā	tċtġċċttċġ	ċtġċaatġġt	tāġċġaaċġ
102781	tġċaatġġat	cġċgagċġat	atġatġaaġċ	ċaaagacġtċ	ġċgaacċaaā	tġċttċċagat
102841	ċaatċċġċat	ġaaċċġtċġġ	ċatġġġċttt	gatġġċġġtċ	atċtċċċact	tġagagġċga
102901	ataċġatġtt	ġaaaaactaa	tġċġtġċġġċ	ġġċċttġtċġ	acatġġġaaċ	aaaacċċaaā
102961	cġtċġatċat	ċtġattġġtċ	ġċaaacttċtċ	tġagaagtat	cġċtċċċċġ	aaġgtġtġċ
103021	ġtatċaaāac	ċtġġċactċġ	atġtġatċċ	tċtġċacttġ	ġċċċċċagċt	tċċaactċċċ
103081	ġċaaġacatġ	ċtġċġattġġ	ġċġagġaaġā	gatċġġttġġ	ġaaatċċċġġ	ġġġagġtġġċ
103141	ċaagġċagat	ċċataċaatġ	tġġttġċċtā	ċaaċċtġatġ	acġċtċċtġġ	atċgaacċċċ
103201	ġaagttċċacċ	ġttttġaaac	aagacġġġat	tċaagġċċċċ	atġġacċċāā	ċċgaagċċāā
103261	actċtatġġċ	gatġċġġtġā	tġġagttġċt	tttġġatġċċ	aagċaagġtċt	tġtġċġagaa
103321	ġtacċagċag	atġċċġġāċā	aacċċatċtt	ġġtċġagatċ	ttċċċacacċ	aaaacċċactt
103381	tġċċattċċġ	acġtttġġtċ	tġċċġġġtġġ	ġġċagġġtat	ttġġġċġttt	ttġġġċċċġ
103441	agġċatċacġ	ġċgaacagċċ	cċċċċtċċā	agġċgaacċċ	ċċatċaaact	ġġaaāagċġt
103501	tttatġġċat	ġagttċtġtċ	atġtġġtċac	ġċtġġagaaā	acċaaċaaċċ	ġaatġċċġċġ
103561	ċtġġċtċagċ	ġaagġċatċt	cġgtttċacġā	agaacċċāā	ċġċaatċċtt	cġtġġġġċga
103621	ġaagatġtċġ	ċċtċaatacċ	gatċġatġtċ	ġċtċtċċġac	gatċtġactċ	cġgtċagċga
103681	ċċtġagġtġċġ	ġċgttċċttt	ċacċacċatċ	cċċċatċċġ	ttġċaatttġ	ċttactċagā
103741	atċċtċatġġ	ġtaatċġagġ	tċċtġatċga	acāacatġġt	ċatġatġċtt	tġgtġċagġt
103801	ġċtċċċatġac	ttġtċċċġġ	ġċattċċċat	ċaaċġatġċċ	ttāacċċċġċ	atacċġġatċ
103861	actġċċagċga	ttġġacġċtċ	agtttġatġā	atāċċāāāā	aaacġagċċā	acċagtttġġ
103921	ġġċtċtġġtċ	ġattġġtċġċ	ġtġacacġċt	ġċċċġaaagċ	ġġtġacċtġġ	cġacċtġġāā
103981	agġttġġacċ	cġagċgaacċ	cġacċaaċtā	ċtġġġġtttġ	cġagagttāġ	ċċaaāagġtġċ
104041	ċatċgaagġt	ġaacagġtġġġ	agċagġċġtċ	tatċċċċċtt	tċtċċgaatġċ	agċaatġġġġ
104101	cġtġatċacċ	ġġċgaacġġġ	ġċċċtċċċt	ġgaatġġċtġ	ġċtċġagċċċ	ġċtċċgaatġt
104161	ġġġacāagac	cġġċaaġaaā	tċċġagċaat	tġaaġacāat	ttġtċċċaat	ċtagċġatġċ
104221	tttġċċġġtċ	ttġċġġċġtt	ġġatċaatat	tġġċċaatċt	ġaagagċagġt	ġġġaaāacġt
104281	tttġġacġċċ	tċċċāacagġ	cġtċċċċat	ċċagċċċttġ	ċtġċċċgaat	ttċatċtċċċ
104341	atċċċċċċtċ	ġċċċċċgaāā	agċtċċatċġ	ċċacġaatġġ	ġċġtġġgaag	ċtttġtċċġċ
104401	ġċtġċtċċā	ttġġatċċċġ	tġġacċċtġċ	ġġċċttġċat	ttċċċtttġġ	ċċaatġċċtā
104461	cġacġāāāā	aacġagġtċċt	tċċċċċċgaā	acacċatġċā	ċtġatġġċat	tġġaatġġġċ
104521	ċċċtċċċtāċ	cġċġacġċtċ	acċġattġġt	ċtġġaaactġ	ċacċacġċġġ	tċtċġġaaġā
104581	ġaatċċġġċġ	ġacġċġġaaċ	agaatġatġċ	cġagaatġtġ	tċagċċġtċġ	aaġagġagġā
104641	agċtċtatġā	ċtċċtāāāāā	ċċtċaaċċtā	atġġġċatċt	tġċġagċact	tġċtċġġġġċ
104701	agċġtċċatt	ċċċattċacċ	tċtċċċċċga	ċċatċċtċċġ	ġġġagagġtċ	ġġacġċġġċġ
104761	ttċagċċċtċ	ġtċċġġġtġā	ġġġġċċġat	ċacatġġċġġ	tċġaaatċċċ	tatġċċacag
104821	aaċċċċċċat	ġtċacġċġġā	cġċċċċċtċā	ċċċagċāāċ	ġċtġaaġġġ	cġtġċċċagċ
104881	ċtċtċċċċā	atġaaattġġ	ġġġagagġtġ	acāactġċġt	tċacġġtċġġ	tġāāagacġ
104941	ċaaactċċċċ	agċaatċċac	ċċċtċtāacċ	ttċtċtċāā	aacċattċċġ	ċċacċġtċġt
105001	tġġatttttġġ	ċċċċġttġat	tġtċttġatġ	ġġċġġġċċġ	cġtttġċtċā	acġagġttāċ
105061	tġġġġacġtċ	ġċaaċċġatċ	ġċttċċċacċ	ġacċċāāāċġ	ġtġtċċāāċ	atġġġaaġtċ
105121	ġatċċacġat	tċċċāāāāā	ċagċttċacġ	ttċċtċċāā	tċġaatāċġā	ttċċtāċċġċ
105181	ġtċċagġġac	ġagġtġġċġġ	agġċtġċtġġ	acċġactatċ	ċċġacagċā	tċtċāacttċ
105241	ttċacttċġtt	tġċagċāact	ġacġtċactġ	aaġgtċaatċ	ċtġatċċġġt	ġġtċattċċċ
105301	ċtġacċġatġ	atġaatġtt	cġactāċċā	ttċatċtāā	tċatċgaacċ	cġġġġċċtċ
105361	ġtċttttċag	aāāāāāāāā	ġaaāāāāāā	cġāāāāāāā	ġċċtċāāāāā	cġġċtċċtā
105421	atġġtġġatġ	atċttċtġġġġ	cġactċċāā	tāċāāāāāā	tġċġāāāāā	actċāāāāāā

105541	faōgacctcā	aagāāāaacc	tcaggtcōcc	gcgatcāact	ccgōcāgacg	ccgcgcccāc
105601	ggcagtgtcg	gttcgtggga	atggtcgcgt	gacggaagcg	acaccagtgt	tcctcactac
105661	cgagccatca	ccgatgacga	agaccgcctc	atgggttttca	tttgccacaa	caccgacctg
105721	ggcgatggat	gggaacgaga	aggcgaagac	caatggtact	tcgatgagtt	ctccgtcaag
105781	aaagtcttct	cgatgggaat	caacatcgtg	acttatgcga	tgaccactgt	aatcattcct
105841	tgatatcaacc	atcgacgggt	ccgacgctcc	tccaaccgga	ttgcacttca	tgacaacgga
105901	taccatgacc	cacgaagacg	aagcccaagt	ggtggagcaa	attcgcgacg	gacgagaacg
105961	aatcgttcaa	gaattgtcta	aggtcatcat	cggccaagaa	gaagtcatcg	agcagttgct
106021	gatctgcttg	tttgccggcg	gtcattgttt	gatcaccggg	gcaccaggac	tggcaaaaac
106081	attgctggtc	agcagcgtcg	cgaaaatctt	tcatttgaac	ttccagcgga	ttcagttcac
106141	ccccgatttg	atgccggcg	acatcaccgg	aacagaaatc	ctggagcaat	ccgccgacgg
106201	tcaccgacaa	ctgcaattcg	tcaaaggacc	aatcttcgcc	aacgtgatct	tggccgatga
106261	aatcaaccgg	acaccgcccc	agacgcaagc	cgcgttgctc	gaagcgatgc	agaacacca
106321	ggtcaccgcg	ggaggccaac	gatttgaact	ggaagaaccg	ttctttgttt	tggccacgca
106381	aaatccgatc	gaaatggaag	gcacttacct	gctgcccgaa	gcccactcgc	atcgtttcct
106441	tttcaatgtg	ctgatcgact	acttgccgcc	caaagacgaa	ctggcggtgg	tcctgcaaac
106501	gacatcgacg	aagcccgaac	cgattcagcc	aatcttcacc	ggtgaagacg	tcgctcgctt
106561	tcacgcgcgc	gttcgacgcg	ttccgatctg	ggaattcgatc	gccgcatacg	cgtgcggtt
106621	ggtcgcgcgc	actcggcgcg	gacgagatgg	aacgcgggac	ttcgtcaacc	aatacgcttc
106681	ctgggggtgca	gggcttcggg	ccgctcaaac	attggtgctc	ggtgccaaag	cgagagcttt
106741	gctcaacggc	cacgctcatg	tccgaacgga	agacatccag	gctctcgcgc	acccgacgct
106801	ccgacaccga	gtcttgctga	gctatcgagc	cgaggccgaa	ggtttcaacg	ttgagaacct
106861	ggtcacacga	cttcttcaag	aaatccccac	ggaagtctga	attgagctgg	ttccaacgtc
106921	aatctcgcct	gtcgttcaaa	gccaccaacg	gcagcacggg	tacactccag	ggcaactcct
106981	cgaagtgcgc	gcccggctgcc	gcttcgcgcg	cgggtggcaa	cggtaaaaac	gccgcctcga
107041	tggaccgcga	tgctctgatg	cggatcaaga	atctgcaact	gcgatccaaa	cttgtcgtgg
107101	aaggtttctt	tggcggactg	caccgaagcc	ctcttcacgg	ggcctccgct	gagttcagcg
107161	aataccgagc	ctactcgcgc	ggcgacgatc	cacggggact	ggattggaaa	ttgttcgctc
107221	gcacagatcg	ctattacatc	aagaagtctc	aggacgaaac	caaccgtcgc	tgctacttgt
107281	tagtcgacca	aagtcatgct	atgggttacg	ggctactcga	atacaccga	atggaatacg
107341	cgagaacgct	ggccgcgacg	ctcgcttact	tcctcactct	gcaacgtgac	catggttgac
107401	tgatgacgtt	cgacgatata	atcgccgacg	tcgtcccggc	gcgcagccga	gtcggccacc
107461	tgcgtaaaat	ccttgccctg	ttggctcgct	caacgctcgg	atctggaacg	gatgtcaacg
107521	gaccgatctc	tcaaattgcc	gcgatcacc	gtcgcgcgag	tttggtgggt	ctgatcagcg
107581	acatgctctc	gccgaccgaa	atcctgcaac	ggtctctcgc	actgctcgct	tcgcgacaa
107641	atgaagtgat	cgtgttgaga	atcctggatc	ctaacgaagt	gaatctttcg	tgggacgaat
107701	ccaaggtctt	ggtggacatg	gaaacgggac	gcaaaatcca	agtcgatccc	gatgcgactc
107761	gcaaagccta	tcaggccgcc	ttccaagaac	acgcgcgagc	gattgaatcg	atttgcaacg
107821	ccgtaggagc	cgcgattttac	accagcacga	ccgatcgccc	tctgcaggaa	gcattgtctg
107881	atttcgctct	cgctcatcaa	cgctcgtcgg	tgggtgccag	tcgatcgggc	atgctgagtt
107941	caggaggaac	cttcgggatga	gcattgctcg	cccgtttttc	ctagccgggt	cactggcctg
108001	cgcggcgaacc	atcttggttt	acctgattcg	gcagcaccgc	aagggtgccg	tgccgttcag
108061	ctcgggtgat	ttcctgcgag	aggtcccgcc	acgactgacc	cgccgcagcc	gtttggatca
108121	gtggccattg	ctgctccttc	gagcactcgc	gttgttgttg	ttggccgccc	cctttgctag
108181	accgtttctg	cgtggtgctg	acgaccagtt	caacaacaca	cccgttcggc	ggatcgcggt
108241	gtttgtcgac	cgaagtgcc	gcattgcaac	ggaagacctt	tgggaacaag	caatccaaaa
108301	agctgaaacg	ggtctgactg	atctatcagc	gcaagaccaa	ttcgcggtgt	ttcgcttcga
108361	caccaaataat	gaacgcatac	gggaaacatc	gctcgcggca	acatccgatg	aacgtcagaa
108421	cgcactcgct	ctgcaagctc	tcacggaagt	tcaacccact	tggcgagcca	ccgatctggg
108481	aaccgccctt	cgcgaagccg	ccgattgggc	acagtggccg	accgagtcac	cgacagcggg
108541	agaagacgga	ttagccgacg	aagaagcgat	taccgcaggc	cagctaccgg	gtcctgccag
108601	catcgttttg	atttccgatc	tgcaagacgg	ttccaaactc	gatgcactgc	agcaaaacac
108661	tggcccgaac	caagttacct	tgcaacatcc	gcgagtgggt	ccgaaggaa	aaggctatgc
108721	gaccgcgatc	atgatgaatg	atcaaacctt	gggaacttgg	caagaatcat	ccgcgtccaa
108781	tgccaatcgc	aagcttcggg	tcgggtcgct	caattccaaa	ctcgcttccc	agttcgatct
108841	gacgttgcaa	tggaaacgac	ccagtgcaca	acaaacgac	caggtcgaag	ctgatgcaac
108901	ccagatcatc	cgtctcgacc	agccggcgga	ttccgtcacc	gcaatggtcc	tgtccgggtg
108961	caactcgcgc	tttgacaata	cgttctcact	ggttgctccc	gagaaacgct	cgtatcgact
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132901	ātcgātccgag	cċctcgcċcċ	āāācācggaċ	ċaccgcāāgc	ċgaagcċgāāt	gātātċċtga
132961	tccgcgaaac	gagcatgatt	tgcctgaggt	ttcttccgca	agcaaccatc	gcttttcaacc
133021	ttcatccaac	aggcaacgag	tcaacatgca	tccctggatc	gcggatcgaa	cggcctcctt
133081	tgatagcagc	ggaattcgaa	aagtċttcga	tctcgtcgcg	aaactgaaag	accgatcaa
133141	cttgtccatc	gggcaaccgg	actttgatgt	cċccgaggaa	attcaggacg	caccgctcga
133201	tgcaattcga	tcggggcaaaa	acgcatactc	gccaaccċag	ggtatcgcgc	cgctgċgtga
133261	gaaactgctg	gcggaaatca	acgċcaagta	tcccgċcaa	aatcgcgacg	tgtttgtcag
133321	cagcggcacc	tcggggcgggt	tgggtcċttt	gctgċtttcg	atgatcaatc	cgggtgacga
133381	ggtcatċttc	ctggatcċct	atttċgtċat	gtaccċggċt	ċtċgtgagċt	tgtgċggtgg
133441	tatccċcċgtg	acggtċgatt	cgtaccċgga	tttċcċggtg	gatċcagċca	agatċgaagc
133501	cgċgatcaca	cccaaaacca	agatgatċct	ggtcaacagt	cccgċcaatc	caaccċgċgt
133561	gāccgcċgtc	gagcaagatc	ttċgagatgt	cggcċgattg	gcggċcaaagc	acaacatċgc
133621	gċtċgtttcċg	gacgagatċt	acagċċgatt	ċttċtacgac	ggċgacttċg	catċtċcċgc
133681	ggċcaccaat	ccċgacacaa	tcgtgatcga	cggtttċagc	aaatċgcacg	cgatgaccċg
133741	atggċgagtg	ggċtacgtċc	acggaccċċc	cgagatċatt	gcgacċgatċ	tcaagatċca
133801	acagtattċg	ttċgtċtċgt	cċċccċagċc	cgċtċagtgg	ggagċtċtċc	gtgċgatgga
133861	aatttċgtċt	gacggċcaca	ttgacgacta	cċgtċgċaaa	cċgċacttċa	tggtggaaca
133921	acttċċcċg	caċttċgaac	tċaccagċċc	cggcċgtċg	ttttatċtgt	tccċgaaagc
133981	ccċcċgċacc	gaagggggga	cggcċgtttgt	cgaaagagċg	atċċcċgacg	gċctgċtgat
134041	cattċcċcċg	aagattttċa	gcagċċgċga	ttċtċacttċ	cċgċtċagċt	tċgċċgċcag
134101	cgatgacacg	ċtċgċtċgċg	gtċċcċgaacg	ċċtgatċaag	ċtgċgtggċg	acaatċgċtg
134161	accgattttgt	tagċċtċgtċ	cgċtċcċaac	gcagaaattt	ċċtactttċa	aacatċċċtg
134221	atċgagtttt	tċgatgtċċg	cċgatċċgac	ċaaaatċat	cgċtċggċca	ċċgtċgtċt
134281	ċcatċgċcċga	caagtċgċtg	acċcaacċgac	ċaaaagċċg	cċggtċgċcga	tċtatċċcċc
134341	caccagċtċac	gaċttċgata	gcacċgaaca	cċgċgċgċċc	ċtgċtttggac	tagċtgaatt
134401	tggcaacatc	tacagċċggt	tċgatgaacċc	aacċgtċgat	gtċgtggaaa	aacċgatċgc
134461	ggċactggac	ggċggtgtaa	cgggattgtg	ċttċgċċtċc	ggċcaggċg	ċcatċacċgċ
134521	agċggttttg	gcċgatċgċac	acagċggtċa	aaacattgtċ	agċagċacċt	cċgtċgatgg
134581	cċgaacatgg	acċċtċgttċa	cacaaacċgt	gaagaacċt	ggtatċgaag	tċgċttċtċt
134641	cgatċċggat	caċċċgagc	aaatċcācċg	ttgtgtċgat	gaaaacactċ	gactggtċta
134701	catggagagc	atċċgċaacċ	caagaaacċga	tgtċċċtgac	ttcaaggċaa	tċgċċgacċg
134761	agċtċactċg	gcacċacacg	ggċċgatċċc	agtgttċgtċ	gacaacacċg	tċgatgacċċ
134821	ttacttċgtċ	cgċċċgatċg	atċacċgċat	cgacattgtċ	atċtacagċa	cgacċgaagt
134881	ċttaggċcċga	cacċgċactċ	acatċggtċg	ċtċgatċgtċ	gatagċgċga	atttċaaatg
134941	ggċċgacċaa	ċċtgaaaagt	ggċċtgagt	tċgċgċċċc	agċċċtċtċt	accacċgtċg
135001	cgċtttċgaa	gagċacċtċg	gtċgċatggg	caacatċgċc	tacaacċgttċ	acatċċgċac
135061	ċċactggttg	cgċgacacċg	gcċgċgċċat	gagċċċtċtċ	gcċgċgttċc	tgttċċtċga
135121	aggċatċgag	actċttċacċ	ttċgċatċċc	tċgċċactċg	gaaaatċgċa	tgaaggttċg
135181	tċagttċċtċg	gaagċtċacg	acċgagttċga	gtċgggtċaat	tacċċċgċgat	tċgaaaacċga
135241	ċtċgċacacac	aaattċgċtg	agċagċacċt	gacċaacċgċ	aaaggċgċga	tċċttgċċt
135301	tċgċcatċaaa	ggċggċatgg	aagċggċcaa	gaaatttātċ	aacċgċtċgċc	aactċgtċtċ
135361	tċacttagċc	aacattċggċg	atċċcaaaac	attggtċatt	catċċċgċca	gcacċacaca
135421	ċcaacagċtt	gcċgaagacg	aacaacċgċg	agċggċgċtċ	agċċċagagt	acattċgċgt
135481	ttċggttċgga	atċgaagaca	tċgacċgatāt	ċċtċgatċgac	ttgaaacagċ	ċtċttċgtċgt
135541	tċgċgacċgċg	tċgacċgtċaa	agċaatċgaa	acċttċgttċ	cċgaacaattċ	atċċtċċċgċ
135601	gaaatċgatċ	cċgggagatċ	ċactċgggtā	acċgatgttċg	agagċċaaċg	ttċtatgggt
135661	gagċċttċca	acċgagatċt	gtċċagċacċ	gatċgatċgtċ	ggactċgatċ	gċcatċggċg
135721	tacċċcaagt	acċgtċgċgt	tċaccagċtċg	ċtċċċgċtċg	aacċgċgċgċg	cċgaactċgċc
135781	gaaattċgat	gċtċgtċacċga	aacċgtgggċg	acactċaacċg	acċgacċgatċ	caacċgċċgtċ
135841	ttggtċtċgċc	acċgċgttċtċ	aggċgactċa	catċgċgċtċc	gċcacċgacċga	agacċgacċaa
135901	ċcaggttċggt	gggacċgċtt	gatċċgċċċc	ggacttċċca	tċgacacċgga	tċggttċgtċc
135961	gtggtċtċgtċ	ċcaatċgtċċt	ggċċggttċgt	cċgċgċcagċa	cċggċċċagċg	tċgacċgċgac
136021	ċcaacċċtċg	cċgatċggċaa	acċċtċacċgċ	gċċaacttċc	ċtċgċgatċac	catċgċgċgac
136081	atċgtċgaaċ	ċċcaaaaact	ċċtċgċtċgac	cacċtċgggaa	tċċggċagċtg	gċgggċċgtċg
136141	gtċgċgċggt	cgċtċggċgċg	tċaccaagtċ	ttċgagċtċgga	tċaatċgċtā	tċċċgacċgċg
136201	gcgaaaacċt	gcċtċgċċat	cgċtċacċtċt	ċċtċgactċga	acagċċaaċg	actċggttċtċ
136261	gatċgtċatċg	ċtċgċaatċg	gatċċaaacċ	gacċċgċact	acċċgċgċgċg	ċcagċtactac
136321	gacaaagacċ	aacċċċċgga	cacċgggattċg	gċaatċgċac	ggatċgtċggg	tċcacatċact
136381	tatċċttċċg	tċgaagċgat	ggagċċċaa	ttċgacċċċg	atċgċċacċga	ċċacċgċcag
136441	atċċċatċac	agttċċgagċa	acċgattċagċ	atċgċtċċtċ	acttċggċaca	ċcaaggċċaa
136501	aagttċacċga	cacċgttċcga	tċgċaatagċ	tacċgtċactċ	tgtċgatċggċ	gatċgċatċtā
136561	ttċgacċtgċg	gcċgċacċgċg	actċgaagċtg	atċgċaaacċgt	ttċgacċgaagċ	aacttċgċgat
136621	ttċċtċgttā	tċagtttċcag	cagċgattċgg	ttgttċċċac	ċtċgtċaatċ	cagagaaatċ
136681	gtċaacċgtċ	tċgacċgċttt	ggacaaacċgt	gtċacttātċg	ċċgaaatċac	cacċaatċgċc
136741	ggċċacċgatċ	ċattċċtċgat	cċgċgaaagac	attċgċagċt	atċgacċgċt	ċċacċgċgaa
136801	gcċcatċgag	acacċgaaac	gċatċċċgċg	gttċċatċċg	acatċacċgtt	gaacċgtċgac
136861	gaagaatċaa	tċċtċggagat	ċattċċagċc	ggatċċagċg	tċgtċggacċt	cċgggtċgtċgċ
136921	aacċgacac	tċgtċgċċgċ	gatċċgtċgat	cgacatċgċa	cċċcagċgacċ	gċċaaacacċg
136981	gaacatċgat	tċgatċggċgt	cċgaggtċgċa	cagċgagacċ	tċgtċggċaac	ggċaatċgċga
137041	ggċatċgatċg	tċgattċgactā	cċgacċtċaac	caċgċactċgċ	ċċgċattċat	cgatgacċag
137101	ttċgactċag	tċgatċċtċcaa	cċgċgacċgtċg	caagċggtċg	agaacċgtċgt	ggaaactactċ
137161	aacċgagatċg	tċgċgagttċgg	cċgacatċgċc	atċatċagċt	ttċċċaactt	tċgċtatċgċc
137221	ċcaactċagag	atċactċagċt	gacacatċggg	cgatċgċċga	aagċċċċċgċg	cgagtċtċgac
137281	ttċgattċggċ	acaacacċċc	taacċgacċgċ	ttċċċċacċga	tċgċċgacċgt	tċgċgacċtċ
137341	ttgggċċaac	tgaacċgtċgt	gatċgatċgaa	gaagtċtttt	gggatċgtċga	tċagggtċcaa



137461	cġcgaaāacc	gtġgaactġg	attcacaatġ	accġcgġcg	acġaġġġcg	tġcgaaggtc
137521	aatcgatcaa	aattcggtat	cgatgatttc	gcgtgcgġcg	cgagtġccca	aggtcġccca
137581	gacaccgaac	ggtgacttcg	aaccagġcgt	caaaaatġcg	ccaccttġcg	gaacttgagc
137641	gctgttgctg	tttccagctt	cgatcgaatc	ggtgatgaac	ttcaccġctc	catcġcacat
137701	caggacġtg	actccacctt	ggtġġcġat	actagġcġt	acatcacctt	cġcġttġtg
137761	gtġġcġtg	aaacaaagct	catcattġġg	ġcġcaacact	gtgacġaaac	ġġgtgtacag
137821	cġgacġġġg	agġġcccat	tgaatġġġg	acġctġctcc	ġcatctġġġ	tgaagġgtġt
137881	cgagccatġg	ttġġġcġga	actgagġacġ	ctccacatġg	atgaattġac	ġġcacġacaa
137941	cġcġttġct	tġtġġġcġga	cġtcaaccġġ	actġtġġaca	ġcatġġcġac	ġġgtġtġta
138001	gtġġġcġaag	tġagtġatga	tttġġġccat	agġgagġġta	ttġġacaaac	catġgagġat
138061	gtġtġġgaac	ttġġtġtġġg	ttġġtġgaat	gaaġcġacca	cġġcagġcac	tġtġctġata
138121	aatġġtġaga	ccacġactġġ	taccattġtġ	agġġtġtġg	cġgacatcac	acagġġttġc
138181	cgagtġġcġc	aacġacacġġ	catagtġctġ	acġġġġtġga	ġġġġcaagc	caacġġcagġ
138241	atġactġġġġ	caacġgaagc	tġġgaagġtt	cġtcaaccag	ġġġtġtaag	gaatġġġġc
138301	gtġġtġġġc	aactġacġġt	tġġġccatġġ	ccccattġġt	tġaaaaccġġ	tġtġġtġġg
138361	attġġtġgatt	acttġccġata	aacġttġttġ	ctġgatġaat	ġġcaacatġc	caaccaaagc
138421	agacaagtġg	gaccġġttac	cġcġġġtġġ	gtġgatġcġt	gtġtġtġġtġ	gatactġtġt
138481	gtacġtġcġc	gatġcġtġct	tġġġcġcġ	gtġtġacġc	gagtġatagt	tġtġġattġc
138541	tāaacġaagt	tġġttġaaat	tġttġtġġca	actġattġġg	cġagcġġctt	ccġġġcġġc
138601	ttġcacġġġg	ġġcagaagca	aaccaaccag	aacġcġaatġ	atġġcġatca	ccaccagġaa
138661	ctġccacġaac	gtġaagġccc	ġġtġġttġt	tġgaaaactc	attġaaaaga	cġttġaagġa
138721	gaaagatġtġ	cġatġaaaag	ġġġġġġcġtġ	acagġtcaac	gacġagġatġ	ccġġtāaac
138781	aattagġġct	tġġtġġgatc	cġatġġagaa	acġtġġġct	tġġġctġttt	cagctġtġġġ
138841	ttġctatġca	gaaactġġct	caactġġcġ	gtġagagġġg	cttġcġġctc	ġgaagaacca
138901	cġġcaccġac	tġatġġcġġc	gacaccġagc	aacġcagġca	agġcġcagcġ	tttġaaacġa
138961	caaaaattġca	cagġcaaaac	tġcatagact	tġtġattġat	cġtgacaacġ	ccagatcaag
139021	aaaactġtġtġ	atttttġcġt	ġġccacaaac	cactcagġca	agtġagagġt	caagattġġc
139081	caaaagġtġga	aaagġcaatta	acġagcagġa	atcattġtġca	aaagacacġt	tāaatcaacc
139141	gattttġcaca	ttagġatġca	aatatġcac	gttttġġcc	atġtttġact	ccġgaaactġ
139201	tatġgatġttc	aagaagttġg	cġtġttġcġa	tatġġġġcca	ġccatacġaa	ġgagġaaaga
139261	gtġcatġġtġc	gaaaaccġġt	ġccaaaaacġ	catġġġcġġa	ctgaaaaccġ	ctġctġctāa
139321	ġcgaagġaag	ġcaccġcaaa	ġcagġcġtat	agagagactc	agcaactġtag	agacacagġt
139381	ctġttġcġġg	ġcgaacġġtġ	tacġagccag	atcagġtttġ	cttġtġtġca	ġcġatcagaa
139441	tġactġgatc	ccġgattttġ	accġġcaccġ	cġġtġcagġt	gacttġġtġc	ccġtġactġc
139501	ġcttttġġġc	ctġcġatġag	agtġccatġt	cġagġġtġat	catġttġtġc	ccġtġġtġct
139561	tāaactġġac	gactāagtġt	tġtttġccac	ġġacġttġġc	agtġttġġtt	gactġaactt
139621	gaccġġtġta	cġgactġcġġ	gagcġttġga	cġttġtacat	tġcġtġcttġ	ġġtāaatġga
139681	cagcġġtġcġ	cactagcact	tġcttġctġc	ccġtġtttac	catcġġtġca	tāgaagġtġġ
139741	cġtġġtġatc	tttġaatagc	tġġactcġġġ	ttġcatġtġc	ġccġagatca	atccagacġt
139801	cttttġcġġt	ttġcġacttġ	acġtġcatca	tcaacġagta	ctcġttġcġt	cġttġaacġġ
139861	ttttġatātġ	ġcgaaccġtġ	ccġttġactt	catġacġttt	ġccġctcaag	cġġtġtttāa
139921	cġġctġtġġc	gatġcġġgac	ġġtġġacġc	cġttġtttġa	cġtġctġccc	agctccġaat
139981	agtġġtagġt	ttġctacacġ	ccatġcġcġt	cttġcatġtġ	gtagġtġacġ	tagġcġtġat
140041	ttagġtāatc	accġtġactā	tġgatġtacc	ġcġtġgatġg	ctcġtacġtt	ccġtġctġat
140101	cġcġatġcġt	gtagġacaca	tagġttġcġt	tġtagtġcġt	ġccatagaaa	gtatcġġcġġ
140161	ġġatġatcag	ctġġtġttġ	tġtġagtġcġ	tġcttġttġc	agcġtġttġa	tagġaaaaga
140221	tġtġctġcġt	ccāacġtġcġ	atagcġtġt	cġġtġġġtt	gtāatcġttġ	cġġtcaaacġ
140281	atġccġagat	ġcġtġaccag	ġcatġtġcġt	caacttġtġt	ġccġcġġtġt	tġcġġġtġaa
140341	agtġcġcġġt	ttġtġccatc	ġcġaccġġcġ	tġcaagġcaa	cġgaaaagag	acġġcġġcġġ
140401	tġcġgacġaa	ġgaacġaagġ	agtġġttġtt	ġġcġatġaag	gaatttġcatġ	ġġgtġaacġt
140461	tttġattġġt	gttġtġcġagt	ġccġcġgact	ġctġcġġaca	tġġġtġaaaa	caccacġaaa
140521	gaagġcaaac	ġġcġcġccac	cttġcġcġtt	tacġġcġcġa	tġacagacġt	cacġcġattġ
140581	caccacġtġga	tġtġcġacġa	ctġġcġtġcġ	cġagcġatca	tttġcġatcġ	tġcġcġgaaa
140641	tġgactġcġga	ccġgaaaaat	ġcttġġcatc	ttġcġġcatc	cġġcatcaaa	tġcġtġaacġ
140701	agacġġtttġ	cġġtġtġctġ	aaccġaccġġ	tagactcġġġ	cġatttġġcc	tttttġacġc
140761	tāacaagaga	ttġcġagġat	gagcttġġġt	ġccġġtġcag	acacġcaatt	cġaaaccatġ
140821	cġcġġtġcġġ	aatttġcġtġ	gattġcġtāa	ttcaccatġt	tġctġgagaa	ccġagtġġġġ
140881	cagtġtġctġ	agġtġttġcġ	ġcġattġtag	ġġġactġġġa	tġcġaatġtġ	ġġccġtġtġc
140941	atcaacġagc	cġġcġgaatġ	tġcġttġcġtt	cġcttġtġga	tġagcġacġc	ġġaccġcġġc
141001	cġagagattġc	ttġagcġagc	cġġġtġġġc	atcattġgaat	cġġatġtġġt	tġġcġtġġag
141061	cttġccġgaag	ġccġccāacc	actġtġcġġt	gtttġcacġġ	cġttġttġca	agcġġaactġ
141121	aacatġatġc	agġcġtaccġ	cttġtġtġatġ	cġtġcġcagġ	ġcaagccagc	ġġtġcġgatc
141181	atġġtagaga	acatġgactt	ġġcġatġaaa	acġtġagġġ	agaaagġttt	ccġaatġatc
141241	accġagġatġ	acttġġacġc	tġacaatġtt	cġcġcġcāag	acatġtactġ	agtġgacttġ
141301	cttġtġcagġc	cġcaccġtat	gatġġttġgat	cġctġcġtac	gatġġcġttġ	caagġcġtġc
141361	gaatġcġatġ	ctġġcġactt	ccacġġġcca	tġtġaatcag	cagġttġcġac	agcġttġġgaa
141421	ġġacatġcġca	catġtġatġc	aactġcġcġc	ttġttġactt	ccġġccatġa	gtġaactġcc
141481	tġcttġacġat	tġġtttttġc	tġġtġtġcġt	tġġagġccġġ	gagġġġcagġ	acġatġtġat
141541	ġccġtttġctġ	gaaaacġttt	tġcġagġcāa	gaacġtġccġ	cġcġaaccġġa	tġctġġaagt
141601	cġccġagcāc	tacāaacact	tġġġcġġtġt	cagccġcatc	aacġagcāaa	accġtġcagct
141661	tatġcġagca	ctġcāaaagc	gaatttġacġc	caacġgaatc	gacttġcġga	tġctactġġġġ
141721	caatġcġgaac	tġġġatġccat	acttġtġcġga	cacġctġcġc	caaatġaagġ	cġġatġġcāa
141781	gaagcġgatġc	ctġġcġtttt	tġaccagġat	gttġcagġtġc	tacagcġġtt	gtġcġcagta
141841	tġcġgāaaac	atcattġcagġ	ctġcġgaaga	agtġġġcġag	ġġagcaccġc	tġġtġgagaa
141901	agtġcġġatġ	ġġcttġaacġ	atġctġġġt	catġcġtġcġ	atġġcġġaca	acġtttġaaa

142021	cātēccgatg	ggcatgḡctḡ	acaaṯtgōga	ctācgaaaaa	āaāctēcgag	aatcatgcccḡ
142081	tttggṯtgcc	gatgcttḡcg	gtgḡggtgga	ttgggacttg	gtttaccaaa	gtcgagcggg
142141	gccaccatcg	cagccttggt	tggaaccaga	cgtgctggac	gḡgatcgccg	agatggacga
142201	cgctaaaaaa	ttggaatcgt	tggtgatcct	tccgatcgga	tttḡtcagcg	accacatgga
142261	ggttctgttt	gacttggacg	aggaagccgc	ccagctttḡc	cgagaacgcg	gaatcaaaat
142321	ggcacgagcc	tccgcggcgg	gaacccaccc	agatṯtcḡtc	gagatgatct	gḡgḡattggt
142381	gcaagaacgg	ctcggaaaac	tgaacgaaaa	acccgctcta	ggtgaactgg	gtccctggca
142441	tgatgtctgc	ccgcaggatt	gctgcttgta	cacgcccacg	cgḡcctccgg	tgḡcgḡggcg
142501	gḡgaccggtt	caagccaatt	gatgḡggcgg	ctagaatcac	cgacgagcca	tcttgattcc
142561	ggccacatcg	gcttcḡtcgt	ctgtccacga	agcḡgtgṯtt	ctgccccctt	ttcgatcctt
142621	cgtgagcacc	atgḡctcgac	tcgcccacca	agtcttcttc	acgaccaaaḡ	accgcagcga
142681	cgaaccatc	aacgcḡttḡt	tḡgacgattḡ	ccaaacctat	ctgaacgatc	atcccgḡttt
142741	ggtgagcttc	gḡcḡtgggac	gctgḡcgagcc	cgaatacgat	cḡtcḡggtca	acatggactt
142801	cgatgtggtg	ctgcatacag	tcttcgaaga	ccḡtgccḡcc	catgacḡctt	atcaaacagc
142861	acctcgḡcac	ctḡgaattca	tḡgagcḡtca	aaaacccaat	tḡḡḡccgaag	ttcgḡḡgtt
142921	cgattcgaat	cttcḡcgact	gatḡccatcc	aaccttcaca	accacḡtttc	actcttttta
142981	aaaagctaat	atcaccatga	gtḡttttggt	cacccaaaaa	gccccḡgatt	tcaccḡccac
143041	cgccḡtcatg	cccgatggca	cgṯtcaaḡg	cḡactṯcaaḡ	ttḡtcḡgatt	acaaggcga
143101	gtacḡtctcg	ttḡttcttct	ggccactcga	cttcactttc	gtctḡcccaa	ccgaatcat
143161	cḡcḡttcagc	gaccḡggcca	aggacttcga	agacctcḡḡc	gtgaacattḡ	tḡḡḡḡtttc
143221	gatcgacagc	catttcactc	acttḡḡcatg	gaccaacacḡ	ccacḡcaacḡ	aagḡtḡḡcat
143281	tḡḡcaagacc	gcttacccat	tḡḡtcḡccga	cttgaacaag	caaatctcḡc	gtgattacga
143341	cḡtḡctgttg	gacḡḡcḡḡc	tcḡcactḡcḡ	tḡḡttḡttc	ttgatcgacc	aagaaggcḡt
143401	tḡtḡcḡtcac	caagctḡtca	acḡactḡcc	gctḡḡḡcḡc	agcḡtcḡacḡ	aagcactḡcḡ
143461	aatḡḡtcaaa	gccccḡcḡt	acttcgaaac	caatḡḡcḡga	gtctḡcccaḡ	ccaactḡḡca
143521	agaaggctcg	cḡtacaatca	aagcḡḡacḡt	ggaaggcagc	aaagagṯtct	tḡḡḡcḡccga
143581	atacaaaaḡc	taagcaagca	atcgagctga	tcccatḡtḡḡ	caattṯtcaaḡ	attṯtcḡcḡḡc
143641	gcccaccctt	ggctccḡctt	gtgaccagaa	cḡcagḡccag	tḡcttcaccḡ	cḡcactḡḡaa
143701	tḡcḡḡagcgg	cacḡactḡḡḡ	tttḡccacac	cḡcḡḡḡcḡḡt	tccaaaggaa	tcagctcḡḡ
143761	cgatcccgat	ggṯtctttḡc	acḡtḡaacct	gttḡcḡḡḡt	ggcḡacḡacḡ	cḡcttcccḡt
143821	cḡccacḡḡaa	caatccḡtcc	gagḡcḡacḡt	ttḡgaacḡtḡ	acḡcttccctc	aagccḡacag
143881	ccagtactca	cttcḡtctḡḡ	ctctḡcḡagṯ	cḡtḡḡaaḡcc	acḡḡaaactc	gactḡḡtcat
143941	tgaaccacag	ctḡtcḡattc	aaacactḡtt	ḡctḡḡacacḡ	cacccaacḡc	tḡgacctḡac
144001	cḡccttḡḡḡc	gattḡcḡḡcḡ	tḡatcttcga	cḡagḡḡcḡac	accctḡḡḡtḡ	acḡḡcḡtcc
144061	accḡatttca	accḡttcaat	tḡcatḡḡtḡa	aacccḡctcc	atḡcḡcḡtḡc	tgḡcḡcacc
144121	caccḡagcc	ccḡttcaccga	ccḡattṯḡcḡ	tḡḡagaaggḡ	cacctḡcaac	tḡcḡtctctt
144181	cḡḡcḡaattc	ctagaaaaag	ḡcḡtḡatccḡ	caaggctcḡḡ	ccttḡḡattḡ	tḡctḡḡatcḡ
144241	ctccḡaacag	ḡḡcḡtttccḡ	aggcḡḡatct	ccaagcḡtat	ttḡaaacḡat	tḡtḡcḡaaac
144301	gccccḡcct	ttḡacḡḡctt	ḡagctṯtḡcḡt	ttṯtḡḡacct	ccagḡctḡcc	tḡcḡcḡattḡ
144361	agṯttḡḡctt	ttcaagaacḡ	cḡtcḡḡḡcḡḡ	caagaatagc	ggḡcttcccc	acccḡcctcc
144421	cttctḡattḡ	ḡccḡacagṯt	cagṯḡḡaacḡ	ccḡactattt	tḡḡttcatcc	ttcḡtḡgat
144481	ggcḡttttt	ctgatctaca	tḡtcccttḡc	gacctḡttc	ḡcḡccaccac	tḡccaccḡḡa
144541	ggaagacḡcḡ	atcḡccḡaaḡ	tḡcagḡḡcḡa	aaccḡttḡaa	ccagccḡagḡ	actḡḡḡttḡc
144601	cḡacacḡḡat	ḡcatccḡagc	ccḡḡcḡaaḡḡ	tḡaaḡḡcḡaa	gaagctaacḡ	aagacacḡḡa
144661	tḡcḡḡttḡag	cḡtcccagct	cḡccaacatḡ	ḡtcḡaccctc	ḡḡttccatḡḡ	atccḡaccag
144721	tḡḡctatḡtḡ	atḡctḡḡtḡa	cattḡaacag	tḡcḡḡḡcḡḡt	ḡḡcatcḡaac	gaattḡaact
144781	gaccḡaacḡc	aaagagaacḡ	ḡacḡctḡḡaa	ataccḡacḡc	ḡtcḡatḡttc	ḡtcḡcḡḡta
144841	cctcḡḡctac	tḡḡḡcḡcḡḡ	acccḡaccḡc	cacḡḡatctc	ḡḡgatccḡag	tcaacḡtḡḡt
144901	cḡḡaccḡḡḡa	actcccḡcḡḡ	atctḡḡcḡac	cḡcttccḡḡc	ḡtḡcaaggṯḡ	ḡcctḡaaacc
144961	cḡḡcḡacatc	atcaccḡḡḡt	tcaaccaaaa	caacḡtcaac	aacctḡtcca	tḡcttḡcḡḡa
145021	agcḡatḡctḡ	gaaaccaaac	cagḡcḡaatc	cḡccaccḡtc	acḡḡttctḡc	ḡḡaacḡagaa
145081	atcḡatcgac	ttcaccḡacca	cḡctḡaccḡa	acacccḡctḡ	gactṯḡattc	ḡattḡḡctḡa
145141	acacḡḡtḡḡc	ḡacḡatḡaaḡ	tḡgaagḡcaa	cctctcḡcḡḡ	cttctcḡtḡc	tḡtḡcḡḡḡt
145201	ggḡacḡcḡtc	ḡḡtcḡcḡcḡ	aaattcaatc	cḡḡcḡagaag	accatcḡaaḡ	ḡcatḡḡtḡcḡa
145261	caccḡḡcḡat	ctḡattṯḡḡḡ	atḡcctccca	agacḡḡḡḡac	aacḡtttctt	accagctḡca
145321	ḡttḡtccḡac	tctḡagatḡa	agccḡḡcttc	ḡḡḡtaaataca	ḡtcḡḡactḡc	aacḡḡaccta
145381	ctcḡctḡaaa	ccagacagct	actcḡctḡḡa	catḡḡacḡtt	cagatcḡaca	accḡcḡccḡa
145441	ggaagcccaa	ḡagctḡḡctt	accḡaatcḡa	agḡtḡccaac	ḡḡcatcacḡc	tḡḡaagḡctḡ
145501	ḡtḡḡtacagc	aacaaaaatca	ḡtcccaactḡ	ḡḡcḡḡḡctcḡ	ḡccḡctcḡcḡ	acatcḡtcta
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145621	gaacḡaatcc	ḡaagcḡḡatḡ	accaaaact	ḡttcḡctccc	ḡattccḡcac	caccḡḡctcḡ
145681	caacctḡagṯ	tacatcḡḡcḡ	tḡgatḡccca	ḡtacttcacc	ḡtcḡcḡatḡt	tḡccaccḡḡa
145741	aggacaagag	tactcaaga	cattccḡtḡcḡ	tḡccḡccḡcḡ	aatattatcḡ	ccḡaccccaḡ
145801	tḡctḡttccc	ḡacaacaaḡḡ	aacḡcḡccḡt	caacḡccagc	ttctatctcḡ	acagṯcccat
145861	cḡcagacḡtḡ	ccccḡḡḡat	cḡtcḡctcaa	acaactactc	cḡattḡttcḡ	ctḡḡḡcccaa
145921	acagcccḡac	ḡtḡatḡḡaaḡ	cctacḡḡttt	ḡḡḡcḡactḡc	atctactacḡ	ḡttḡḡttctc
145981	ḡttcḡtḡcḡt	aaacctcttḡ	ḡcḡḡḡttḡct	ḡcacctḡttt	tccaacḡtḡcḡ	ḡcaactacḡc
146041	cttḡḡcaatc	ḡttctḡtḡtḡa	cactḡtḡtḡt	ḡcḡagḡtctḡ	atḡttcccḡc	tttcḡcḡaaa
146101	agcḡḡcḡatc	aacḡctcaac	ḡcatḡcaaga	ḡttḡḡcacct	ḡagctḡaaḡa	agattḡccḡa
146161	gaagcacaaa	ḡacḡacatḡḡ	aagctcḡcḡt	ccḡagcccaa	cḡḡḡaactḡc	aacaacḡcḡt
146221	cḡḡḡttcaac	ccḡatḡḡcḡḡ	ḡctḡtḡcccc	catḡttcctḡ	cagṯtḡccaa	tttctattḡḡ
146281	cttḡtaccḡa	acactctcḡḡ	tḡcagattḡa	actḡcḡacaa	ḡctḡcḡttḡḡ	cctcḡtḡḡac
146341	cactḡḡḡḡcḡ	tcaaacctḡḡ	ccḡctcccḡa	catḡatḡtat	tactḡḡḡḡcḡḡ	actḡḡatḡtḡ
146401	ḡḡactactṯḡ	ḡḡagḡccḡcḡ	ḡcaccḡḡttḡ	ḡttḡḡḡtccḡ	tactṯtcaaca	tctḡcḡcḡat
146461	gatcḡtḡḡtt	tḡḡttḡttcc	tḡḡctcagca	aaagatḡttc	atḡccaccḡḡ	ctacḡḡacḡa

146581	cttccgtgtc	ccggctgggt	tgtgcatcta	cttcatcac	agcagtctgt	ggggaatcgg
146641	cgagcggatc	ttggtcaaga	aaacgctgcc	atcgaagcct	cacttcgata	cagcaaccct
146701	gcagggcgcc	gccgcgggtg	gcggcacggt	cgatggcaaa	gtcaacaatt	cggcgggtgc
146761	caatggaaag	aaaagctccg	acggcaaac	caaaacgatg	gccgaccgac	ttcgcgagcg
146821	attgggaact	cccgaagaag	aagccgcccc	gctacccaaa	gatcgcaaac	gcccaccatc
146881	gaagaagccc	ggcaacaaga	aacgcgcta	gcgtcttaag	acccccgacc	gcgcagcggg
146941	agggttcgga	taacgagcgt	tcagcgagat	ttctggggga	gggcaatccg	cgccacgtcc
147001	cacgctcggc	ccccctccct	gcgtatgcct	gaacggcgct	gcttgacctc	ccccaaaact
147061	tcgtttcggg	agaggtgcgc	agggtgaaaa	tcggccggaa	agcgttctct	gaaaacggca
147121	ggccgcagct	tcgcgtactg	cgaggccaga	gtagaaccgt	tgtctcaact	gttccgcggg
147181	gcaaccctca	acggccaggc	ctcatcacca	tccatcaagg	tccgaagggg	cgacagatcc
147241	attgtcagag	tcgtcaggcc	ccggaacgat	gaaccactca	aacagctcag	gccgacggag
147301	ggcctccgct	ggcaacagg	aactcaacac	tcccacgaca	acctcgctcg	tgacaatgcc
147361	ggtgaatgtc	gaccgcaacg	cggtgcaggc	gaatacgccg	atttcttgac	gttgcgatcg
147421	gggcagggca	gggcggagtg	tcattccgcc	acttcccaac	ctttctttgt	caaaaccagc
147481	tcctgcgact	tgtccactgt	ccttgcttcc	aagccatcaa	ctcgaaacgt	ggttggaag
147541	cagcgtttca	tgctcacggt	cgtccgtggc	ggcatctcga	actcgtcgac	actcctggtg
147601	gttttcgatcg	acaccgttgc	agctttgccc	gaacggttta	gcaccgagat	ctcaatctgc
147661	gctgatttgg	gtcgacaaa	caaataaacg	gcgtagttaag	tcgtttgatc	tttcgtcgcg
147721	acagccgccc	ccgtttgcgt	gatgtgtttg	gccacgatgt	tctcatgggtg	cggcgggtgaa
147781	tcgatccatc	ccggaacaaa	gatataaatc	aaactcttcg	cagtgacttc	accagtgttg
147841	gtgcgataag	caatgtttct	tctcacgacg	cagtactcgt	accccccgcc	ttcggcacgc
147901	tccgcccggc	tcttgccatc	cgcgatga	ccgtacttgc	ccgattcagc	catgaactcc
147961	gcaaaccttc	tcgcggttgc	ctgcaactcg	tcgtttaccc	gcaactgacc	gagccccttc
148021	tttttgcggt	agtcgttgat	ttgcttgacg	attgcctctt	ccacttgctg	gaccaattcg
148081	ccatcgcttt	ccgaatcagc	agcgaccgcc	gtcgattcct	cttgagccat	caacggaccg
148141	acaaacaaca	gacatccaag	catcaaccaa	ccacgcactg	catcactcct	ggtagagaat
148201	ttgaattgaa	accgaatcac	ccaatgagca	gcgatgagca	atcgatcagc	ctattctttg
148261	cctcgtctgt	ttcgtcacag	cgccgaccca	aatcaatcgg	tcacgaccag	cgattctctc
148321	cgctctcacc	gagctggtaa	aacgtgtcgc	acccctgata	aacagcgccc	ctttcgctgt
148381	ccccactcac	tgatttgaca	ccgtcccaac	tcagcatgcg	aattcaagct	ccttctttcg
148441	tcgatctcga	aacgcccacc	ggtccgatgc	ggacgcattt	gtttcgcccg	gacggtcccg
148501	gccgctatcc	cggtgtgatt	ctttacagcg	agatctacca	gatgacggcg	ccgatcgctc
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192361	ttggcagḡaa	cccatgcccḡ	aattccttcc	agcggcgṫgt	ttggaaattḡ	gagcattcḡa
192421	gcccḡcaaac	gatagcḡḡt	gggtttḡtcḡ	gtcaccḡḡag	gagcatḡcac	ḡtagccacḡa
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192541	tcgaacccṫṫ	ḡattctccaa	cagattccaa	atḡcḡaacct	ṫḡttḡccṫcḡ	atccactṫṫḡ
192601	ḡcḡacḡtcḡc	ḡaatḡatccḡ	ḡcccatcḡtc	aaḡḡṫṫṫḡa	caaaccattc	ḡacctḡcḡaa
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192901	ḡṫḡacatcḡḡ	tcḡḡḡḡṫcḡc	ḡccḡṫcḡḡṫ	ttcagatctṫ	ḡatcaactcḡ	cttcaagaca
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193081	agṫṫccṫṫcḡ	ḡacḡcaatcc	ḡactṫṫṫḡṫca	cccagṫṫṫṫṫ	cccacacḡḡc	acctṫḡḡḡṫḡ
193141	ccḡaaattḡḡ	catcḡatcaa	ṫḡḡctṫcatc	ḡagḡḡatcat	ccḡṫḡatḡcc	agacagagṫṫ
193201	ḡṫctṫctṫṫc	acḡaatcaca	cacḡacḡḡṫc	agḡṫṫḡḡḡaa	tacḡṫactac	accagcḡḡcc
193261	ḡṫḡcḡḡḡca	acaactṫcaa	cḡccḡṫcatc	aaaacḡḡḡṫṫ	ṫḡḡcacḡḡcc	ctḡṫctḡḡcc
193321	ccḡḡctṫḡṫ	tcḡcagḡccc	agcḡṫṫctṫṫ	tcḡagcccḡḡ	ctṫcctṫṫḡc	ggḡṫḡccḡca
193381	tcṫṫḡḡḡcḡa	tcḡaatḡṫḡa	tcāatcāaa	cacacḡḡcca	ḡaacḡḡṫḡṫ	catcacatḡḡ
193441	agcaccḡcḡa	ḡḡcḡḡcaagc	ctḡṫḡṫṫcḡa	ccḡṫcḡaaḡṫ	ṫḡḡaaaaata	ḡḡṫṫcḡcḡṫḡ
193501	ḡḡattḡatca	ctcḡṫṫṫḡṫc	cḡccactṫḡc	accḡṫṫḡaa	aattcattca	agatcḡṫṫṫ
193561	ḡaaatcatcḡ	ḡaatccatcc	ḡagccḡcḡṫ	ctcṫḡcḡcḡa	ctḡḡṫcagc	cḡḡccḡatāt
193621	cḡṫaaacccṫ	ṫccattṫṫcḡḡ	ḡccḡaaatḡc	cḡatḡṫcacc	atccatcḡcc	ṫḡattṫḡṫḡc
193681	cctṫḡcaagā	ḡaccaaaatḡ	accḡaaacḡc	agḡaaactcc	ḡṫaccaaaac	cccṫṫḡattḡ
193741	agcḡṫṫacḡc	ḡṫcacḡagaa	atḡḡcḡṫṫṫc	actḡḡḡḡṫcc	ccagcḡḡcḡa	ttcḡcatcct
193801	ḡḡcḡaaagḡṫ	ctḡḡattḡcḡ	ctagcḡḡagḡ	ccḡaaacaagā	ḡctcḡḡaatc	ḡcaatcaccḡ
193861	atḡcccaaat	cḡaaacaactḡ	aagṫcḡṫṫcḡ	aaaacaaatṫ	aaatctḡḡac	ḡcḡḡcḡḡcca
193921	aatacḡaacḡ	ṫḡaaactṫcḡc	cacḡatḡḡḡa	ṫḡḡcccacḡṫ	ccacḡctṫac	ggcḡatcagṫ
193981	ḡccḡḡagcḡc	cḡḡṫḡḡatc	atccacctcḡ	ḡcḡcḡaccag	ttḡṫṫṫcḡṫḡ	accḡacaacḡ
194041	ccḡacctḡṫ	ḡctḡattcḡc	ḡaagccctḡḡ	agctcactḡc	ṫaaacḡctḡḡ	ḡcḡḡccacḡa
194101	tcḡaccaaat	ḡḡcaaaatṫc	ḡcḡḡccḡagc	accḡcḡacct	ḡccctḡṫṫṫc	ḡcctṫṫṫacc
194161	actṫṫṫcāacc	agcccagccc	acaacḡḡṫcḡ	ḡcaagcḡagc	atḡṫṫṫḡḡḡ	atctacḡacc
194221	tagṫṫctṫḡa	ṫctcḡaaḡcḡ	atcḡaaatcṫ	ḡṫctcḡaaac	ṫctḡcḡṫḡca	cḡṫcagcca
194281	aagḡcaccac	ṫḡaaaccḡag	ḡcḡagctṫṫṫ	ṫḡḡaatḡḡṫṫ	ctccḡḡcḡac	cacḡacaagḡ
194341	ṫccḡṫcḡṫṫ	ḡḡaaaaacḡa	atcḡṫḡaa	agctctcḡṫṫ	ṫḡagṫcḡḡṫc	ṫacḡccḡṫca
194401	ccḡḡacāaac	ctaccctcḡc	aaagṫcḡacḡ	ctcaattḡṫṫ	cḡacḡccctḡ	tcḡḡḡḡatcḡ
194461	ḡḡcaaagcct	ḡcacaagatc	ḡccaccḡaca	tcḡḡṫṫḡṫṫ	ḡḡccḡḡṫcḡc	aaḡaagṫcḡ
194521	aagagccḡṫṫ	ṫḡagaagaaḡ	caaatcḡḡcā	ḡctcḡḡcaat	ḡḡcctacāaa	cḡcaaccḡcḡa
194581	ṫḡcḡḡagcḡa	ḡcḡaatctḡṫ	ḡcactcḡḡṫc	ḡattṫḡṫcat	ḡagcctḡcāaa	ḡagcctcḡccḡ
194641	cḡatḡaccḡc	agcḡaccḡag	ṫḡḡatḡḡaa	ḡcactctcḡa	cḡacagcḡcc	aaaccḡccḡṫ
194701	ṫḡḡṫcatccc	ḡcaagcḡṫṫc	ṫḡḡḡcaatcḡ	accḡcḡcact	cḡṫḡṫṫḡatḡ	caaaacḡṫṫḡ
194761	ccḡacḡḡaat	ḡḡṫcḡṫctac	ccagccacḡa	tcḡcaaaaaa	ctṫḡḡḡḡḡcc	ḡagctṫccḡṫ
194821	ṫcatḡḡcḡac	cḡagaacatc	ṫḡatḡcāag	cḡḡṫcḡṫḡc	ḡḡḡcḡḡḡḡac	cḡṫcaagatt
194881	ṫḡcacḡagcā	aattcḡcḡṫḡ	cacagccaag	cḡḡcagcact	agaagṫcāaa	cagaacḡṫḡ
194941	ḡcḡacaacḡa	cctḡṫḡḡḡaa	cḡṫctcāagḡ	ḡcḡacḡagaa	cttcḡcḡḡcḡc	atcḡactḡḡḡ
195001	aagctḡcḡat	ṫḡatccḡcāc	ḡctṫacḡḡḡḡ	ḡḡcḡagctcc	ccaacaagṫc	ḡacḡagṫṫca
195061	ṫḡḡaaḡcḡat	catcacccccc	atccḡccacḡc	ḡṫṫactctḡḡ	cagcḡacagc	ṫṫḡagcḡṫḡḡ
195121	aagṫcacḡḡṫ	ctḡattṫṫcḡa	cḡḡḡcḡactḡ	cccṫṫaaacḡ	caaagatctc	ḡccḡḡcḡṫḡṫ
195181	catatcḡccḡ	ḡcḡagatcāa	atḡṫctṫṫṫṫ	ṫḡḡatcḡṫṫ	ḡṫṫctagāaa	caataagṫṫṫ
195241	tagaacaagā	agatcḡṫḡṫc	aatḡccḡaaṫ	ḡṫḡḡṫṫḡḡṫ	cḡṫctṫḡḡṫc	ḡṫṫṫṫccaag
195301	atḡccḡḡṫca	cḡṫcḡḡṫṫc	ḡṫctḡcccag	ṫccagcḡaa	ṫṫṫcḡḡacḡ	ḡatcaagacḡ
195361	ṫḡḡcḡṫcḡḡ	ḡṫṫṫḡacṫṫ	ḡḡcaccāag	ḡṫṫaatḡcḡṫ	agacḡṫcāac	ḡṫṫcḡḡṫḡḡ
195421	aagacaccḡc	cḡṫcḡḡcḡṫc	ataccactcḡ	aagcḡactḡc	ccaagccāaa	acaatcḡṫṫḡ
195481	accḡṫḡṫagā	ṫcagḡṫagṫṫ	ḡṫṫcagḡccḡ	tagḡṫṫṫṫṫṫ	ṫḡaagṫṫḡcc	accattḡccḡ
195541	ṫṫṫṫṫḡcḡṫ	ccatḡṫaatc	cḡactḡcāag	acataactḡca	ḡṫṫḡatcḡḡṫ	caacḡcḡatḡ
195601	ṫcḡḡḡacḡa	ṫcḡagṫḡcat	ḡtagccctḡc	ḡacḡṫḡḡṫc	cḡḡṫḡḡṫṫc	atccḡcaaaa
195661	cḡṫccagcḡa	cagṫṫḡcḡṫa	ḡḡṫcacagṫḡ	accḡṫcḡṫcac	ṫcatḡḡḡṫaa	cḡagacaccḡ
195721	cccaagaacḡ	agṫcḡccḡṫṫ	ḡṫctṫṫcḡaaa	cḡḡṫṫṫṫṫṫ	aaaccāagḡṫ	ḡṫaaccaccḡ
195781	ṫaaacḡḡṫca	agṫcatcḡṫ	agcḡṫṫḡtag	ḡṫcḡccaatḡ	caccḡḡṫḡḡḡ	ḡḡṫḡaagḡḡc
195841	ṫcḡṫḡṫṫḡṫ	acatcḡṫḡṫa	agcḡṫḡḡṫḡ	tagaagaagṫ	ṫḡṫcagḡagc	ḡḡcaacaact
195901	ṫcḡtagccāa	ṫḡatcḡṫḡaa	ḡaagṫḡacca	aactṫcaccḡ	acagḡṫcḡcc	ḡtagccaaact
195961	ṫcaccḡṫagā	ctṫḡṫḡḡcag	ṫḡcactṫṫccḡ	ṫactcḡccat	ḡctṫccaacc	ḡḡṫḡṫcccag
196021	ṫḡḡccattḡṫ	cḡatḡccḡaa	cḡcctḡṫḡḡḡ	ṫcctḡagcḡṫ	cḡatḡccḡṫa	ḡḡḡṫaatcḡ
196081	atḡcḡṫccḡc	cḡaagṫcḡaa	accḡṫṫcḡag	ḡṫḡṫcḡatḡḡ	cctṫṫṫcagc	ḡṫagaaccaaa
196141	ḡctṫḡatḡcā	ḡḡṫṫḡṫattc	ḡṫcḡḡḡacḡa	ṫḡḡṫṫḡaaā	aagḡcaatḡc	ṫṫṫḡṫṫḡḡḡ
196201	ṫagcccattṫṫ	ḡaaccāaac	ḡccḡacḡḡag	ṫagccacaag	ctṫcaccḡaa	ḡagcḡḡḡaac
196261	ḡḡatcḡccḡa	ḡḡṫcacaatc	aaacatccḡc	caaccḡccḡṫ	catcāaacag	ḡccḡccaccḡ
196321	atḡṫcḡccac	agcccātḡṫc	ḡccḡcaacca	ccatcḡcagḡ	ccaactcacc	ḡcagccacat
196381	ṫccattṫṫcag	ḡaaatḡṫḡṫc	acagḡattca	ṫcacagctḡḡ	catcāaagṫc	cccḡactḡḡa
196441	acḡactṫṫcḡḡ	ctḡactḡḡṫ	ṫḡḡcattccḡ	ccctḡḡṫaac	ṫṫḡcḡṫcḡḡc	cacḡaatcḡḡ
196501	ṫcḡḡcagcag	aagcḡccatt	ḡagḡṫṫṫṫṫ	aatccaacca	agccaccḡag	ḡḡccaaccac
196561	aaagcagctc	ḡṫṫṫṫcḡattṫ	catctṫḡṫṫc	ḡṫccctḡatc	ḡattṫṫcāaat	ḡḡattcḡccḡ
196621	cḡṫccacagṫ	ḡactḡccacc	ṫṫccatḡḡca	ḡcāaacagṫ	caaccḡṫḡṫc	ḡaccḡccaag



196741	ccātāgāāāc	cccagcccgā	ātccāccgāa	aatccgḡcāc	agcgṭtaaac	tttḡcgḡgtt
196801	aggggattga	tccgḡcgatc	cacgagcgṭ	cggccgātcg	gcctgagatc	ttgagcgcaa
196861	acgaaaaaaa	gcccḡctcat	cgcattttctḡ	cggṭgaaccḡ	gcctcttgga	tctcacgaaa
196921	tcttcḡttcg	ggḡcagctta	gaacḡtgaag	atcḡtatcga	aaccḡaagḡṭ	gḡtttgatcg
196981	tcḡtcatcat	tttccaagat	tccḡḡtcḡḡ	tcḡccatcaa	cccagṭccca	ḡcgaacttcḡ
197041	ggacḡaatca	agacḡttgḡc	ḡtḡagḡagcḡḡ	tagṭḡgatac	cagṭcḡtcag	agcḡtagacḡ
197101	tcḡttcccgḡ	tḡṭḡḡttḡcc	atcatcgaag	acḡccttcḡṭ	ttḡḡṭacca	ctcgaacḡḡḡ
197161	ccacccaagḡ	acaagcaatc	ḡttḡacḡcḡḡ	taaaaccaagṭ	actḡḡṭḡgat	accḡaacḡḡḡ
197221	tcacḡḡcḡḡḡ	tḡḡcaccagṭ	ttcḡtcttcḡ	ḡḡṭccagca	agṭcḡḡactḡ	gatgatḡtac
197281	tḡcaagṭṭḡṭ	cactḡacagc	ḡtagṭcagca	acḡatcḡagṭ	ḡcatḡtagcc	ctḡctcaact
197341	ccaccagcḡṭ	tḡtcttcḡcc	gaagcḡaccḡ	atḡḡṭḡḡṭḡ	cḡṭaagṭcag	agṭcagḡtcḡ
197401	tcḡḡṭcaaac	cḡḡccḡagaa	cccḡcccagḡ	aagṭṭḡtcḡc	cattḡtcttc	gaatccḡctḡ
197461	tcccagccca	tḡḡḡḡtatcc	accaaaḡacḡ	ctcagṭcat	ccḡagacḡṭṭ	ḡtacḡṭḡcc
197521	aatḡcacccḡ	tḡḡḡḡḡḡaa	tḡḡctcḡcḡḡ	ttḡṭacatcḡ	tḡḡagcḡḡḡ	ḡctḡḡagaag
197581	aagṭṭatccḡ	ḡagcḡḡcaac	ḡacttcccaa	ccḡatgatcḡ	tḡaagaagṭḡ	accactṭḡḡ
197641	accḡacagḡṭ	cḡccḡtagcc	catttctḡḡḡ	tacagctḡag	gaatḡḡcḡḡḡ	accḡtagtcḡ
197701	ccaccḡṭṭḡṭ	cccagṭcḡṭṭ	ḡtcccagṭḡa	ccḡṭṭḡṭḡḡa	tcccḡaacḡc	ttḡcḡḡḡṭca
197761	ḡḡṭccḡṭcḡḡ	taccḡtagac	ḡtaatcḡata	cḡṭccaccḡa	tḡṭcḡaagcc	acacḡaagṭḡ
197821	tcḡatḡḡcṭṭ	tttṭacḡcḡṭa	caacctḡḡct	tḡḡṭḡcagct	gaacḡṭṭḡṭc	ḡḡḡacḡḡṭḡḡ
197881	ttḡaacaagḡ	ḡcaacḡcctt	cḡṭḡḡḡḡag	ccḡatcḡacḡ	cccactccacc	ḡactṭcḡatḡ
197941	ccacaacacat	cḡccḡaagcḡ	cḡṭḡṭaagḡḡ	tcactccaagc	agcagṭcḡcc	caaaccḡḡḡḡ
198001	aagcagcttc	cḡagḡccacc	ḡccḡcagagc	gaatcacaac	cḡctḡtcḡca	acctḡcḡṭṭḡ
198061	cagccacagṭ	cḡcccaagca	ḡccḡacḡḡṭṭ	tcḡcaaccḡc	aagṭcactṭc	ḡṭṭctcḡcaa
198121	ccḡḡṭḡṭcḡc	agccḡccaac	agḡctcacaa	ccacacacḡḡ	ḡctcaccaca	atcḡcaaagc
198181	ḡacḡagḡḡḡc	aagagacca	ttccaatatca	ttḡḡṭḡaag	cḡccḡctcag	ḡṭṭcḡḡḡḡḡ
198241	ttaacḡccḡc	atḡcaaccḡc	tḡcḡatcaga	ḡctagṭṭṭac	taagḡṭṭcat	tḡctṭṭctcc
198301	ḡṭṭgatattcc	caatccaatt	ḡḡḡṭcḡṭṭṭ	ḡḡṭcaccaa	gattcaaaat	ḡḡatḡctḡṭṭ
198361	agaacḡḡḡḡa	ḡctḡḡḡcccc	caaaatḡṭḡḡ	ḡḡagḡḡccḡa	tctctcḡctc	acaacḡatḡa
198421	aacaaacḡca	ḡtccatcḡct	ttttcaacḡc	acacḡctḡcc	tḡccḡccḡat	ḡḡcacatcḡa
198481	aactṭccagḡ	caatcḡcttc	ḡḡaattcḡaa	tcaatcacct	cḡaaagattṭ	cḡagṭagṭṭ
198541	gaaagcaatc	catcatḡṭcḡ	tcḡḡḡagaat	tcctcḡḡṭḡḡ	ḡṭṭṭḡcḡaga	tctḡctcṭca
198601	accḡḡṭḡctc	aaaacḡactṭ	agaaaccḡcc	cḡcḡḡḡḡḡḡc	ḡcaaccḡcḡcc	tḡṭṭaatcct
198661	catctḡcḡḡḡ	tcḡctcccaa	cḡṭṭccḡṭct	ḡḡḡcaaactṭ	tḡacḡctṭcc	cḡaccḡgaac
198721	acḡccccḡca	tctḡaaaatc	ctḡctṭṭcaa	taaaacḡṭṭc	caccḡcḡtat	cctḡcḡḡḡḡḡc
198781	ttctccctḡa	aatcagḡḡḡat	ttḡḡaccḡṭc	tcaaatcaca	ttcatḡacaa	tcaccḡcḡḡag
198841	cḡḡṭḡḡḡcḡḡa	gaatcagatḡ	ḡcacḡacagṭ	ḡcḡaagcḡḡḡ	cḡḡcaaaaaa	ḡtccaaatḡḡ
198901	ḡcaacc					

201301	ftggggtca	cggggatcg	tggatcca	aaaccgacca	agtaatgagc	tgacactcgt
201361	ttcccgaccg	ttccgatgca	cgccgctcag	gcaggggcga	tcaactccgc	agccaatcga
201421	cacgcgtcca	agaactcgte	gaccatcagg	tactcgtcga	ccgtatgaat	ggacgcctga
201481	ccacacccca	atgtgaccgc	ttcgattccg	tgcagcatca	accaattcgc	gtccaaaccg
201541	ccattggcga	cttcacactg	tggagagcgc	cccaattgcg	aatcaattc	cgttgccgcg
201601	agaactgacg	gatgatcctc	cgctaatacg	aacgcttcac	aatcgactcg	gctggtgaat
201661	tcaaagctgc	ctgttcggcc	ctgaacgtcc	ttgaccgact	gaaccgcatt	ttcgatcgcc
201721	gttcgcatct	gagacacgat	ttcggcccga	aactcggcat	cgtgactgcg	agcctccgcc
201781	cgtagctgta	cttctggcgt	gatcacgttc	gtcgcgtcgc	caccctgaaa	aacccccacg
201841	ttcgcggttc	cgcgacgccc	gtccttttca	accagtccca	gccaaccggt	gcgatgcaga
201901	ctgctgatcg	cttcggatgc	aatcacaatc	gcactgacgc	ctttctcggg	agccacgcgc
201961	gcactgagaa	cgtggcctgt	aatggtcacc	tgcactcggt	cgccaccgat	gcctccatga
202021	cggattttat	cgagtgtctc	gccatcaaaa	ttgaatgctc	gatcaacatg	gccgactttg
202081	gacacgtcca	aatgacgagc	ccctcccaac	ccgacctctt	cctgaatcag	gaatgtgact
202141	gcggcaggag	ccagtttcaa	atcagggttc	tttgccctgcc	gtgatagtcg	ctcgacgatc
202201	gcactgagaa	tcaccgcgca	accgctgcgg	tcacggcac	ccaagccggt	cggcccatcg
202261	gccacgacaa	ttcggcccga	ttggtcatcg	tctcgaagct	gtggattgca	accaacacag
202321	atcggaaccg	tatccatatg	agcggaaagc	aacgtccgcg	gcaacgaatc	gtcgctggc
202381	aacgtgacaa	tcaaattgccc	cgcgttgcca	tccaaacgag	tcttggtgcc	agcgtcatcg
202441	gattgaaatc	aatccggatc	cactcccgcga	tccaccagca	ttttctcaat	cgcggccgaa
202501	attgcggctt	cgtcgccact	cttaccagga	atccgcgtta	gctcgagaaa	gcgatccaag
202561	gcagcggact	catcgatcgc	agccccagac	atagcaccct	tcccgccatc	atttatcgct
202621	tcggactggc	tcacgcgctg	cgattggcac	ggcggaggca	ctgatcttcc	acacgaattg
202681	gctgtgctgc	ggtgcccagt	tgcgactggg	ttaaaccgtc	cattgcgaac	cacccaacgg
202741	ccaacagcaa	tcgcgtggcg	gcaaacgagg	ccaacattgg	aacaacgtga	gcgggttccg
202801	tggcgtagt	agtcaaacct	tctgtgctgc	catgccctgg	gtgagccgaa	gcgggaacgg
202861	caaaaaccaa	agcggcaatc	gagccaatga	gtgaacgcga	caaaatgaac	tcacaagaat
202921	caagagaaat	gagaagagcc	gattcacccg	cggatttcac	cttcggcgac	caaacccaat
202981	gcacctgcca	accgatgagc	gggatcgtgg	agccggatca	gccgactgat	tataccctct
203041	ggtcgagctg	ttggtgacgc	atccgtcgac	gttttcgctg	ttcgtaggtc	acttccgcgg
203101	cacaacgcga	acaagccacg	ccacgttcgt	aatcggaatg	ctgcttcatt	tccggggtca
203161	acggccatcc	acatccgtga	cacaactcat	acgccccagc	ctgcaattgg	tgatcgaccg
203221	cgacacgatt	gtcgaacaca	aaacattcgc	cctgccaacg	agaatcctct	tccggcatct
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203401	ggtgcttctg	cgggttccaa	ttttcttcga	caaacttggg	gaattctcga	aaggattccg
203461	tatgaggggt	gattgacccc	tcgaacgtgc	caatctcgat	ctcgtagtcg	tttcgggtat
203521	cgatcagcgt	gacatccgga	tcacgcacca	aagcgttcca	atcctggggc	tcgatgtagg
203581	tgccaaccga	tcgcagcgga	tcaatgctcg	acacgcccac	cgttacgatc	tcacgcttca
203641	gccgaacttt	ggtttttgcga	aacgggatct	cttcgcagta	cgaccatttg	acatccattc
203701	cgcgaaaagg	agtggccttg	tcacgaagct	ccatcgaccg	gagccagtcg	ataaacggtt
203761	ccatcaactc	tcgaggtccc	gcgatgcgtc	cattgatgcc	ttcgccggcc	agcaacaacg
203821	atccccgaat	gccatcatct	gacattcgct	ggcggaaacg	ctctcgcagc	gattcaaact
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203941	cctcggcagg	cgattcggcg	ggcaattcgg	cgggtacgga	agaagcgtgt	gattcgggtc
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204241	tcaagctccc	caccgcgggt	accaactcgg	cctgccgtcg	catattctca	tttcgatcgc
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204481	tccagtgaga	ctgccattcg	gcaggaaact	tccatccttc	gaccattttc	gcaaactcgc
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204781	ccgcacgcgc	ctgactgacc	tcggagggaag	cgcgcgcgga	caaccaagct	tgagcagtg
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210481	ctgaact̄tt̄t	ct̄t̄ct̄gḡt̄cc̄	cgcacccacc	gc̄ggt̄gt̄t̄ct̄	cgḡc̄ct̄gḡaa	ccaaḡtt̄cac
210541	gacgaagc̄tt̄	cc̄gḡc̄gḡaga	cgt̄c̄ct̄caat	gḡḡc̄c̄ḡc̄c̄ḡc̄	cgt̄t̄c̄tt̄gat	cat̄gc̄gagac
210601	tgḡtt̄gḡaāḡ	aaḡc̄c̄ḡcc̄ca	gt̄c̄act̄ḡc̄ḡḡ	aaaaḡc̄tc̄ac	cc̄gc̄ḡtt̄tḡc̄	caacatt̄gat
210661	cgagcc̄ct̄cḡ	gt̄tt̄gat̄caa	t̄ct̄c̄ct̄tt̄tḡ	t̄cḡgḡḡct̄gt̄	tḡc̄c̄gḡc̄ct̄a	tt̄gḡatt̄t̄c̄
210721	cat̄c̄gc̄gac̄c̄	tḡct̄gt̄tt̄cca	ccaacc̄gc̄cḡ	gaact̄ḡct̄ct̄	tcaac̄gḡtt̄t̄	ct̄t̄c̄ct̄gḡga
210781	cgt̄tḡtḡcc̄ḡ	aagt̄cat̄gḡt̄	gcaacaaat̄c̄	gḡc̄gaagac̄ḡ	agt̄cc̄att̄tḡḡ	cacc̄gt̄gḡac
210841	gacgaat̄cc̄ḡ	ct̄c̄ḡct̄tḡc̄ḡ	gcaaat̄cat̄c̄	gḡcac̄ḡct̄ga	ac̄ḡact̄ac̄gt̄	cgḡct̄acc̄gc̄
210901	ccaḡtc̄ḡc̄ḡḡ	t̄c̄ct̄cḡaaaa	t̄c̄gt̄ḡc̄gt̄ḡc̄	caac̄ct̄tac̄ḡ	cac̄ac̄gaat̄t̄	cgt̄t̄c̄ḡacc̄ḡ
210961	at̄cc̄c̄ḡcaaa	tḡgt̄cc̄aḡgḡ	tḡct̄gḡtat̄c̄	acc̄gc̄c̄gḡḡac̄	c̄ct̄at̄c̄ḡc̄ga	att̄gat̄c̄ḡaḡ
211021	c̄gc̄ḡc̄gḡtḡc̄	gaḡc̄gat̄c̄ga	agaaḡct̄ccc̄	gaḡḡac̄at̄cc̄	tḡc̄gt̄t̄cc̄gc̄	gḡc̄tat̄gḡat̄
211081	ccaaaḡcaac̄	tḡc̄gḡḡaḡct̄	t̄tḡct̄tḡḡac̄	cc̄ac̄ḡaḡc̄gt̄	at̄ḡact̄tt̄ga	cc̄at̄c̄cḡgt̄c̄
211141	aat̄c̄gt̄cḡac̄	cgaact̄at̄ca	ct̄tt̄gḡc̄ḡga	tḡgḡat̄gaac̄	at̄ḡc̄gat̄c̄ga	tt̄cc̄gat̄ḡga
211201	c̄ḡct̄ac̄gat̄c̄	gḡtt̄cat̄c̄ct̄	t̄c̄ḡc̄aḡtḡt̄ḡ	acc̄ct̄gḡatt̄	catt̄ḡct̄c̄gc̄	ac̄ḡaḡt̄caac̄
211261	gaḡac̄ḡcc̄aḡ	aact̄gc̄ct̄cḡ	tḡac̄gaact̄a	ct̄c̄gaagaaḡ	cc̄ḡct̄t̄c̄gḡt̄	gt̄t̄gḡc̄c̄gḡc̄
211321	acaat̄ḡct̄ca	tḡḡcat̄c̄gḡḡ	cat̄ct̄c̄cḡgt̄	tḡgḡgḡcc̄ct̄ḡ	gt̄t̄ḡct̄ac̄aḡ	caḡc̄gat̄gt̄ḡ
211381	ac̄ḡct̄t̄cḡat̄	cact̄gat̄gḡt̄	t̄cc̄gat̄c̄ḡc̄c̄	aact̄t̄cc̄ḡtḡ	at̄ḡaḡtt̄tt̄a	caact̄gḡc̄ga
211441	att̄t̄c̄ḡcḡaa	t̄c̄gḡt̄gḡtḡa	ac̄at̄gḡcc̄aa	c̄ḡtt̄tḡct̄cḡ	ac̄gaaḡt̄caa	aac̄gc̄ḡac̄at̄
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211561	caḡtt̄ḡcaac̄	ac̄gt̄t̄caact̄	c̄ḡct̄c̄ḡcat̄c̄	t̄ac̄ḡc̄c̄cḡct̄	tḡgḡat̄at̄cc̄	c̄ḡatt̄c̄aḡc̄ḡ
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211681	gḡgat̄ḡac̄ac̄	t̄c̄gḡc̄ct̄ac̄ḡ	c̄ḡc̄c̄ct̄c̄cḡc̄	ac̄gḡat̄c̄ḡct̄	t̄cc̄cc̄gat̄ḡc̄	gḡtḡgaaḡt̄c̄
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211861	cac̄ḡac̄aḡcc̄	gact̄c̄gat̄ga	gt̄tḡct̄gt̄ac̄	at̄cat̄c̄ḡaga	acc̄t̄c̄t̄t̄c̄gḡ	ct̄ac̄at̄c̄ḡct̄
211921	c̄gc̄gt̄at̄ḡga	gt̄gaaḡc̄gḡc̄	c̄ḡct̄c̄ḡc̄gat̄	gac̄gaaḡtt̄ḡ	c̄ct̄ac̄gaac̄ḡ	aat̄gḡat̄c̄ḡc̄
211981	caat̄acc̄ḡc̄ḡ	aaḡtt̄ḡcc̄ca	gt̄gḡtḡgḡc̄ga	ac̄att̄c̄ḡc̄ḡḡ	ct̄cac̄ac̄ḡgt̄	t̄gaat̄cc̄ḡt̄c̄
212041	gaaḡcaac̄ḡḡ	at̄c̄ct̄t̄gḡga	at̄c̄gt̄ac̄ḡaḡ	t̄cc̄ḡct̄c̄gt̄t̄	tḡgt̄c̄ḡct̄ca	aḡct̄c̄t̄ḡc̄gt̄
212101	tt̄gt̄gḡc̄acc̄	gt̄gḡc̄gḡtḡc̄	acaac̄ḡaḡgc̄	gac̄att̄ḡc̄gt̄	t̄ct̄gḡgḡc̄acc̄	t̄c̄ac̄ḡc̄gḡat̄
212161	ct̄ḡtt̄tḡatt̄	cacc̄ac̄ḡaḡc̄	ct̄ac̄at̄ḡct̄c̄	gt̄ḡat̄ct̄c̄cḡ	cact̄ḡct̄ḡga	ac̄gc̄aaaḡac̄
212221	tt̄cat̄cc̄cc̄ḡ	ccc̄aaḡc̄act̄	ct̄tḡat̄cc̄ac̄	tḡgt̄c̄t̄gt̄ḡc̄c̄	aaḡc̄c̄gat̄c̄ḡ	gḡtḡgḡact̄ḡ
212281	c̄gc̄aḡc̄gḡaḡ	c̄gaact̄c̄att̄	ḡc̄ct̄c̄gt̄ct̄ḡ	acc̄gaac̄ḡct̄	gḡtt̄ḡct̄ḡca	act̄t̄c̄ḡc̄gat̄
212341	cac̄at̄ḡc̄gḡḡ	agḡact̄c̄ḡca	c̄ḡaḡct̄c̄tḡḡ	cc̄ac̄gt̄gt̄ca	acaaḡtt̄c̄ct̄	tḡact̄at̄c̄t̄c̄
212401	gaaḡccaat̄ḡ	c̄gḡaat̄c̄gt̄t̄	tt̄gḡt̄cc̄ḡca	c̄ct̄c̄ḡct̄t̄cḡ	aaḡtt̄gḡc̄ga	c̄gat̄ḡaḡccc̄
212461	c̄gt̄gat̄c̄gḡc̄	at̄c̄ḡc̄ḡac̄aa	ct̄gḡgḡaḡcaa	gaatt̄aḡcc̄ḡ	aaḡccaac̄ga	aḡat̄c̄cḡtt̄t̄
212521	gḡat̄c̄acc̄cḡ	aagaaḡat̄ga	c̄ḡaḡgc̄gḡga	ct̄gt̄tt̄tḡat̄ḡ	c̄ḡgc̄gt̄ac̄ga	aaac̄gt̄c̄aḡc̄
212581	t̄at̄c̄ḡcḡaca	c̄ḡacc̄gat̄ga	c̄gḡaaac̄ḡaa	gḡtt̄c̄gat̄ct̄	tt̄ḡatact̄aḡ	caḡc̄ḡac̄aḡc̄
212641	aḡc̄aḡtḡt̄cḡ	ac̄gaact̄c̄ga	aḡcc̄gaaḡtḡ	aaac̄ḡact̄c̄ḡ	cc̄aḡc̄c̄gt̄ct̄	c̄ḡact̄t̄c̄tt̄ḡ
212701	caḡt̄c̄ḡct̄gḡ	ct̄c̄gaat̄gt̄ḡ	gḡc̄gḡtt̄gḡt̄	ḡcc̄gat̄gt̄tḡ	cact̄ḡacc̄ga	aatt̄cat̄ḡcc̄
212761	gc̄ḡac̄ḡḡaḡt̄	c̄ḡact̄gat̄t̄c̄	aḡct̄ḡact̄c̄ḡ	t̄cc̄ḡacc̄c̄ḡc̄	aac̄gc̄c̄ḡaca	ḡcaac̄aḡat̄c̄
212821	gaaḡc̄att̄gt̄	cc̄gc̄at̄gḡgḡc̄	t̄c̄gc̄c̄ḡaḡc̄ḡ	gt̄tḡccaacc̄	gaat̄c̄gḡgt̄t̄	ḡct̄c̄gaact̄ḡ
212881	ct̄t̄gḡtḡat̄ḡ	t̄cc̄ḡaḡct̄ta	caaaāt̄caaa	c̄c̄gḡc̄gḡḡca	cc̄ḡac̄aaaḡa	tt̄cc̄at̄ḡc̄ga
212941	at̄ct̄at̄gat̄c̄	ḡcc̄gc̄c̄ḡc̄gt̄	c̄ct̄c̄c̄ḡc̄ḡac̄	aḡt̄c̄gt̄gat̄gḡ	aaac̄gḡgt̄cat̄	cacc̄ac̄c̄ḡc̄ḡ
213001	gt̄gḡaaat̄gḡ	ct̄gat̄ḡc̄ḡaḡ	ac̄ḡatt̄gat̄c̄	ḡcaaḡc̄ḡct̄c̄	t̄c̄gḡtḡcc̄ct̄	cc̄aḡgḡcaaa
213061	ct̄ḡcc̄agaaḡ	ac̄gt̄gḡḡc̄ga	agaatt̄tt̄ḡcc̄	gaaḡac̄gat̄ḡ	ct̄gḡc̄ḡc̄gat̄	c̄ḡaḡct̄gt̄t̄c̄
213121	t̄cc̄ḡc̄ḡct̄ca	t̄c̄ḡc̄c̄gḡc̄ga	c̄ḡcc̄gaac̄ga	ḡcc̄c̄ḡc̄ḡaḡc̄	gḡtt̄cc̄cc̄ḡac̄	gt̄t̄cat̄c̄ga
213181	gc̄gat̄c̄ct̄ca	at̄c̄ḡc̄aḡtt̄t̄	ḡct̄tt̄ac̄at̄c̄	cc̄act̄tt̄c̄ac̄	gt̄gḡc̄gḡtḡa	cc̄cḡgt̄caaa
213241	att̄t̄at̄gt̄ga	cc̄cḡgt̄tḡc̄ḡ	agaac̄gt̄tḡt̄ḡ	ct̄cc̄ḡac̄acc̄	tḡtt̄ḡc̄act̄ḡ	gt̄tḡcc̄ac̄gt̄
213301	c̄gc̄ḡc̄c̄ct̄gt̄	t̄c̄ḡc̄agaac̄	ct̄ḡcc̄ḡḡct̄ḡ	at̄c̄gaac̄c̄cḡ	ct̄c̄ḡcc̄aaat̄	ḡgaac̄aac̄ḡḡ
213361	cat̄ccaat̄cḡ	gt̄ḡcc̄gḡtḡc̄	c̄gt̄ḡac̄aḡaḡ	tt̄tḡac̄ḡḡct̄	tḡtat̄c̄ḡaḡc̄	tḡgt̄tat̄c̄ga
213421	t̄ct̄tt̄gḡtḡḡ	gḡt̄c̄gat̄c̄ḡc̄	c̄gaaḡc̄c̄gt̄t̄	tt̄ḡcat̄ḡc̄ga	cc̄ḡc̄c̄gḡc̄ga	acc̄gc̄c̄ct̄cc̄
213481	c̄ct̄ḡcc̄cc̄ga	ct̄gaac̄ct̄ca	at̄cc̄ḡcc̄ac̄ḡ	c̄ḡaḡaḡct̄ca	ḡc̄gt̄c̄ac̄ḡga	ccaaḡac̄ḡc̄ḡ
213541	at̄c̄ḡcc̄ḡat̄c̄	gḡtt̄gat̄t̄cc̄	act̄act̄gḡaa	c̄ḡact̄ḡacc̄ḡ	aaac̄gat̄ḡct̄	c̄gḡc̄aḡct̄gḡ
213601	ct̄ḡcc̄cc̄aca	gt̄caaacc̄ct̄	t̄c̄gc̄ct̄gt̄ca	c̄cḡct̄c̄gaaḡ	cc̄gt̄c̄aḡtḡa	t̄c̄ct̄ḡcaaaḡ
213661	tḡgḡaac̄ḡtt̄	taḡtt̄gaatt̄	cat̄caaact̄t̄	t̄ac̄gḡc̄ḡacc̄	caat̄c̄tt̄c̄ac̄	ccaaḡgt̄tt̄c̄
213721	ct̄ḡcaact̄ga	ḡcaac̄gt̄t̄cḡ	c̄gc̄gḡtḡct̄ḡ	cacc̄aaḡac̄ḡ	t̄ct̄c̄gt̄cat̄ḡ	ḡct̄gḡaac̄ḡc̄
213781	ḡcc̄at̄ḡacc̄ḡ	at̄gḡc̄ḡac̄ga	ct̄t̄gt̄tt̄gḡaa	ḡac̄acc̄c̄aḡc̄	tatt̄tt̄c̄ḡc̄ga	t̄ct̄c̄gaat̄t̄c̄
213841	gḡcaaḡat̄ca	aḡat̄caac̄ga	aḡc̄ct̄c̄ḡc̄ga	tḡgat̄cac̄ḡc̄	tḡgt̄gt̄tt̄ga	at̄c̄gt̄ḡct̄c̄
213901	gat̄cacc̄ac̄ḡ	c̄gḡaatac̄ca	aḡact̄acaac̄	aḡcac̄ḡac̄ga	cac̄aaaḡc̄ga	t̄c̄ḡc̄gḡc̄ḡaa
213961	ct̄gat̄ct̄aca	c̄gt̄t̄c̄ct̄c̄ga	tt̄tt̄t̄c̄t̄cḡt̄	ct̄ḡc̄gaact̄c̄	ḡatac̄gaac̄ḡ	c̄gt̄c̄ḡc̄gt̄gḡ
214021	aātt̄taaaac̄	c̄gat̄cat̄gt̄ḡ	ḡac̄cc̄ac̄ḡaa	gt̄c̄ct̄c̄gt̄ḡc̄	gḡat̄gḡgḡc̄ct̄	c̄gat̄caaac̄ḡ
214081	t̄c̄act̄gḡgt̄t̄	gḡc̄gt̄ḡaaaḡ	c̄ct̄caac̄ḡaa	c̄gc̄at̄c̄ḡc̄aḡ	ct̄gaaḡcc̄ga	ḡct̄at̄at̄gt̄t̄
214141	c̄agaaḡc̄tt̄c̄	gt̄gaatt̄ḡca	ac̄gt̄c̄ḡac̄at̄	t̄cc̄at̄ḡc̄ḡaa	tḡccaac̄gat̄	tḡcc̄gat̄c̄ḡc̄
214201	at̄c̄gaagaac̄	gat̄t̄c̄gt̄tt̄ca	accaat̄ḡac̄ḡ	at̄c̄ḡacc̄ḡaa	tḡc̄gat̄c̄ḡct̄	tḡt̄c̄gaac̄cc̄
214261	ḡcc̄at̄gḡgḡc̄ḡ	at̄ḡc̄gḡaaḡc̄	gḡacc̄ḡct̄tt̄	aḡtḡcc̄ḡc̄gt̄	t̄c̄gaac̄aact̄	c̄gaaḡc̄aḡaa
214321	ḡccaac̄gaac̄	tt̄t̄c̄ḡc̄gaac̄	t̄cc̄cḡtt̄gḡc̄	gt̄c̄gḡact̄c̄ḡ	at̄c̄t̄ḡc̄c̄ḡcc̄	tt̄gḡtt̄ḡaḡt̄
214381	ḡct̄c̄tḡgaaḡ	at̄gaaḡtḡga	aaaḡat̄c̄gḡḡ	aaac̄ḡaaat̄c̄	taat̄c̄aḡc̄ga	gat̄tḡacc̄c̄ḡ
214441	caagaatt̄ga	tḡacc̄att̄cc̄	c̄gt̄c̄aḡcc̄ca	ct̄ḡac̄ḡct̄gḡ	ac̄gaact̄caa	aac̄gc̄aact̄c̄
214501	gc̄ḡac̄ḡḡct̄c̄	aaac̄cc̄aaaḡḡ	cc̄gc̄c̄ḡgt̄tḡ	c̄ct̄cat̄at̄ḡc̄	gt̄c̄ḡcc̄ḡcaa	at̄c̄ct̄aaḡtt̄
214561	gc̄gc̄gt̄t̄cc̄ḡ	t̄ct̄ḡgt̄t̄c̄ḡc̄	gḡt̄c̄gḡct̄tt̄	gc̄gc̄gt̄ḡacc̄	ḡct̄ḡcac̄gḡḡ	t̄gaac̄gaacc̄
214621	ḡcaaact̄tt̄ct̄	t̄c̄gc̄ct̄cc̄cc̄ḡ	gt̄tḡc̄gt̄ḡca	t̄ct̄c̄gt̄tt̄t̄c̄	gaaaḡtḡaca	aḡcaaaac̄cḡḡ
214681	c̄gat̄gat̄tt̄t̄	t̄c̄aḡc̄ḡgaat̄	ct̄c̄ḡaaaaḡt̄	caaaaaaact̄	tt̄ḡact̄caaḡ	t̄cc̄ḡact̄ḡaa
214741	aat̄gḡc̄gt̄cḡ	c̄ḡaḡgc̄ḡaḡḡ	tt̄t̄c̄aḡaḡgt̄	caac̄cc̄c̄ḡaaa	ḡac̄att̄ḡc̄aḡ	gaact̄c̄aḡgḡḡ
214801	gaat̄gat̄cc̄ḡ	ct̄c̄ct̄c̄taaa	ḡac̄cc̄caaact̄	ct̄cc̄cc̄cat̄cc̄	ct̄c̄ct̄att̄tt̄t̄	at̄c̄ḡc̄gḡc̄at̄
214861	cacc̄att̄caa	caḡc̄gt̄gat̄t̄	caaḡtḡaaḡc̄	gc̄ac̄aḡgḡtḡ	cc̄gat̄ct̄aga	tt̄gḡct̄ct̄cc̄

214981	tccaacācgc	t̄t̄t̄ccgctcc	gc̄c̄ḡaatgct	t̄ctccḡaccg	āc̄ac̄ct̄c̄gt̄t̄	tccacāt̄ct̄t̄
215041	gattt̄gtcat	c̄ḡgaactagc	t̄c̄gt̄cac̄ct̄g	ac̄gat̄cac̄gc	taḡgacac̄ga	ct̄t̄cac̄aggc
215101	gact̄cgact̄g	ac̄aaac̄aaaa	c̄aḡc̄gaat̄ac	ct̄tt̄accaag	c̄ct̄t̄gḡcgat	tac̄aḡtt̄c̄gc
215161	gacc̄ḡct̄tḡg	t̄ḡccaat̄ct̄g	ḡct̄ḡgaaact	t̄ḡgaagaaga	c̄ct̄ḡc̄ct̄gag	c̄gaagat̄c̄gc
215221	aaḡgt̄ctact	ac̄ct̄gt̄cact	t̄gaat̄t̄ct̄t̄g	at̄c̄gḡc̄c̄gt̄t̄	c̄ḡct̄cac̄caa	c̄gc̄ḡgt̄cgaa
215281	aac̄ct̄cgact	t̄ggac̄gaaga	c̄gt̄c̄cḡcaaa	ḡct̄ct̄ḡcgag	c̄ct̄ac̄aḡc̄gt̄	c̄ḡgaat̄ggaa
215341	gaaḡtc̄ḡct̄g	ac̄aaaḡaact	c̄gat̄ḡc̄cḡgt̄	t̄t̄gḡḡcaat̄g	ḡt̄gḡc̄ct̄c̄ḡg	c̄ḡct̄t̄gḡc̄g
215401	gcat̄gt̄tt̄t̄cc	t̄ggac̄aḡct̄g	t̄ḡcaaac̄ct̄g	c̄aḡct̄t̄c̄c̄ḡg	t̄c̄gt̄t̄gḡc̄t̄a	c̄gḡcat̄c̄c̄gt̄
215461	tac̄gaatac̄g	ḡaat̄gt̄t̄cca	c̄c̄aḡcac̄at̄c	gāagac̄ḡḡgc	ḡccaaḡtc̄ga	aḡacc̄c̄ḡgat
215521	c̄ḡct̄ḡḡt̄t̄gc	ḡt̄gat̄gḡcaa	t̄c̄ct̄t̄gḡḡaa	at̄caaac̄ḡcc	ct̄gaaḡac̄ac	t̄c̄ḡc̄c̄ḡc̄gt̄t̄
215581	c̄ḡct̄t̄ct̄ac̄g	ḡc̄c̄ḡcac̄c̄ga	aāact̄act̄ac	gac̄gaac̄ac̄g	gāact̄t̄t̄ḡc̄g	acc̄ac̄gt̄t̄t̄g
215641	ḡt̄c̄gact̄c̄gt̄	ac̄gat̄gt̄t̄ct̄	t̄ḡc̄c̄gt̄t̄cca	t̄ct̄gac̄at̄ḡc	ct̄gt̄t̄c̄ct̄ḡg	gt̄acc̄ḡcaac
215701	gac̄ac̄ḡgt̄ca	ac̄ac̄gt̄t̄ḡc̄g	at̄t̄gt̄gḡaaa	ḡc̄gt̄cḡac̄ga	c̄cḡac̄gt̄c̄t̄t̄	cāac̄ct̄c̄aḡc
215761	gaatt̄caat̄g	c̄gḡḡct̄c̄gt̄a	c̄cc̄c̄gaaḡcc	ḡt̄c̄ḡc̄ḡḡcaa	agāac̄ḡac̄gc	c̄gaac̄aaat̄c
215821	t̄c̄gat̄ḡgt̄gt̄	t̄gt̄at̄cc̄caa	c̄ḡac̄ḡcc̄aḡc	ḡaaaat̄gḡca	aḡgaact̄ac̄g	act̄gaac̄aaa
215881	c̄aḡt̄act̄t̄t̄c	t̄t̄gt̄ct̄c̄aḡc	at̄c̄ḡct̄cc̄aa	gac̄gt̄gat̄c̄g	c̄cc̄gt̄t̄gḡgt̄	t̄gaac̄aḡcac
215941	ḡgt̄ḡagḡact̄	t̄c̄aḡt̄ḡact̄t̄	t̄gḡac̄ḡcaaa	aāct̄ḡc̄t̄t̄cc	aāct̄caat̄ga	cact̄cacc̄cc
216001	ḡc̄ct̄gt̄gt̄ct̄g	t̄t̄cc̄c̄gaact̄	cat̄ḡcḡatt̄g	ct̄gat̄gḡac̄g	aḡcat̄gḡact̄	t̄gaat̄gḡḡac
216061	gac̄ḡc̄ct̄gḡg	ac̄gt̄ḡgt̄ḡac	ac̄gt̄t̄ḡcat̄g	ḡct̄tac̄acca	acc̄ac̄ac̄gt̄t̄	ḡct̄t̄cc̄cḡaa
216121	gc̄gt̄t̄gḡaāc	gat̄ḡgt̄cc̄gt̄	c̄ḡgt̄ct̄gt̄t̄c	aḡt̄c̄ḡct̄t̄ḡc	t̄ḡc̄c̄ḡc̄gt̄t̄t̄	ḡct̄c̄ḡac̄at̄c
216181	at̄ct̄ac̄ḡaga	t̄caac̄ḡct̄c̄g	ḡt̄t̄ct̄t̄ḡaaa	ct̄c̄gt̄c̄gat̄c	aḡc̄aḡt̄gḡcc	c̄ḡgt̄ḡac̄gt̄t̄
216241	gc̄gat̄ḡc̄gt̄c	ḡc̄ḡaaat̄gt̄c	ḡt̄t̄gat̄t̄ḡaa	gāaḡgt̄ḡaca	acc̄c̄ḡcac̄at̄	c̄c̄gaat̄gḡc̄g
216301	tac̄ct̄gḡcca	t̄t̄gt̄c̄gḡaag	t̄t̄t̄ct̄c̄ḡgt̄c	aāc̄ḡgt̄gt̄t̄g	c̄c̄ḡgt̄ct̄ḡca	cācac̄aḡt̄t̄g
216361	t̄t̄ḡgaat̄c̄ag	ḡc̄ct̄gt̄t̄caa	ac̄act̄t̄caac	ac̄ḡct̄gt̄gḡc	c̄cc̄ḡcaaḡt̄t̄	cāacaac̄aag
216421	ac̄aaac̄gḡc̄g	t̄ḡacc̄caac̄g	tc̄gt̄t̄gḡt̄t̄g	t̄c̄ḡc̄act̄ḡca	acc̄c̄aḡḡc̄ct̄	t̄c̄gt̄ḡac̄ct̄c
216481	ct̄caac̄ḡaaa	c̄c̄att̄gḡc̄ga	aḡgt̄t̄gḡcaa	aāaḡac̄ct̄ca	c̄caaaat̄caa	aḡaḡt̄taact̄
216541	c̄ct̄t̄ac̄ḡc̄ga	c̄c̄ḡac̄ḡcc̄ga	ct̄t̄cc̄ḡcaāg	aāgt̄gḡat̄c̄g	at̄gt̄caaḡca	aḡaaaac̄aaa
216601	ḡct̄c̄ḡct̄t̄gt̄	c̄aḡact̄t̄gḡt̄	ḡgt̄c̄ḡc̄ḡḡaa	acc̄ḡḡc̄gt̄t̄c	ḡct̄t̄t̄ḡac̄ac	gt̄catt̄c̄at̄g
216661	t̄t̄c̄ḡac̄gt̄t̄c	aāgt̄caāac̄g	gat̄t̄cac̄ḡaa	t̄ac̄aaac̄gt̄c	aāct̄ct̄t̄ḡaa	c̄gt̄t̄t̄t̄ḡcat̄
216721	at̄c̄gt̄ḡc̄acc	t̄gt̄ac̄gat̄c̄g	cat̄t̄t̄t̄ḡc̄gt̄	ḡgt̄ḡaaac̄c̄g	c̄ḡgḡcat̄gḡt̄	c̄cc̄ac̄gt̄t̄ḡc
216781	gt̄c̄ct̄gat̄c̄g	gc̄gḡc̄caāaḡc	aḡc̄cc̄cc̄c̄ḡgt̄	t̄acc̄ac̄gt̄c̄g	c̄caaatt̄gat̄	c̄gt̄gaaḡct̄g
216841	at̄caac̄gat̄g	t̄t̄ḡc̄gaaḡaa	ḡgt̄caac̄aat̄	c̄ac̄cc̄c̄ḡc̄ag	c̄caat̄ḡac̄ct̄	ḡct̄caaḡgt̄g
216901	gt̄ct̄t̄t̄ct̄t̄cc	c̄gaact̄at̄c̄g	c̄gt̄t̄t̄c̄gt̄c̄g	at̄ḡgaaḡt̄ga	t̄t̄t̄ḡcc̄c̄aḡc	aācc̄ḡaḡt̄t̄g
216961	t̄ct̄ḡaḡcaaa	t̄t̄t̄caac̄c̄ḡc	ḡgḡcaāaḡaa	ḡct̄t̄cc̄ḡḡca	c̄gḡḡcaac̄at̄	ḡaaatt̄cat̄g
217021	at̄gaac̄ḡgt̄g	c̄gt̄t̄ḡac̄gat̄	t̄gḡcac̄ḡct̄c	gat̄gḡt̄ḡcca	ac̄at̄c̄ḡaaat̄	c̄cḡaḡaaaac̄
217081	gc̄gḡgt̄ḡc̄c̄g	agaact̄t̄ct̄t̄	ct̄t̄gt̄t̄c̄ḡgt̄	t̄t̄ḡḡac̄ḡct̄g	c̄c̄gaaḡt̄aac	c̄c̄gaatt̄ḡaag
217141	aāgḡact̄at̄c	gt̄cc̄caac̄ḡa	aat̄cat̄c̄ḡcc	ḡct̄gat̄ḡaḡg	ac̄at̄c̄gt̄t̄c̄g	cat̄cat̄ḡaac
217201	ct̄ḡct̄ḡḡaaa	ḡc̄gḡac̄act̄t̄	caat̄c̄ct̄ḡac	aāt̄cc̄aḡgt̄t̄	t̄gt̄t̄c̄ḡatt̄t̄	gt̄tḡacc̄aḡc
217261	gḡc̄ct̄ac̄ḡca	acc̄ct̄c̄aḡga	t̄c̄ct̄t̄gḡgt̄c	acc̄at̄c̄ḡc̄c̄g	ac̄ct̄t̄c̄gt̄ḡc	gt̄ac̄at̄c̄ḡac
217321	ḡct̄caaḡc̄c̄g	aāgt̄t̄gḡcaa	ḡgc̄atacc̄caa	gac̄gt̄c̄gat̄c	act̄ḡgaat̄ca	gat̄ḡaḡcat̄c
217381	ct̄aaat̄ac̄c̄g	c̄agḡc̄aḡc̄ḡg	ct̄ḡgt̄t̄c̄aḡc	aḡc̄ḡac̄c̄ḡaa	c̄ḡatt̄c̄aḡca	at̄ac̄ḡc̄c̄ḡac
217441	gac̄at̄ct̄gḡg	ac̄gt̄ḡc̄ḡacc	act̄gt̄c̄gt̄aa	ḡcc̄cc̄aāc̄ct̄	gat̄t̄gḡt̄cca	aāc̄ḡaaaaḡg
217501	ḡct̄c̄ḡgt̄ḡag	aāat̄c̄ac̄c̄ga	ḡcc̄ct̄t̄t̄t̄t̄t̄	ḡt̄t̄gt̄t̄t̄ḡag	aāc̄gaatt̄ḡc	ct̄aḡt̄act̄ac
217561	aḡc̄ḡct̄aāct̄	ḡgt̄gt̄t̄gt̄ag	aḡgḡc̄c̄ḡḡgc	t̄t̄t̄t̄c̄ḡct̄ga	gaat̄aḡc̄aḡc	t̄gḡaḡat̄t̄t̄t̄
217621	ḡt̄t̄t̄ḡct̄ḡca	c̄gḡaḡaḡct̄t̄	ḡgc̄at̄ḡgat̄g	t̄c̄ḡct̄gaact̄	ḡgaac̄aāct̄c	gāaḡat̄c̄ḡgt̄
217681	t̄aaat̄ḡct̄t̄a	ct̄t̄gḡct̄c̄ḡc	t̄t̄t̄gḡc̄gat̄t̄	ḡt̄t̄t̄t̄c̄ḡac̄g	aāḡc̄ḡac̄ac̄g	aḡgḡct̄c̄att̄
217741	t̄ḡac̄ḡac̄cta	t̄gt̄c̄c̄gt̄gḡt̄	caact̄t̄t̄t̄c̄c̄g	ac̄ct̄gḡac̄ḡc	cāaḡaḡt̄gt̄g	gaḡc̄c̄gat̄t̄g
217801	c̄gt̄t̄ḡcaaḡc	c̄gḡt̄ac̄ac̄c̄g	gt̄ḡc̄gaac̄ct̄	t̄ḡc̄aḡgaatt̄	t̄at̄c̄ḡc̄c̄c̄ag	cat̄c̄ḡgt̄gḡg
217861	ac̄gaaḡat̄gḡ	act̄t̄c̄ḡc̄aḡg	aḡḡct̄gat̄cc	ac̄at̄c̄gt̄c̄c̄g	t̄gat̄ḡaḡcat̄	gt̄caac̄aaga
217921	ac̄act̄gt̄c̄ḡc	gat̄catt̄ḡac	ḡaaacc̄aḡc̄g	ac̄gt̄caaḡaa	ḡgḡc̄ḡac̄aaa	ac̄ḡc̄ct̄gḡc̄g
217981	t̄ḡcaac̄ḡaca	gt̄gḡt̄ḡc̄ḡḡc	aāaḡt̄c̄ḡḡca	aḡc̄aḡḡaḡaa	ct̄gt̄at̄c̄gt̄c	ac̄ḡgt̄t̄cat̄c
218041	t̄gḡct̄ḡc̄ḡḡc	gaac̄ḡaaḡac	t̄t̄t̄c̄act̄ḡca	t̄gḡt̄c̄gat̄gḡ	t̄gaact̄gt̄t̄c	ct̄cc̄cc̄ḡaga
218101	ḡct̄ḡḡaḡtaa	c̄ḡacc̄ḡc̄ḡag	c̄gt̄t̄gt̄ḡc̄c̄g	c̄c̄ḡc̄c̄ḡḡcat̄	t̄cc̄c̄gat̄ḡag	at̄ḡgt̄ct̄at̄c
218161	ḡcc̄cc̄aāct̄g	gc̄aḡat̄c̄ḡc̄g	t̄t̄gḡaātt̄ḡc	t̄t̄gat̄c̄ḡc̄ag	taaḡḡaḡḡag	gḡḡatt̄ḡaat̄
218221	at̄c̄ct̄t̄gḡct̄	aācc̄ḡct̄ḡac	gāaḡḡct̄ac̄g	ḡc̄ḡgt̄aāacc̄	t̄gḡatt̄c̄ct̄ḡ	gāaḡct̄ct̄t̄ḡ
218281	c̄c̄ḡacc̄ḡc̄ga	t̄c̄agaaḡt̄t̄t̄	gt̄ḡct̄t̄ḡaaḡ	t̄ḡc̄c̄ḡc̄gaac̄	ḡt̄t̄t̄t̄c̄ḡgt̄t̄	t̄gḡḡagaaḡc
218341	at̄cc̄c̄gaaḡt̄	gac̄c̄ḡaḡc̄aḡ	c̄c̄ct̄at̄c̄ḡca	aḡgḡc̄ḡḡc̄c̄g	c̄ḡḡc̄c̄ḡaḡgt̄	c̄ḡcaaḡac̄ac̄
218401	c̄cc̄ḡc̄gt̄caa	gaḡc̄ḡḡḡḡaa	aḡt̄t̄c̄ḡc̄c̄ḡc	gāaḡt̄gt̄t̄ga	aāc̄aḡt̄gt̄t̄c	t̄gḡc̄ac̄ḡḡc̄g
218461	aāc̄gat̄ḡaa	aḡc̄ḡaaac̄ḡc	t̄gḡaaac̄ḡct̄	acc̄ḡc̄gt̄caa	aḡac̄ḡḡc̄ḡag	aāaḡgt̄cc̄ca
218521	t̄cat̄ct̄gḡga	aḡcc̄aāḡc̄ḡg	ḡt̄t̄c̄ḡc̄gt̄ca	cact̄caāaḡg	c̄aḡc̄ḡac̄ḡga	ct̄acc̄ḡḡḡḡc
218581	t̄gt̄ct̄ct̄gt̄g	ḡt̄t̄gḡt̄gḡt̄c	gc̄ḡḡaaac̄ḡ	t̄ḡct̄t̄ḡac̄ḡg	c̄gaact̄ḡaaa	t̄t̄ct̄t̄c̄gt̄ca
218641	ḡcaac̄ḡc̄ḡaḡ	c̄ḡaḡt̄t̄c̄ḡct̄	t̄c̄gat̄gḡc̄ga	t̄ḡct̄ḡct̄aca	ḡgt̄t̄ḡc̄gt̄t̄t̄	c̄aḡc̄gat̄gḡc
218701	gaḡt̄ḡgaac̄ḡ	t̄t̄gt̄t̄t̄c̄ḡaḡ	gat̄c̄agāaac̄	aāḡaḡgt̄c̄ḡg	ct̄taḡact̄gt̄	tac̄ḡaḡgḡḡc
218761	ḡcc̄ḡatact̄t̄	ḡgḡt̄ct̄ḡaaa	c̄ḡcc̄act̄t̄ga	t̄cat̄c̄ac̄gt̄c	ḡt̄t̄ḡaḡct̄at̄	ct̄ḡt̄t̄t̄ct̄t̄t̄
218821	c̄ḡcaaac̄ct̄ḡ	c̄c̄aḡc̄aḡḡaḡ	c̄gḡḡaaaaaa	aāt̄c̄c̄ḡḡaḡt̄	gḡacaatt̄t̄ca	ḡḡaaat̄t̄c̄ḡc
218881	gac̄ḡc̄ḡgt̄c̄g	ac̄gc̄caat̄c̄gt̄	t̄gt̄c̄aḡct̄gḡ	t̄c̄act̄c̄c̄ct̄c	gt̄ḡaḡaḡt̄c̄g	t̄c̄ḡcat̄gt̄t̄ḡ
218941	ct̄t̄gat̄c̄aḡg	t̄c̄ḡc̄ct̄c̄ac̄ḡ	gat̄caact̄ac̄	cat̄caat̄cac̄	ḡcaac̄ḡtaḡc	ḡḡct̄c̄ḡcat̄c
219001	aḡcc̄atac̄ḡc̄	aāac̄ḡaaḡct̄	c̄ḡac̄aḡatac̄	ḡcc̄gaact̄c̄g	gt̄at̄c̄ḡac̄cc̄	c̄ḡaaaḡcat̄c
219061	ac̄ac̄gat̄ḡcc̄	gat̄gḡcc̄caa	aāct̄taḡc̄ḡc	t̄gt̄aḡt̄act̄a	ḡc̄aḡḡct̄gt̄t̄	ḡgt̄t̄taḡac̄g
219121	cat̄acc̄ḡatt̄	ḡacaat̄c̄att̄	aḡcc̄gt̄t̄gḡḡ	c̄gt̄taḡcc̄cc̄	ḡgt̄t̄gḡc̄gt̄c	tāat̄caac̄c̄ḡ
219181	c̄c̄ḡct̄aāc̄ḡc	ḡgt̄ḡc̄ḡḡct̄c	aātaaāt̄caa	c̄aḡc̄ct̄ḡcta	gḡac̄aāac̄ct̄	ac̄ḡct̄gḡcc̄c̄
219241	gaḡcc̄cc̄at̄c̄	gc̄ac̄gt̄c̄ḡc̄c̄	aāḡc̄act̄ḡaa	t̄t̄gḡc̄ḡcat̄ḡ	t̄gaaḡcat̄ca	t̄gt̄gḡc̄c̄gt̄
219301	caḡgt̄aḡaaa	c̄c̄gt̄ḡc̄aḡc̄ḡ	at̄ccaac̄c̄gt̄	ḡct̄ḡaāct̄t̄t̄	t̄c̄ḡc̄gaaḡat̄	gt̄t̄c̄aḡt̄c̄ḡg
219361	gt̄t̄c̄ḡḡc̄gt̄t̄	ḡaaaac̄ac̄c̄ḡ	c̄gt̄c̄gt̄c̄ḡḡc	at̄t̄c̄aḡcaat̄	ḡc̄ct̄c̄gat̄c̄g	ct̄ḡc̄ḡc̄cat̄ḡ
219421	c̄ḡac̄ḡagaaḡ	aāct̄t̄ct̄cca	c̄c̄act̄t̄ct̄t̄c̄	cat̄t̄gḡc̄ḡga	tac̄aḡc̄gt̄ḡc	cat̄t̄gḡgat̄c̄

219541	cgaggtgttg	gctcāāāctt	gctcāāgcac	tgggcatgga	tacagcāacā	āatgccccāg
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219661	ctgctcctgc	gtcactcccg	tcatcagtcg	tttggcgat	ccgatgcaaa	gctgaccaga
219721	gtcagcgate	atltgtccga	tcatgttgtt	tctctaagag	gtgcaaatca	atccttctgt
219781	tttagctacc	ttccaaaccg	aaggtaagcc	agcgacaccg	cccagacgcg	gcatgcacac
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219901	ctaccaaacg	acaaccccg	tgccaaccca	gacaagcatt	tggccgggca	cgccgttgat
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220021	gccccactgg	cgctgtgccc	caaccaataa	gcgcggaccc	aatcgacggg	accacgaccg
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220381	cccaggatcg	atccctgaac	gccgcgatcg	ggacgcactc	tcaaaggagc	caaattccat
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220561	gccggcaaca	cacccggtgc	aaggattgac	aactctcgcc	agcaaccttt	ttgctgcgct
220621	tgcataggaa	tccccaaatc	gggcatttgg	actccttcga	caccatccgt	caaaccagcc
220681	acattatcgg	tgacgcaaac	aaaacgggtga	ggacgattca	agttggccgc	aacggcggtc
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220801	gccatgatga	tttcgccatc	catgattgag	ttgagttggg	gggcggttcc	ccttctaggt
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221941	atgccgatgc	gggacatcat	gagatcgatt	tgctagcaaa	ctgaaaagcg	tgaccagagt
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222121	caagtgcatt	cccaaaccgc	gcgaatagat	cgctaactgg	ggaccactga	actgggaatc
222181	aagtctcatt	gcttcgtcgt	cagtcaacca	ttcgcgagat	tgccaccgcc	gcgtagcagc
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222421	attggaacat	cggttgcgtt	cacgaagagc	tttcacctgc	cggcgtcgat	atttcattca
222481	gaaggcggag	cgtacacggt	tgtccgttgc	aaatcgacga	acacgttccc	gatgagatcg
222541	gtttgcaagg	cacgactgaa	accatcggcc	aattgcaccg	ggcgggcaca	caccagcaa
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222661	caaacgttgt	tgctgccatc	gatcgatata	ggttcgacga	tagtgggtct	gtcgttgagc
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222781	cgcggaacc	aaagcttcca	cgtctgccga	aagttcagca	gccagatttt	gctcacctct
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223141	caactgccgt	tccaccgcc	tcatctcggc	gaccaaacca	gccatctcgt	tttcgacggg
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223921	aatgttccca	accaagcttg	gatccgattg	gcaccgtcgg	cgtgcgagtg	gtgagttgca
223981	acttcgctgg	cgtaattgat	taaategtaa	actcgagctt	tgctggggcag	aatccggcga

224101	agcgaacgga	accgcccgat	cagtcacatcc	tgcgtcagct	gcttggtcccg	acgtagaagac
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224281	acgatgcaat	gctccatggt	ctttccaacc	ggcacatcgc	tgcggaatgc	tttggcgctgc
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259141	caaagccacc	tcgagacgṭṭ	cgagagattc	gggaaccgaa	gacacgtcag	accaaacgga
259201	ccgctgagaa	agagagaaga	aatgctṭḡca	ggccactata	gcagccccgt	ccagattṭḡṭ
259261	cccgagcgga	gccctgcgaa	accgacgcag	aatcaccagg	actcgcgaaa	aacgcggatc
259321	aacggggccg	atgtctcggt	ctccgtccgc	aggactgggt	ggatcacgct	gcaacgagac
259381	aatcgacgga	aatcgṭcatt	tccgctctcg	actṭṭṭḡgat	tcgcggṭcga	tatctṭccgc
259441	agccgattga	aaaacagtga	gcgtgcaatc	acattṭcagt	gatgcgaacc	gactcactgc
259501	ggtṭcaatca	gcacgacacc	aggtctcgcc	catcacgggc	gcggcggaag	tḡṭḡṭḡḡca
259561	ggcagṭṭṭcc	tagcggaatc	gcccactcca	aacgcacaac	gtṭḡccatac	cgcaaggṭgc
259621	cgcaacctcc	attgcgatct	ccccaaagṭc	aacacgṭṭat	tḡcgcccagg	acgcggctcg
259681	ataacagcga	agaagaagtc	ggccagggtṭ	ccatcggaac	cctcagacga	agccaccggg
259741	cttcgaagṭṭ	ttgactḡṭat	ttcgṭṭṭctc	aactgacctṭ	ggṭccccaat	tggaggcacc
259801	ccagccgcat	gatcgcacṭc	accattctgc	gcgcacccaa	cgccccgaac	gctcagccga
259861	acctṭṭcctt	cgacctcgcc	aaagagctcg	ctgaaaaaca	cggcacacct	ttḡctṭḡṭc
259921	tatcacgatc	caaagccatc	gaaacctact	ggcgatgaa	gaacgccctg	ccaggtḡṭṭg
259981	atctṭṭacta	tgcggcgaaa	gccaaaccgg	acctgcattṭ	cctḡṭcgacg	ctcaacggcg
260041	aaaatgcatt	catcgacgṭc	tḡctcgctḡ	gcgaattgaa	ggcagcactc	gccgctggṭṭ
260101	tcacgccaga	ccgcatgctg	cacacgcacc	catgcaagac	cgatgcaaac	ctṭṭḡḡḡaat
260161	gctatgaagc	cggcgṭgaac	tḡḡṭṭcḡṭc	tcgataaccc	aatcgaaagc	gaaaagattc
260221	gccgactgac	tcccgatḡḡ	aaactḡṭṭḡ	tḡcṭṭṭḡḡc	aacgaccgga	gcctccagcc
260281	gaatcaacct	gtcggcgaaḡ	ttcgḡṭḡcc	ccatḡcagca	agcgctḡḡaa	ctattḡḡcaa
260341	cggcaaaaagc	caaagccctg	aaagtccgcg	ggṭṭctcḡṭṭ	ccatḡṭcggc	agtcaḡṭḡcc
260401	tcaaccacaca	agactatḡṭc	gaagtḡctcc	gcagcgṭṭcg	cgaagtctḡḡ	gacgaagcca
260461	ccaaagccgg	acaccactḡḡ	gaagtccctg	acatcgṭḡḡḡ	cggṭṭṭcccc	gctccḡṭatc

260581	ĕċġtġġgġġa	ċttġġġgatt	ġġttġgacġ	ċġġaaċcagg	cġġġġġtġ	tġġaċġġaa
260641	ġġġtġġġġġ	ġatġġġġġ	ġtġatġġġġ	agagġġġġ	atġġġaattġ	cġttġġttġ
260701	tġġtġġġġġ	tġġġatġġ	ġġatġġttġ	cġġġġaagat	cġttġġġġġ	acġġactġġ
260761	cġttġġtġġt	cġġaaacġat	ġġġtġġġġ	agacġġttġġ	tġġġtġġtġ	ġġġġtġġaa
260821	cġtġġġġġġ	cacġġatġġ	ġtttġġġġ	atġġtġġġt	tġġtġattġ	ġaagtġġtġ
260881	aattġġtġġt	ġġttġġġġ	atġġġtġġt	acġtġġġġ	cagġġġġġ	cġtttġġatġ
260941	ġattġġġġat	ġġġġacagġ	ġtġġġatġġ	cġtġġġġġ	ġacacġġġġ	tġġġattġat
261001	cġġġġġġtġ	cġġġġtatt	tġġttġġġġ	ġatġġġġġ	ġġġttġġtġ	cagġġġġġ
261061	cġtġġġġat	ġġġġġġġ	tġatġġtġġ	ġġġġġġġ	cġttġġġttt	acatġaactt
261121	cġttġġġġtġ	tġġġġactt	ġġtttġġtġ	cġġġġġġġ	cġttġġġttt	cġġġġġġt
261181	tġġġġġġġaa	ġġactġġtġ	cġatġġġġġ	cġġġġġttt	ġġġtttġġġ	tġġtġttġġt
261241	ġġtġġttġġġ	tġtttġttġ	cacġġġġt	cġatġġġatġ	ġacttġttġġ	cġatġġġġġ
261301	tġttġġtġġġ	aaacġġġġġ	ġacġġġġġ	cġġġtttġġ	acġtġġttġ	tġatttġġġ
261361	atġġatġġtġ	ġġġtġġġġġ	cagġġġġġ	cacġġġġt	ġġtttġġtġġ	tġtġġġġġ
261421	tġġġaaġġġ	atġġġġġġ	aaacattġġ	cġtġġġġġ	ġġcġtġtġġ	tġġtttġġġ
261481	cġtġġtġġġ	tġttġġġġġ	tġatġġġġġ	cġtġtġġġġ	ġtġġġtttġġ	cġġacatġat
261541	tġaaacġttġ	ġtġatġġġġ	tġġtġtġtt	ġġtġġtġtġ	ġtġtġatġġ	cġcġtġġġġ
261601	cġġġġtġtġ	tġġttġtġġ	tġġatġġġġ	tġġġaattġġ	ġġġġtġtġġ	agġtġttġġ
261661	cġactġġġġġ	ġaatġġġtġ	agġtġtġġat	cġacattġġġ	ġġattġġtġġ	cġġġġġġġ
261721	ġġġttġġġġ	cġġġacagġ	atġtġtttġġ	ġġtġtġġġġ	agġġġġaaġ	acġaaġġġġ
261781	cġġġatġġġ	ġġaacġttġġ	tġġtġġġġat	ġttġtġactġġ	atġttġġġat	tġtġġġġat
261841	ġttġġatġġġ	tġġġġġġġ	tġtġatġġġ	tġġġatġġġ	tġġġġġġġ	tġġġġġġġ
261901	cġacġtġġġġ	ġaagtġġġġ	ġaacactġtġġ	ġcġġġġġtġ	atacagġtġġ	cġġġtġtġġ
261961	ġġtġġaaġġ	ġttttġtġatġ	ġtġġtġtġġt	cġġġġġat	cġatġġġġġ	cġġġġġġġ
262021	ġttġġtġġġ	cġġġġġġġ	tġġatġġġġġ	aaacġtġġġ	cġtġġġttġġ	ġġtġġġġġ
262081	cġġġġġġġ	aaacattġtġġ	ġġtġġġtġġġ	aatġtġtġtġ	cġġatġttġġ	ġtġġattġġġ
262141	ġttġġġġġġ	ġġttġġġġġ	ġġaaġġġġġ	ġatġtġġġġ	atġatġġġġġ	agġġġġġġġ
262201	cġtġġġġġġ	ġttġġtġġġġ	tġġtġġġġġ	ġġġġtġġġġ	cġġatġttġġġ	aaġġġġġġġ
262261	cactġġġġġġ	ġġatġġġġġ	cġatġġtġtġ	cġġġtġġġġ	acġtġġttġġ	cġttġġġġġ
262321	ġatġttġġġġ	ġaattġġġġġ	tġġġtġġġġ	acġatġġġġġ	cġġġġġġġ	cġttġġġġġ
262381	aatġġtġġġġ	ġtttġġġġġ	tġġġġġġġ	tġġaaacatt	cġġġtġatġ	cġtġtġġġġġ
262441	tġġactġtġġ	ġatġġġtġtġ	ġttġġġġġ	tġtġġġġġġ	ġġttġġġġġ	tġġtttġtġt
262501	cġaaġġġġġ	ġġġġġġġġ	tġġġtġġġġ	cġtġġġġġġ	ġġtttġġġġġ	acttġġġġġ
262561	tġtġtġtġtġ	ġcġġġatġġ	ġagatġġġġ	tġtġġġġġġ	ġġaaġġġġġ	ġtġtġtġtġġ
262621	atġttġġġġġ	cġttġġġġġ	cacġġġtġtġ	aaactġattt	ġcagtttttġ	ġagttġġġtġ
262681	tġġaattġġġ	tġttġġtġġġ	cġġġaatġġġ	tġġatġġġġġ	ġttġġġġġġ	ġġġġġġġġġ
262741	taactġġġtġ	cġaaacġġat	cagġtġaaġġ	atttġtġġġġ	agagġacatġ	ġaattġġtġġ
262801	acġġġtġġġt	acġġġtġġġġ	ataatġġact	tġacġaaġġt	ġctġġatttġġ	cġġġatġġġġ
262861	ġġtġġġġġġ	cġġġġġġtġ	cġġtġġġġġ	acttġġġġġġ	ġatagġtttġġ	ġġġttġtġt
262921	ġtġttġġġġġ	cġġġġġġġġ	cġtġġġtġġ	ġġġtġġġġġ	cġġġġġġtġ	ġġġttġtġt
262981	tġġġġġġġġ	cġġtġttġtġ	cġġaaacġġġ	ġġġtġġġġġ	agttġtġtġt	ġġġġġġġġġ
263041	ġtġġġġġġġ	ġtġtġtġġġġ	cġġaaactġġ	tġagġtġtġġ	ġaaacġtġtġ	ġġatġġġġġ
263101	tġġġtġtġġġ	aatġġatġġġ	cġġġtġġġt	ġatġtġġġġ	aagġġtġġġ	cġaactġġġt
263161	tġtġġġġġġġ	cġtġġaactġ	tġġġġġtġġ	acġġtġġat	acġacttġġt	ġaaactġttt
263221	aacġatttġġġ	cġġġġġtġġ	acġttġġġġġ	cġtġġġġġġ	ġacttġġġġġ	acġġġġġġġ
263281	ġġaaactġġġ	ġġġġġatġġ	cacġġaaact	cġtġġġtġtġ	tġġatġtġat	cġttġġġatġ
263341	cġġacagġġt	tġttġġġttġ	ġaaġġġġat	atġtġtġġġġ	cġtġġġtġġġ	cġatġatġtġ
263401	tġttġġġttġġ	tġttġġtġġġ	tġġġtġġġġ	agġġġġġġġ	cġġagġtġġġ	aagġġtġġġ
263461	cġġġtġtġġġ	cġacġatġġt	ġġġtġġġġġ	cġġġtġtġġ	aaacġġġtġ	cġġagacġġ
263521	cġttġġġġġġ	ġaacġtġttġ	tġġġacġġġ	ġaatġtġġġ	cġaagtġġġt	tġġġġġġġ
263581	tġġġġġġġġ	cġacġġġġġ	taacġġġġat	cġġtġġatġġ	cġġġġġtġġ	ataaagtġġt
263641	ġtġġġġġġġ	ġtġġtġtġġġ	ġġtġtġtġġ	agġatġġttġ	cġatġtġġġġ	tagġttġġġ
263701	tġġġġġġġġ	cġatġġġġġ	ġacġġaaġġ	ġtġġġġġġġ	cġatġġaaact	cġġtġġġġġ
263761	ġġatġġġġġ	ġcagġġtġtġ	tġġġġġġġ	cġaaagatt	cġttġġttġġ	tġġġġġġġġ
263821	ġtġtġġġġġ	atġġġġġġġ	tġatttġġġġġ	acttġtttġtġ	ġaacġactġġ	tġatġġġġġ
263881	tġtġġġġġġġ	cġġġġġġġ	agġġactġtġ	cġġġġġġġġ	ġagtġġtġġġ	tġġġġtġġġ
263941	ġġġġġġġġġ	tġġġġġġġġ	agġtġġġġġ	cġġġġtġġġ	tġġatġġġġġ	ġġġtġġġġġ
264001	cġtġġġġġġġ	cġġġattġġġ	ġġġaagtġġġ	cġġġtġġġġ	tġttġġġtġġ	atġġġtġġġ
264061	cacġtġġġġġ	cġagġactġġ	aagġġacġġġ	ġagġatġġġ	cġġġġġġġġ	tġġtġġġġġ
264121	cġtġġġġġġġ	acġaagtġtġ	cġtġġatġtġ	ġġaaacġġġġ	tġġġġġġġġ	cġtġġġġġġ
264181	cġġġġġġġġġ	cagġtġġġġġ	atġġġġġġġ	cġttġġġġġġ	ġacġtġġġġġ	tġġġġġġġġ
264241	agġġġġġġġġ	aacġġtġtġġ	ġatġġġġġġġ	aatġġġġġġ	cġġtġġġġġġ	cġtġġġġġġ
264301	cġġġġġġġġġ	ġaactġġact	atġtġġaaac	ġaacġatġġġ	aacatġttġt	attġġġġġġġ
264361	cġġagġtġġġ	tġagtġġġġġ	tġtġġtġġġġ	attġġġġġġġ	ġġcġġġatġ	tġacġġġġġ
264421	cġacġġġġġġ	atġatġġtġġ	cġtġġġġġġ	agacġaaatġ	ġġcġġtact	tġatġġġġġ
264481	cġġtttġġġġġ	ġaagġtact	tġġġatġġġ	ġtġġaaacġġ	cġġacġġġġ	ġġaaagtġġt
264541	ġttġtġġġġġ	tġġagtġġtġ	tġġġġġġġġ	ġaacġġġġġ	ġagtġtġġġ	acġaagacġġ
264601	agtġġġġġġġ	cġttġġaaag	ġġġġġġtġ	ġatġġġġġġ	ġacttġġġġġ	acġaagġatġ
264661	cġġġġġġġġġ	agtġtġtġtġ	tġtġġġġatġ	ġġaagġġġġ	aagacatġġġ	ġttġġtġġġ
264721	cġaagtġġġġġ	cġġġatġġġġ	atġġġġġġġ	ġtġtġġġġġ	tġttġġtġġġ	ġtġġaaġġġ
264781	ġaagaaġġġġġ	tġġġġttġġġ	tġagġacttġ	cġġġġġġġġ	aagacġġġġġ	agcactġġġ
264841	cġġtġtġġġġġ	tġġtġġtġġġ	aaactġtġtġ	agcagaaġġġ	ġġcġatġtġġ	aacġatġġġġ
264901	tġactġġġġġ	aacġaatġġġ	tġtġġġatġt	ġaacġġġġġ	tġġġġġġġġ	tġcġġġġġġ
264961	ġaaattġġġġġ	ġġtġġġġġġ	cġtġtġġġġġ	tġġtġatġġġ	cġġġactatġ	cġġġġġġġġ
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276781	aacatcgaa	gcgtacagag	caccggtttc	atcgttgccc	aaatggatca	gcagacgatt
276841	cccatccacg	acgggtgagc	aactggcgcc	ccactttgga	tgattgatcg	aaaatcgctt
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276961	gttgatgctg	gccgtgaaga	ggcgtccgctc	cgccatcacc	ggattggctt	tgggcccctgc
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277621	cgtgatggat	tgaaaaagtg	aaattgacaa	ttgcaaaatg	caaaattgat	tcgctgggca
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278881	cġtġtgatgc	ggcgċcċttt	tcgtċcāt	gcgagacgat	gaaattgctg	gtċcġttga
278941	ggatgċċtc	caacgattca	atġtgattgg	ccgacaaaca	ctggctgatg	ttggcaatga
279001	tcgggatgcc	accggċcacg	gċcgċtċga	acgċgatgċt	gċgtċċgagt	tcgċgggċtċ
279061	gggtgaacaa	ttcggċaccg	tgġttcggċca	acaatgċttt	gtċcġcggtg	acaatgtċtt
279121	tgċcagċttc	catċgċċcg	agċatgactt	cġcgagċcg	tgacaaccg	ċċcatċaatt
279181	ggatgacaaċ	gtċgattċg	gggtċattca	ggagċċatc	gatċgaatcġ	gtċaggactċ
279241	cġtċgggcag	atċaattċcg	cgaggtġtgċ	tgagatċgċg	gacgacagċċ	ttggacaacc
279301	aaatggġttt	gċċcgċtgā	cġagċggtċ	gatċgċċtg	atċgatċaac	aaacgagċca
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279421	gċttggtgga	tgtagċgtċ	atgtgggggā	tgġtaatċag	agċċċacgat	catġgaacac
279481	gggggtċatc	cagattċċtċ	gacgaagtċċ	acggġaccgġ	acggagattċ	cggġgċgtċg
279541	ggġtċgtġcġ	gċċċċaaaa	aagċatċċgċ	ċatċagaatg	aggċggattt	gtġggċaatċ
279601	aaagaaaaċ	ggċggtgċaa	cġtgċċċaaa	cġgtgċċċg	ċġgtġċċat	ttċaatċgċ
279661	aagaaċatg	cagċgggtċ	tcgggtgċgċ	aatċċċacac	ċacgacagċt	gċċċċgċtċ
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279901	ċttċċgatċt	tgtagċċgat	ċċgattgċtt	tgagaaċċt	gagċaagatt	cgaaactġtċ
279961	cġtċċċgaat	attċċċgacċ	aatċgċttċċ	gċċgtġgċaa	ggatgċtċċg	atggċaatċg
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280081	ttgġtgaacg	ggaccatgċg	ttċċgtċtgċ	aagġtċaata	cggċagċacg	ċċgċċtċċā
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280201	acgactċgċt	tċċtgċċgā	gtgggċgċċg	ċgtġċċgċgċ	ċċgtġtgċā	cġċċaagċgg
280261	aagċttacgġ	cġtgġatċċt	ttgagċaagā	ċactċaaċā	aactċaagċt	gċċtgatgāg
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280441	gċaattgċtā	cggċaccċā	ċtċgġattġt	ggċgggtgċā	aaagatċċċg	acgtgċgtġt
280501	tcgċgattġtċ	cagaaġċacg	tggtgċatgt	cġacgacggċ	tactgggggċg	gċgċaccacg
280561	cġtċgġtċac	cagtggtacg	accċgtġgċā	gċgtġacċtġ	ċacċaatċac	gtġttgacgā
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288181	g t a t t g g t g g	g a t t a t t g c t	g c c a g c c g t g	c a a t c c g c t c	g c g a a g c a g c	a c g a c g c a t g
288241	a g t t g c t c c a	a c a a c a t g a a	g c a g c t t g g t	c t t g c a a t g c	a c a a c t a t c a	c g a c g c t t t t
288301	c g a a g c t t t t c	c c t a t g g t c a	c c t c a a a t c	g g a c t t t c c g	t g a c c c a c a a	a c g g g a t t c c
288361	t g g t a c c a a a	a c a t c c t c c c	t t t t g t t g a a	c a a c a g g c a t	a c g c c g a a a a	a t a t c g a a a c
288421	g c t g c c a c g a	t c t a c a g t g t	c t a c g a a g c g	g a a t g g a t t c	a t c g c a t g c c	c c t g g a a c t c
288481	g c a g g g g t c g	c c g t c c c c a c	g t t c a t g t g t	c c g t c c g a a c	c c t c c g g c c c	a g c t c t c g g t
288541	g g c g g c g g g t	c c g a c a a t g g	t t t c c a a g g t	a g t t a c g g t g	t t t c c g c t g g	t g g a g g c a c t
288601	t t g c c t c a a g	a t c t t c t a g g	a g g g a t c a c t	c c g g a t g a g a	t c a a c a t c a t	t a a a c c g g a t
288661	c c g g g a g g g a	t g t t c g g t g a	g a c g a g g a c c	t a t a a g t t c a	g a g a t t g t c t	c g a t g g a a c g
288721	t c t a a c a c c c	t a c t c g c c a g	c g a g a c g a t c	a t t c g c g g c g	c g a g c g g c g g	a a g t t g g g g a
288781	g g c a t g g g a g	g c t a t t g g g g	t g g t t c t c c t	c a c g g a t c c t	t c g g t t t c t c	t t c a g c a g a g
288841	c c c c c a a a c a	c a t c c g t t t c c	c g a t c g t g t g	t a t t c c t g c a	a a a g c a c a a a	t t t c c c g a a a
288901	t c a c c t t g c g	a a a a c g g g a a	c g c t g a c g g t	c t c a c g g g c c	g a t g g a a c t t	c g c c c g c a g c
288961	c a t c a c a c c g	g t g g t g t a t t	a a c g g c t t t c	t g t g a t g g a t	c c g t t c g g t t	t g t t a c c g a t
289021	t c g a t c g a a c	g t c a g a t c t g	g a g a g a c t t a	g g c a a c c g t g	c c g a c g g t c a	c g t c c t g g g t
289081	g a g t t t t a g g	g g g g c a t a a g	g g a g t c t t c a	g a t a t g t g a g	c c g c c t a g c g	t t c g c c a a g g
289141	t c t c t a c a c g	a a a a c g g g g c	t a a c g c c c a a	a c g g c t c g c a	t t c t t g c c c c	c a a t c a t t c c
289201	a g c c a a a c g g	t t t g a g a t a c	g t c t a c c t g a	c g a a c a g g a g	c t t c g t t t c t c	a a a t c g t g a a
289261	a c c t t c c c a c	g c c g t a c a c a	t c a a a t t t t g	t t g a g a t t c a	c g t c a a t g t a	a a g a a t g c a
289321	g t t t g t t c t a	t c g g g c t c t t	t a t c a c g c c g	t t g a t a c t a a	c t g g t t g c c c	a g c g c g a g c
289381	g g t c t c g a g t	t g t a t c c g g t	g a c t g g t a c t	g t g a c a t t c g	a g g g c a a g c c	g a t c g a t a c c
289441	g g c c g a a t t c	a a t t c c g c a c	t g c c t c g g a a	g a g a g g c g a a	g t t t c a g t g c	t g c a a t c g a g
289501	a a t g g c a a t t	a c g a g a t g g a	a a c c c t c a c c	g g t c c g a t g a	c a g t t g a a g t	c c g g g c c t c c
289561	c g g t t g a t t g	a a g g c a a g t t	t g a c a a g t c c	a a c c c c g a c g	a a c t c a c c c c	a g c g g g c g a a
289621	a t g t a c a t t c	c t c a a a a a t a	c a a t t c t c g c	a c t g a a c t a a	c c g c g g a c g t	g c c a g c g g g c
289681	g g c g a c a c a a	t c g a c t t c a a	c t t g c t t g g t	t c c t a a a c a g	c c c g c t a a t t	c a g t t g t g c t
289741	c t g c c a a t c a	c g g c a g c a g a	a c c a t a c c c a	a c a a a t g c a a	g c a a g t t c c g	c c t t g a g a t c
289801	a c t t g c t t g c	g t a t g t t g a a	a t t a c g t t g t	t t g t c a t t c g	g g g g t g a c g a	c a g c g t a a a t
289861	c c a g t a g g g a	t t g t g t t a c t	g a g c a a c g g c	c c a a g c c a g g	c c c g g g a a t a	t c a a g c c g g a
289921	t c g t a a g c t t	c g c t g c c t a g	t c c c c t g c c c	c g t g g c a t g t	a c g c g c a c a t	c a c g a t g c c g
289981	a g g a a g t a c a	g g a a t a a c a g	c g g a a c t g c c	a g a g c c a c c a	t g c t a g t c a c	g t c g g c c g g t
290041	g t g a c a a t c a	t c g a t a t g a c	g a a g a t t a c c	a a c a c c g c g a	c t c g c c a a c t	t t g t a t g t a g
290101	t c c t g c g t t t	g a a t c a a a t c	a a t g c g t t g c	a g g a a c a g c a	t c a c c a a t g g	c a a t t g g a a g
290161	g c g a c g c c g a	a t c c c a a t g g	c a a c a t c a a c	a c a a a g t t g a	c g t a a t a g g t	c a g c c g a g g c
290221	t c c a c c g c g a	c g t c c a t c g a	t c c a t t g a a t	t g c a a c a a g a	a c g t c a g c a c	g t a g t g c a g c
290281	a c c a a c c c a a	a c g c g a g c a c	g a c g c c c g a g	a c a a a c a g c a	c c a c g c t g a a	c g g t a g g t a a
290341	a c g t a g a c a t	a a c g t c g t t c	g t g a c t a t g c	a a a c a c a g c g	c c a c a a a c g a	c c a c a g g t g a
290401	t a g a a g a t c a	t g g g g g a g g c	a a g c a c c g c g	c c a a c a a t c a	a a c c c g c t t t	c a c c c a a a t c
290461	a t g a a c g g c t	c t t c g a t c t t	c a a t g a a c t c	a g c c c g c g t t	c a c t g c g a c g	g a g c t g a a t c
290521	a t g g g c a c c a	a t t c a t c g g g	g t t g g g g a t c	g t c c c c a t c g	a t t t c a t c a a	t t c c g c g g t g
290581	g t g a t c c t c t	c t g g a a t g t c	c a g c g c a g c c	g a c t c g c c t g	c t t c g g c t t c	g a c a t c g g g a
290641	c t g t t c t t t t	c a t c c g g t t c	a g a t t c g a c g	g c c g t g c c a g	t g g c c t c c g g	c g g t t c c a c c
290701	a t g t c t c c g g	t c g c c a c t g g	g a c g t c c c c c	a g a t g c a g c g	t g t a c a c c a c	t g t c g c g a c c
290761	a g a g a a t t g g	a c g t c a a g a a	t t c g t a g a a c	c g a c t g a c c t	g c g g a t c t t c	c t t g c g g t c g
290821	g g t a g c c c c a	t c t c t t t c a g	g t c g c g a t c g	g c g t t g t a t t	c g a t g a t c g c	c t g t t t g a g c
290881	g g c t c c t g g a	t g a a t c g c a c	c a c t c g g t t g	g c g a a c a t c a	a t c c a a c c g c	c a a t c c g a t c
290941	a a c a a c c a a a	t g a t t g c t t t	g a c c a g a g a g	c c a c g g a g t t	c t t c g a g a t g	c t c c c c g a a c
291001	g t c a t c g t c g	a a t t g t c g a a	c a a a t c g t c t	t t g g g t c g c g	t c a g t g c t t c	c a c g a g t t t c
291061	a a t c c a c c a g	g g g a g g g a g g	g t a c c a t t g t	g t g a a c t a c	t c t g c a c c g a	a c t a c t c g a t
291121	g c c a a c t a c t	c g g c g t c g a g	c c a t t c t a a c	t g a c c a t t c c	a a t c t c g c a c	g g t g c c a t t c
291181	a t g a c c g a t c	c a a c t t c c t c	t t c c a a t c c c	g c g a c c g c c g	t t t c c g t c g a	t t c g g t t t c g
291241	c c t c a g a c a c	t c g t g g g a a a	a c g a g t t c t g	t c g t t t g t g g	g c g a a a t t t a	c g a g g a c t t g
291301	g a g c t t t g g t	a c c c c a a a c t	a c g c c t g a t c	g a g g c g g g a g	c a g a a t t t t t	t g t c g c g g g c
291361	c c a a a a g c g g	g c g a a a a a t a	c g a c g g c a a a	c t g g g c t a c c	c c t g t g t a a g	c g a c c t t g c c
291421	a t c g a c g c t t	g t g a g g t g a	t t c c t t t g a c	g g g t t g c t g g	t t c c c g g c g g	g t t c a t g c c g
291481	g a c a a a c t g a	g g c g a g a c c c	g a a g g t a t t g	c a a c t c g t c c	g t g a c t t t g a	c g c g g c t a a a
291541	a a g c c g a t c g	c c g c g a t t t g	t c a c g g c g g c	t g g a t t c c c a	t c t c a g c a g g	c g t c t a c c g c
291601	g g c g t t c g c g	t g a c c g g a t c	c c c g g g c a t c	a a g g a c g a c c	t c g t g a a c g c	g g g a g c a a t c
291661	t t c g a a g a c g	c t t c g g t c g t	g g t c g a c g g g	c a c c a c g t c a	g c a g t c g c c g	c c c t g a c g a c
291721	c t g c c c g a t t	t c t g c c g c c a	c t t c a t c g c c	c t g c t c g c g t	a a t c c c a a c c	t g t a g c t c g g
291781	t g c t c c c c c a	c t g a g a c g a g	c a t g g a c c a g	c c g t c t t c a a	c c g t t t g c g t	c g c a g g g g g g
291841	a c t t g c c t c a	a a c g g t c g c a	c g a a c g a c g c	g a g c c t g t g a	g a c g a t g g a t	c g t g c t t g g
291901	c g g c t g a g c g	c g g c g a g a c g	g a a c a a t t a g	g g a c a a t g g t	t c t a c t c t g g	t g c a a t c a c c
291961	g a a c c c c a a c	a t c t c a c g g c	g g g g a c c g c c	g t g c t a c a g g	t t t t t g g t g g	c t g t g a c a t t
292021	t t g t g a a a c t	g a a g c g t c g t	g a t t c c t t g g	c g g a g t t g a c	t t g a c a t c g a	t t g t c g c g g a
292081	t t c g t a g g g t	c g g c t c g a t g	g a t g a t t c c a	a g g t t c t t t c	c g a t t t g g t t	g g a c g g c g t t
292141	c c c g c g t g t a	t t t t c g t t c c	c a c g a a c g a a	t g a c t c t c t c	g g c a c c g a t g	c g g t g t t g g t
292201	g g g c a a c c t g	c g c g c t g g c a	a t t g t g a t g c	t t g g t t c a g g	a t g c t c g c t g	t t t c g a a a c g
292261	g t g t t t g g t c	c g a t g g a t c g	t c c g g c g a a t	t g a a t t c g g g	g t c g a a t c a c	a c a c a a g t t t
292321	c a a a g c t c a c	c c a c a a g a g c	c g a a a g a c g a	t t t c g t t g c a	g g c g g a t t t t	c g t c a c g t c g
292381	g c a c c c a a g a	c c t g g a c g a a	t c g c t g t g g c	a g c a c g t t g a	t g a a a c c g c t	t t t c c g c c a a

292501	cċttgċċgā	aācggċāgāā	ġagaatġttg	cctċgggċgā	tgaċccaātċ	aatcgċttgċ
292561	tttcaaccgċ	cggggtgġtg	ggacgċagtc	catcgġgtat	cgaaaccatt	ccgttgċgċ
292621	catċgċagċg	acacgaactt	ccgatċtcca	cggtgċtgga	tgggtċtcat	gtċgtactgg
292681	ċtcaagagaa	cggcaagċtċ	accggċcgċt	cattgġattċ	gċccċagatg	tċgċgtċgt
292741	tgaċaccaac	gġtgggċċċċ	ggacċtgggċ	aagtċacċtt	ggagatċcgġ	ċċgaaatċċ
292801	agċatgġttċ	ggtċċagċaa	cġtttċatċa	gċagċgaagċ	ggċgacacġt	ttggċgacċg
292861	gacġtċċac	ttgggaactg	ċċggaatga	atċtttċgtg	ggċċgċcaat	ċċgċatċtga
292921	cġttgġtgat	cġtċċgġtg	catċaaccag	acgaaaacġa	accaacġttt	ggattggċċa
292981	ggċaaatgċt	tċgċgacġċċ	gatċacatġċ	aagacġacca	acatġtgatg	ttġtġtġtċ
293041	gaatċaacġa	tttgċċġtċt	tċċtgatċtċ	cggaaaaatt	ċtġtġggġtg	gattċġtġċ
293101	cġtgċaaacġ	aggċgġċtag	ċtċatġtċtt	tċacacġagċ	gagattttċg	ċgatċċacġċ
293161	aġċċċċċċg	gaagġtttġċ	cacċatttġċ	tāaaċttċtt	ttttċgatga	ċtġtġgatċġ
293221	catċtġtgatċ	ggatggaactt	cġttċatgaa	agacġċtċac	tttgġġtgac	actċċċtċtċ
293281	ċċgatċċċċg	gċċgacċġtċ	aacġcaccac	cġgtċtċċċċ	acċċgġċċaa	gċġtġtċġa
293341	tġgacġaagġ	gacċġtġċġg	ċaatċċacċċ	ċġtagacġċ	ċċagġċċatt	cacġċtttga
293401	tġċġtċċġtt	tġtttċċgċag	catċtġġtġċ	tġtċċgġgac	ċgaagċċgaa	atċatċgagġ
293461	tgaċċċċċa	cġgġttċġtċ	gċgatġgġtċ	ġtċċacġġtġ	catċġġċttt	tċċċċatċġ
293521	agġtċtācag	tċċaaġċtġ	gċċgaactġċ	aatġtċttġċ	ċġtġċacċċċ	gaagċċċaac
293581	ġtttġgġact	gggacġċaaa	ttġġtċġgġċ	actġċatċġa	aagagċċċċċ	acġċtċġġtġ
293641	tġatġggaat	ċċtċċġgatċ	agċtċċtċċġ	aagacttċċt	ċaaatċatġċ	ggċttċġatt
293701	actċġttġċċ	ċgaccagaaġ	aaagċċttġt	tċtġċċaact	ċċġtċċtċċċ	aacttċġatġ
293761	accactġaaa	tġċaacċġċt	ċgaatttttċ	aagċaatċċa	ttċtġacġċċ	cagċċċttċġ
293821	ġġttacġaag	aacċgatċċa	aaaactġatċ	ggċgaatacc	tġaaacċċġa	cagċġacġaa
293881	ġtċtċgatċġ	acġtġċacġġ	aaacċtġacc	ġtċċġġtċġ	gċgaagċġġġ	tġġċċċċaag
293941	ċtġatġttġġ	ġtġġtċactġ	tġacċaaatċ	ggċatġġtġa	tttċacacat	ċġacġatċaa
294001	ġġattċttġt	acġċċċaaac	gatċġġġġġt	tġġġacċċac	agċaactġat	ċġġtċaatċċ
294061	aġġacġġtġt	ggacċġacġa	ċġġtċċċġtċ	tċċċċġġtċa	tċagġtċġaa	ġċċaatċċac
294121	ttġttġtċtċ	aacagġaaċġ	ċġġċgagġtċ	ġtċaaġġtġġ	aacaaatġtġ	ġtġġġacatċ
294181	ġġagċċaaag	atġġtġacġa	agċċaaatċa	aaagġċċġa	tċġġġactġġ	ġġtācġttġġ
294241	aaċttġċċt	acċgagaact	ġtġġġċġac	atġġtċagċġ	ġtċċġġġcat	ġġtācācāaa
294301	acġġġcatġt	ggacġġtċat	tġaaacċċċċ	ċġtċġtġtġġ	ċċtċġtċċġa	tċaagċġttġ
294361	ċagġġċgaac	tġċacagċġt	ċġċġactġtċ	ċaagagġġaġa	tċġġtċtġċġ	tġġagċċaaġ
294421	acċġtġċċġ	ġtċġċatċaa	ċċċagatġtġ	ġċċatċċċġġ	tġġatġtċac	ġċatġċatċa
294481	ġactġċċċġa	ċgatċġacaa	ācācācācāa	ggċgatātċa	agatċġġtġġ	ċġġċċċġġtġ
294541	atċttċċċġġ	ġċċċāacat	ċaacġċċāaa	ġtċġċāaagċ	ġactġatġġa	atġġġġgac
294601	ġacāacġācā	tċċġġtatċa	acċtġċġġġġ	ċtċċċċċġġ	ċċġċċċġaa	tġattċċāac
294661	ġtġttġċagġ	tttċtġġttċ	aggċġttġċċ	acaggacttġġ	tċġġattċċċ	ċaacċġtāc
294721	aġġactċag	ċġtċġaaac	gatċagċċtċ	ġġtgacatċġ	aagċġattġċ	ġaaactġġtġ
294781	acġġtġttċġ	ċtċaatċġġt	ġacaccagaa	tġċġatttċa	tċċċċġġttġ	atċġagġtċġ
294841	ġġtgagġaag	ċtġtgacġat	tċġġġttġġt	ggattġġcagġ	ġagagagagā	ġatċtċacġġ
294901	ċġgagacċġċ	ċġtġġtācag	ġttġacġatċ	atċċċagċċt	ġtagġtċġġt	ġġtċċċċac
294961	ċġagġġagġt	ġtċaaacġġt	tċaaacttttġ	tġċċacċġtt	ċtāattċġġġ	āacġġċċtċa
295021	atċċāagaag	catċtċġġġt	ċtċtċġġācā	ġċġġtttġtt	tġċċagġtċa	ċaatċġġtġt
295081	ġtċcagaaag	ttġttċacāa	ācāagċċtġt	agacċġċttġ	ċċgatċċtġġ	ċtġġtġtċċa
295141	ġttċaacġċa	ċċgattċtġġ	ċttttġāaga	actċġacġġt	ċġġāacġtt	tċċttttttġa
295201	aggatācāaa	ċċġġacttċ	aagġtācācā	agttġtġġtċ	ttġtġġtċċġ	ġtġtactttġġ
295261	ċtċgagċċag	aacġġtġttċ	tċcāagaġġt	ċatācġġācā	ttċāagaġāc	ġatċatċttġġ
295321	ġcāactċġġt	ġtċtttġċċa	aacacġtġġt	acacġġtċtċ	ċaagtttġgac	tċċgacċġtġ
295381	ġgaacċċatċ	ġagċāagaāa	ttċċġġttġċ	ċġġtttċġġġ	agtgatċttċ	tċċatċġċat
295441	ċċċgaagċāa	ċttċaccacġ	atċġtactġġ	ġaactāaaat	tċċtġċċġā	atġatċtċtt
295501	ċaatġġċċġċ	ċġġtġġġġt	ċċattġġġtċ	ċġġttċcagċ	tċġċāatāaa	tċġċċġġtċġ
295561	ācāaatġġac	ċċagċċċagġ	tġġġattċġġ	ċċaactċġā	catċġttċċċ	ttċċċċġċac
295621	ċġġgacċċċ	aagċācāaaċ	āacacġttġġ	ġttċġġġġā	tġġāatċġt	ġġatċġġagġ
295681	ġatġaactċac	aacċttġġġt	gaagġagċċa	ġċċttttċtċ	ġtagacatġċ	ċaacġtċġat
295741	ċġtġġġagġ	aagġtċġtċt	tċġġagġtġa	tġtċatāagċ	ġagatġġċċa	tċċagċċġac
295801	āaatċċtċċa	tġagġġatāc	ġtattġġaat	acġacagġġċ	aggacttċtċ	ġġtgatttċċ
295861	catċċġcācġ	atċċċāagċċ	atċttġċċġt	tċċāatāaac	tġġactġġāa	acġġtġċċċġ
295921	attċċġactċ	ċġcagġċġġċ	ġcagtagagġ	ġaācāaaġag	ċċatċċact	tċġġāagġtċ
295981	ċċġacċġat	ċacċtċġatġ	tāgaagġtat	tġġġagġcāġ	ċtċġttċġat	tċagġċatċa
296041	ġġagġāgaāc	ċttċtācatt	ċġttġġġġā	ċġġġtċagġ	ttċagġċġag	ċāaaagġaat
296101	ġġtċtċagċċ	ċagċttttċġ	ġtċatċġttt	ċġġagġġttġ	ċtġġagġġġt	tċagġċaact
296161	tġġtġġġġtċ	tttġċċġċċġ	ġġttġagċċa	tatċċġġċċġ	ġċċacċġċġ	ċtġċċacċġa
296221	ċċacċttġġġċ	ċġċġġacċċġ	acċċagġċac	ċġġċtttċāa	acċacġatċa	acċagatċtċ
296281	ġġtċagġtċċ	acċġacċāac	atġactttġt	ċġttċatċġa	ċgaagċċāac	agċactġġġġ
296341	ttġġġġtġtċ	ġtċtttċttġ	ċgaatttġat	ċġatċċāacċ	tċġġatġatġ	tġġġġttġġ
296401	ċacċġġġġġt	tċcagċāacġ	atċagċāacġ	ġtġġċċġac	ċttġġttċċa	tċtġġġatċa
296461	agġtācċċġċ	ġgāaatċttā	ċċġċċġġġġ	tċacċtġttt	ġagttġġtċġ	acċagċttċġ
296521	atċġatċġġċ	ċaacagġġāa	tċċāagġġac	tġagċacatċ	ġġtgatċġā	acġttċāaac
296581	ġġġagġtċāa	acċġġāacċ	ġċġġacġġā	ċġġġttġtā	atċġtġatġ	tċġġtċġttt
296641	ċġġtttċġċ	agċċttġġġā	tċāaaġācāa	attċagġġġġ	atagġtċċġā	ġċtttġġġtġ
296701	acġācāattċ	tttċttċagċ	ċġġġāactt	ċttċġatċāa	ċġċacċġtġ	ċġġġagġcāġ
296761	ċcācġāagġ	atċġācāattċ	agtttġġġġ	ċcāċċtċġtt	ċagċāacġġt	tġġġtttġġt
296821	ċġġġtġttċ	tttġġġacġċ	tċġċċġtċā	atġġttċġat	ċġġġġagġtt	ċċġtġġāaa
296881	ċġġtttċttċ	ġaccacġācċ	tċāaacġāac	ċġacttġttt	ġġtġttġġtċ	aggġagġttċ
296941	ċacċġcācāġ	ttcācġactġ	aacġttċċċa	tċgāaacċat	ġġgacatġġġ	tċġġġatact

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L3 ANSWER 84 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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CAS REGISTRY NO. (RN): 504700-37-2
SEQUENCE LENGTH (SQL): 27
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 10 Apr 2003
DEFINITION (DEF): Sequence 6 from patent US 6500643.
SOURCE: Unknown.

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Unclassified

NUCLEIC ACID COUNT (NA): 5 a 6 c 5 g 10 t 1 others  
REFERENCE: 1 (bases 1 to 27)  
AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
JOURNAL (SO): Patent: US 6500643-A 6 31-DEC-2002;

FEATURES (FEAT):

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L3 ANSWER 85 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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DIVISION CODE (CI): Patent  
DATE (DATE): 10 Apr 2003  
DEFINITION (DEF): Sequence 5 from patent US 6500643.  
SOURCE: Unknown.  
ORGANISM (ORGN): Unknown.

NUCLEIC ACID COUNT (NA): 5 a 7 c 8 g 5 t  
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AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
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L3 ANSWER 86 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AR268950 GenBank (R)  
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DIVISION CODE (CI): Patent  
DATE (DATE): 10 Apr 2003  
DEFINITION (DEF): Sequence 3 from patent US 6500643.  
SOURCE: Unknown.  
ORGANISM (ORGN): Unknown.

NUCLEIC ACID COUNT (NA): 430 a 570 c 516 g 377 t  
REFERENCE: 1 (bases 1 to 1893)  
AUTHOR (AU): Wu, D.-H.; Gu, Y.; Millard, W.J.; He, Y.-J.  
TITLE (TI): \*\*\*Human\*\*\* \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
JOURNAL (SO): Patent: US 6500643-A 3 31-DEC-2002;

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781 gacatgattg agcgctgcat ctgccttgta tgcctggacg cgccaggagg gctggagctc
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901 aatcgctggg acgacaagt cctgcagttt gtggtgggac gagacggcac ctgcggtgtg
961 gtgtgcgaac actccccatt cgatggcatc gtcctgggtg agtgactga gcatctgctc
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L3 ANSWER 87 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): AR268949 GenBank (R)
GenBank ACC. NO. (GBN): AR268949
GenBank VERSION (VER): AR268949.1 GI:29699686
CAS REGISTRY NO. (RN): 504700-34-9
SEQUENCE LENGTH (SQL): 1743
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 10 Apr 2003
DEFINITION (DEF): Sequence 1 from patent US 6500643.
SOURCE: Unknown.
ORGANISM (ORGN): Unknown.
NUCLEIC ACID COUNT (NA): 411 a 395 c 405 g 532 t
REFERENCE: 1 (bases 1 to 1743)
AUTHOR (AU): Wu,D.-H.; Gu,Y.; Millard,W.J.; He,Y.-J.
TITLE (TI): ***Human*** ***high*** ***affinity***
***choline*** ***transporter***
JOURNAL (SO): Patent: US 6500643-A 1 31-DEC-2002;

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FEATURES (FEAT):
Feature Key Location Qualifier
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source 1..1743 /organism="unknown"

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L3 ANSWER 88 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): E49871 GenBank (R)
GenBank ACC. NO. (GBN): E49871
GenBank VERSION (VER): E49871.1 GI:22554902
CAS REGISTRY NO. (RN): 450667-38-6
SEQUENCE LENGTH (SQL): 1743
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Patent
DATE (DATE): 27 Aug 2002
DEFINITION (DEF): ***High*** - ***affinity*** ***choline***
***transporter***
SOURCE: Homo sapiens.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo

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NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

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COMMENT:
OS Homo sapiens ( ***human*** )
PN JP 2001136976-A/3
PD 22-MAY-2001
PF 27-DEC-1999 JP 1999368991
PI TATSUYA HAGA,TAKASHI OKUDA
PC C12N15/09,A01K67/027,A61K38/00,C07K14/47,C07K16/18,C07K19/00,
PC C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/00,C12N15/00,A61K37/02,C12N5/00 CC
FH Key Location/Qualifiers
FT CDS (1)..(1743).

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REFERENCE: 1 (bases 1 to 1743)
AUTHOR (AU): Haga,T.; Okuda,T.
TITLE (TI): ***High*** - ***affinity*** ***choline***
***transporter***
JOURNAL (SO): Patent: JP 2001136976-A 3 22-MAY-2001; SCIENCE & TECH
AGENCY

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FEATURES (FEAT):
Feature Key Location Qualifier
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source 1..1743 /organism="Homo sapiens"
/db-xref="taxon:9606"

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961 ccaattgttc tgcagtatct ctgccctgtg tatatttctt tctttggtct tggctcagtt
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1741 tga

L3 ANSWER 89 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AB084377 GenBank (R)  
GenBank ACC. NO. (GBN): AB084377  
GenBank VERSION (VER): AB084377.1 GI:22506641  
CAS REGISTRY NO. (RN): 450515-00-1  
SEQUENCE LENGTH (SQL): 291  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 21 Nov 2002  
DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* CHT1, 5'UTR.  
SOURCE: Homo sapiens ( \*\*\*human\*\*\* )  
ORGANISM (ORGN): Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo  
NUCLEIC ACID COUNT (NA): 51 a 123 c 74 g 43 t  
REFERENCE: 1  
AUTHOR (AU): Okuda,T.; Okamura,M.; Kaitsuka,C.; Haga,T.; Gurwitz,D.  
TITLE (TI): Single Nucleotide Polymorphism of the \*\*\*Human\*\*\*  
\*\*\*High\*\*\* \*\*\*Affinity\*\*\* \*\*\*Choline\*\*\*  
\*\*\*Transporter\*\*\* Alters Transport Rate  
J. Biol. Chem., 277 (47), 45315-45322 (2002)  
OTHER SOURCE (OS): CA 138:252025  
REFERENCE: 2 (bases 1 to 291)  
AUTHOR (AU): Okuda,T.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (26-APR-2002) Takashi Okuda, University of  
Tokyo, Faculty of Medicine, Department of  
Neurochemistry; 7-3-1 Hongo, Bunkyo-ku, Tokyo 1130033,  
Japan (E-mail:okuda@m.u-tokyo.ac.jp,  
Tel:81-3-5841-3560, Fax:81-3-3814-8154)

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..291	/organism="Homo sapiens" /db-xref="taxon:9606" /tissue-type="spinal cord"
gene	1..291	/gene="CHT1"
5'UTR	1..291	/gene="CHT1" /note="high-affinity choline transporter CHT1"

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181 cgcggttcca gggggcgggc gcccggggcg gacgccttgc gcgtgcagcc accactccag  
241 aagacttaat gaagtagcca gctgcagaag aatctggatc attagataaa a

L3 ANSWER 90 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BD012719 GenBank (R)  
GenBank ACC. NO. (GBN): BD012719  
GenBank VERSION (VER): BD012719.1 GI:22092908  
CAS REGISTRY NO. (RN): 445761-48-8  
SEQUENCE LENGTH (SQL): 1743  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Patent  
DATE (DATE): 2 Aug 2002  
DEFINITION (DEF): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
SOURCE: Homo sapiens.  
ORGANISM (ORGN): Homo sapiens

Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

COMMENT:

OS Homo sapiens ( \*\*\*human\*\*\* )  
PN WO 0116315-A/3  
PD 08-MAR-2001  
PF 18-AUG-2000 WO 2000JP005545  
PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI  
TATSUYA HAGA, TAKASHI OKUDA  
PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC  
A61K38/17,  
PC A61K45/00, A61P25/28, G01N33/53, A01K67/027  
CC

FH Key Location/Qualifiers  
FT CDS (1)..(1743).

REFERENCE:

1 (bases 1 to 1743)

AUTHOR (AU): Haga, T.; Okuda, T.

TITLE (TI): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*

JOURNAL (SO): Patent: WO 0116315-A 3 08-MAR-2001; JAPAN SCIENCE AND  
TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606"

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L3 ANSWER 91 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC):

BD005267 GenBank (R)

GenBank ACC. NO. (GBN): BD005267

GenBank VERSION (VER): BD005267.1 GI:18633228

CAS REGISTRY NO. (RN): 392945-96-9

SEQUENCE LENGTH (SQL): 1743

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Patent

DATE (DATE): 31 Jan 2002

DEFINITION (DEF): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*

SOURCE:

Homo sapiens.

ORGANISM (ORGN): Homo sapiens

Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

COMMENT:

OS Homo sapiens ( \*\*\*human\*\*\* )  
PN JP 03074455-T/3  
PD 19-JAN-2001  
PF 18-AUG-2000 JP 2000005545  
PR 27-AUG-1999 JP 99P 240642, 27-DEC-1999 JP 99P 368991 PI  
TATSUYA HAGA, TAKASHI OKUDA  
PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC  
A61K38/17,  
PC A61K45/00, A61P25/28, G01N33/53, A01K67/027  
CC  
FH Key Location/Qualifiers  
FT CDS (1)..(1743).

REFERENCE:

1 (bases 1 to 1743)  
AUTHOR (AU): Haga, T.; Okuda, T.  
TITLE (TI): \*\*\*High\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\*  
JOURNAL (SO): Patent: JP 03074455-T 3 19-JAN-2001; JAPAN SCIENCE AND  
TECHNOLOGY CORP, TATSUYA HAGA, TAKASHI OKUDA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606"

SEQUENCE (SEQ):

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L3 ANSWER 92 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308377 GenBank (R)  
GenBank ACC. NO. (GBN): AJ308377  
GenBank VERSION (VER): AJ308377.1 GI:18375495  
CAS REGISTRY NO. (RN): 388546-92-7  
SEQUENCE LENGTH (SQL): 610  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 23 Jan 2002  
DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 1 and joined mRNA.  
SOURCE: \*\*\*human\*\*\*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 102 a 200 c 197 g 111 t

REFERENCE: 1 (sites)

AUTHOR (AU): Wieland, A.; Bonisch, H.; Brüss, M.

TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 610)

AUTHOR (AU): Brüss, M.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (23-JAN-2001) Brüss M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

# FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..610	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
exon	<1..196	/gene="CHT1" /number=1
mRNA	join(<1..196, AJ308378.1:183..411, AJ308379.1:879..992, AJ308379.1:1745..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..>2239)	/gene="CHT1"
gene	join(1..610, AJ308378.1:183..411, AJ308379.1:879..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..2239)	/label=CHT1-mRNA /gene="CHT1"
intron	197..>610	/gene="CHT1" /number=1

# SEQUENCE (SEQ):

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1  cacctgtcaa ctctgcgcgc tcccagggtc ttggagacgc cgagtgcagg gccgccctga
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121  tcgcacccac acccctcgcg gttccagggg gcggcgggcc cgggcgggag gctttcgcgt
181  gcagccacca ctccaggtag gaggcgacgg tcattcctgc gcctacgggc ccgcaccctc
241  ggaaacgcct tgggcaccga gcccgggcgg ttttagaggg gagggacgag cggttttttc
301  ctctcggtgg gatgcgaggg cgggtttgct gtctggcacc gttgctgtca ggggtgaaga
361  ggctacaaag tctgggcgca ggaaatgggt agagggggcc gaggaagggc cgcagggggc
421  cgggagagca tcgggctgct gcggagagga acttgccctg ttggttgctc acaaaggtag
481  agaagaacaa gcccgcgggc gcttcttttg cctcctttta attccggaga ggctgattct
541  ttccccaac gtctctttac ccacctgcac gcacaaatgt gagagtttcc ccagaaact
601  tgtgtgtgag

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L3 ANSWER 93 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308378 GenBank (R)

GenBank ACC. NO. (GBN): AJ308378

GenBank VERSION (VER): AJ308378.1 GI:18375493

CAS REGISTRY NO. (RN): 388546-91-6

SEQUENCE LENGTH (SQL): 1178

MOLECULE TYPE (CI): DNA; linear

DIVISION CODE (CI): Primates

DATE (DATE): 23 Jan 2002

DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 2 and joined CDS.

SOURCE: \*\*\*human\*\*\*

ORGANISM (ORGN): Homo sapiens

Eutelēostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 329 a 210 c 262 g 377 t

REFERENCE: 1 (sites)

AUTHOR (AU): Wieland, A.; Bonisch, H.; Bruss, M.

TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 1178)

AUTHOR (AU): Bruess, M.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1178	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13" /gene="CHT1"
gene	join(1..1178, AJ308379.1:879..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..1421)	/gene="CHT1"
intron	<1..182	/gene="CHT1" /number=1
exon	183..411	/gene="CHT1" /number=2 /usedin=AJ308377:CHT1-mRNA
CDS	join(234..411, AJ308379.1:879..992, AJ308379.1:1745..1900, AJ308380.1:579..727, AJ308381.1:35..178, AJ308382.1:663..816, AJ308383.1:887..1104, AJ308384.1:792..1421)	/gene="CHT1"  /function="re-uptake of choline" /codon-start=1 /label=CHT1-CDS /product="high affinity choline transporter" /protein-id="CAC88115.1" /db-xref="GI:18375494" /translation="MAFHVEGLIAIIVFYLLILL VGIWAAWRTKNSGSAEERSEAIIV GGRDIGLLVGGFTMTATWVGGGYINGTAEAVYVP GYGLAWAQAPIGYSLSLILGGLFF AKPMRSKGYVTMLDPFQQIYGKRMGGLLFIPALM GEMFWAAAIFSAIGATISVIIDVD MHISVIISALITATLYTLVGGLYSVAYTDVVQLFC IFVGLWISVPFALSHPAVADIGFT AVHAKYQKPWLGTVDSEVYSWLDLSFLLMLGGI PWQAYFQRLSSSSATYAQVLSFL AAFGCLVMAIPAILIGAISTDWNQTAYGLPDP KTTEEADMILPIVLQYLCPVYISF FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF RQNASDKEIVVMRITVFVFGASA TAMALLTKTVYGLWYLSDDLVIYIVIFPQLLCVLF VKGTNTYGAVAGYVSGFLRLITGG EPYLYLQPLIFYPGYPPDDNGIYNQKFPFKTLAM VTSFLTNICISYLAKYLFESGTLF PKLDVFDVAVARHSEENMDKTLVKNENIKLDEL ALVKPRQSMTLSSSTFTNKEAFLDV DSSPEGSGTEDNLQ"
intron	412..>1178	/gene="CHT1" /number=2

SEQUENCE (SEQ):

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61 caaggggtgt acctctctctg tgaagtggcac aggaactctgc atgagccagc tgggtttattc
121 ctggctgcct acatgtgcat agtgcttgac tgggtttataa tgcattccctg tattttcttc
181 agaagactta atgaagtagc cagctgcaga agaactctgga tcattagata aaaatggcctt
241 tccatgtgga aggactgata gctatcatcg tgttctacct tctaattttg ctggttgga
301 tatgggtgc ctggagaacc aaaaacagtg gcagcgcaga agagcgcaga gaagccatca
361 tagttggtgg ccgagatatt ggtttattgg ttggtggatt taccatgaca ggttcagacg
421 ccgccggctc catgcagtc tcccttcctt ggcattctgt agtgtgcagc gtgtggcctc
481 agagtgacaa agcaaagtgt ggtctttgtc ctttggggat tctttatgtt cactagttat
541 atataatttta aaataatttt ctattgattt aaaacctaaa aataaattgg tttcaactca
601 gtagtacttg aacaaaaatg atttttataa aaatcactgg actgaacagt cacgaaacaa
661 atcttggtgc cctgggctat tgagtgggtg gaaacagagt aaaaacaaag aggtggggga
721 atgggaagct gtcctagtat tacaagctat gtatctgcta attaattgtg taggcagcat
781 ctcaacgtgt ccggaataac atgcataaag ttgtgacttt gagattttaa taagtgccaa
841 tgaataccat ctagtgatgg tttttaatct gcataaataa atttgggggt gatgatattc
901 ccaattgagt gattccctgt tttgaaacct aattctttca ttaataact aattcctcac
961 aggaagacaa tcacatgtta tgagtccaca gcactaataa agagatttca tgaacctgtt
1021 tataaaaggg aaaagctagg gtgtgtcttc ataggaatcc ccaggccacc atctgcagtc
1081 atctctcatt caaaccttct ttgtgttagc aggaactgat attcttttct tactttgcac
1141 taaagtgggt ctgttttaaag ggtgatttgt ttcttttt

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L3 ANSWER 94 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308384 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ308384  
 GenBank VERSION (VER): AJ308384.1 GI:18369775  
 CAS REGISTRY NO. (RN): 387812-77-3  
 SEQUENCE LENGTH (SQL): 2239  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 23 Jan 2002  
 DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 , exon 9.  
 \*\*\*human\*\*\*

SOURCE:  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo

NUCLEIC ACID COUNT (NA): 664 a 442 c 440 g 693 t

REFERENCE:  
 1 (sites)  
 AUTHOR (AU): Wieland, A.; Bonisch, H.; Bruss, M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and  
 characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 2239)  
 AUTHOR (AU): Bruess, M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
 Bonn, GERMANY

Feature Key	Location	Qualifier
source	1..2239	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
intron	<1..791	/gene="CHT1" /number=8
gene	1..2239	/gene="CHT1"
exon	792..>2239	/gene="CHT1" /number=9 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA

SEQUENCE (SEQ):

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121 ttttggtttt tgctccctgtg ctagtttgct gaggatgatg gcttccacct tcatccatgt
181 ctctgcaaag gaatgatctt attccttttt atggccacat agtattccat ggtatacatg
241 tgccacattt tctttatcca gtctatcact gatgggcatt tgcgttgggt ccatgacttt
301 gttattgtaa atagtgtgc aataaacgta tgtgtgcatg tgtcttttca agagcaccag
361 aaggtggtta gttaaggat ggtagcactt ctacaaagag ataaacatag ggatggccta

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481 tgcctttatta taacctccctg aacacatgtt agctcatcct gcccttgccc ctgtgcattc
541 aggaaaaggc tcaggtggcc tgtgtgtcat acatctggta cacagaaacc cctcccaaag
601 gtccaccacag gaagtcacct tgattgtttg ctttggggtgc ttagctgtga gttgggtttt
661 cccatagatt gagcacattt gaaccaggag aattctttag accagttttg aagcaaaaaa
721 tctgtctcat tctttgccta aatgagccaa gacactgtgc aaaaagctga cactgtggca
781 atttcttaca ggcttcggac aaagaaatcg tttgggttat gcgaatcaca gtgtttgtgt
841 ttggagcatc tgcaacagcc atggccttgc tgacgaaaac tgtgtatggg ctctgtgacc
901 tcagtcttga ccttgttttac atcgttatct tccccagct gctttgtgta ctctttgtta
961 agggaaaccaa cacctatggg gccgtggcag gttatgtttc tggcctcttc ctgagaataa
1021 ctggaggggga gccatattctg tatcttcagc ccttgatctt ctaccctggc tattaccctg
1081 atgataatgg tatataaat cagaaatttc catttaaaac acttgccatg gttacatcat
1141 tcttaaccaa catttgcctc tcctatctag ccaagtatct atttgaaagt ggaaccttgc
1201 cacctaaatt agatgtattt gatgctgttg ttgcaagaca cagtgaagaa aacatggata
1261 agacaattct tgtcaaaaat gaaaatatta aattagatga acttgactt gtgaagccac
1321 gacagagcat gaccctcagc tcaactttca ccaataaaga ggccttcctt gatgttgatt
1381 ccagtccaga agggctctggg actgaagata atttacagtg accccatcta aataaaaatac
1441 tgccttttga aacagaacac tgtaatatgg tagttctgga gagatgggtat gcagcataca
1501 aaaatatatt aaaaatataa acaatgttca ggagagtaaa aattcatata aagtgcattt
1561 gcacaaatac aagccaagct agaaggaagc acctatgaaa gcaacaactt tgtttctcat
1621 ccatagtagt attgattttg atgctagata gttttgctag gtataaaaaa taagtaaagt
1681 tccacttaga gaacaaaggg ccaaatagag tttttatatt tgttatgata aaaggaagta
1741 gatgtgaaaa agcctaagaa aaaggaaatt ggacagtttt gatacaaact ttgtttgcta
1801 atgactgat gagtctagtt tcattatagc acgaagctat gagaataact tcagctcctc
1861 ccttgaatgg tgcaatgaat taaccagctg atttttctta gtgtgatgat taacccttc
1921 tttcatgttc tgagctataa catttgctga atatgcaatt tgttattctt ttattaatgg
1981 catgtaatat tctgagcacg ggcaaagaaa acacacaaaa aattatgtat tggcatttat
2041 ttatgtgcaa ggtgatagga aaactgaatc catctttgta gaagagcact gggctaattt
2101 gtatgtttcc atagctacta tatgcataaa caacagtacc tgaaggatta ttaagcaacc
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2221 tctcaagtat ataaagttt

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L3 ANSWER 95 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): HSA308383 GenBank (R)
GenBank ACC. NO. (GBN): AJ308383
GenBank VERSION (VER): AJ308383.1 GI:18369774
CAS REGISTRY NO. (RN): 387812-76-2
SEQUENCE LENGTH (SQL): 1657
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 23 Jan 2002
DEFINITION (DEF): Homo sapiens partial CHT1 gene for ***high***
                    ***affinity*** ***choline*** ***transporter***
                    , exon 8.
                    ***human***
SOURCE:
ORGANISM (ORGN): Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                  Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                  Hominidae; Homo
NUCLEIC ACID COUNT (NA): 529 a 304 c 287 g 537 t
REFERENCE: 1 (sites)
AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.
TITLE (TI): Molecular cloning of the ***human*** and murine
             high affinity choline transporters and
             characterization of the ***human*** gene structure
JOURNAL (SO): Unpublished
REFERENCE: 2 (bases 1 to 1657)
AUTHOR (AU): Bruess,M.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,
              Pharmacology and Toxicology, Reuterstr. 2b, D-53113
              Bonn, GERMANY

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FEATURES (FEAT):
Feature Key      Location      Qualifier
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source           1..1657      /organism="Homo sapiens"
                  /db-xref="taxon:9606"
                  /chromosome="2"
                  /map="2q11-13"
gene             1..1657      /gene="CHT1"
intron           <1..886      /gene="CHT1"
                  /number=7
exon             887..1104    /gene="CHT1"
                  /number=8

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intron 1105..>1657

/usedin=AJ308377:CHT1-mRNA  
/gene="CHT1"  
/number=8

SEQUENCE (SEQ):

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61 tgcattgtaag caggctttgt gacaattgta atagaaaatg agggagaagaa aaatggtagg
121 atccaaagag aacaattcct atttggtcca atgatcatga tattaaaaaa gttcagcaaa
181 taaaaagccg actatgctaa tgaacattta aggattccat agttcttcaa cacatgctac
241 aactaaccag taaagaagct atgtattcaa agataaatct gtgtttcaag tcttcttacc
301 ctaccacaca ccaaaacttc ctgaaaattt cagccacatg actgtaattt ttattcaata
361 aaaagggact gttctttaacc tagtgaaatt ctatgcaatg tggaaatagg agaaaagtaa
421 tgctgaggca gcttcaaaac caagtattatg tacagagaga tgatggctga gaatagccct
481 actattgtct ttcttcaatt acacatgaat aactgagcct taaagaagaa acagtgagtg
541 tcccaccaca ttccaagtgt gttgaaggaa tactctagaa ttctgtttat gagagtgtgt
601 tttctatgat tctaggcaat gtaacaccat cattgcagaa aggaaatata tatcttacca
661 ccagtgtctg tgcaggcatt gtgaataaca ctaactataa ccaataacct ttagaagcca
721 agagatataa gacatttcca cttgaccagc acatggactt cacaccagac taatgtatat
781 gattctgagt ttatttcaaa acaacctagt aaataggatg accccagatg gataaagaac
841 atttggttcc ttggtggtta taatggttgt tgattctgtt caacagactg gaaccagact
901 gcatatgggc ttccagatcc caagactaca gaagaggcag acatgatttt accaattggt
961 ctgcagtatc tctgcctctg gtatatattt ttctttgggt ttggtgcagt ttctgctgct
1021 gttattgtcat cagcagattc ttccatcttg tcagcaagtt ccatgtttgc acggaacatc
1081 taccagcttt ccttcagaca aaatgtaaga acagtcttct tcaacctgat catttactag
1141 cattgctctt gcatgcttct gatgttgtat ttggtgtata tacagtatta tatatttatt
1201 aatattctat gttaaactct actgtacttt aagcatacga gattaaataa caaattatac
1261 ctatgctgaa tggatgctat cagtacctgt tcttattcat gtcaatacta aagggaacaa
1321 atcaatataa ttatttccca agaggtagag tcacagggct atcatttaac ctttttgtct
1381 ttctgatgaa agagtaatga aacctaaact attcagcaaa acttttagta taattaaatt
1441 ctctatgaca ctggaataatc ttggtggaag cagggcagtg taagtgttgc gacacgtatt
1501 tttgtaactt ctgaactgtt ttatacttgc actccaaagt ccacctttgc aggaagatat
1561 cctctcaatt tgattttctt tattgaatca aagtggctgc aaaacagcat gcttctttgg
1621 ttgattaaag cttttcctct ctctagggtt tagttac
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L3 ANSWER 96 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308382 GenBank (R)  
GenBank ACC. NO. (GBN): AJ308382  
GenBank VERSION (VER): AJ308382.1 GI:18369773  
CAS REGISTRY NO. (RN): 387812-75-1  
SEQUENCE LENGTH (SQL): 1467  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 23 Jan 2002  
DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exon 7.  
\*\*\*human\*\*\*  
SOURCE:  
ORGANISM (ORGN): Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo  
NUCLEIC ACID COUNT (NA): 398 a 326 c 284 g 459 t  
REFERENCE:  
1 (sites)  
AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure  
JOURNAL (SO): Unpublished  
REFERENCE:  
2 (bases 1 to 1467)  
AUTHOR (AU): Bruess,M.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1467	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
gene	1..1467	/gene="CHT1"
intron	<1..662	/gene="CHT1"

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exon          663..816          /gene="CHT1"
                                   /number=7
                                   /usedin=AJ308378:CHT1-CDS
                                   /usedin=AJ308377:CHT1-mRNA
intron        817..>1467      /gene="CHT1"
                                   /number=7

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# SEQUENCE (SEQ):

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121 atagagaaaa cttcaggaaa ttctgcataa ttgaaagtgt atgatacatt gtcttagttc
181 agttgggttaa caaagcatca taaacggagt ggcttataaa caacacagat ttatttttca
241 cagttttttca catggctggg aagtccaaga tcaagggtgcc ggcagattca ctgcctgggt
301 aggattcgca tcctcataga aggcaccttc ttgctgcctc ctcacatggt ggaaggaaaa
361 aaactccttt gactctcttt tataaggact ccaccctcat gggctaatac tctcccaaag
421 ttgccaactt gatacctaata accatcacct tggggatcaa aatttcagtg tatgaattta
481 gggggaacat aaacatcaga tcatagcaaa cataatgata ctaattgata ttgtgggcta
541 catgccacat tttttttact acttctaagt tgtacttagg cctattctaa atgtgattgc
601 aataaaaactc tttaaaaaaa tgaatagatg tttgcctctc catccttggt tttcccgcac
661 agatgctggg tggaaatcca tggcaagcat actttcagag ggttctctct tcttctcag
721 ccacctatgc tcaagtgtgt tccttcctgg cagctttcgg gtgcctgggt atggccatcc
781 cagccatact cattgggggc attggagcat caacaggtaa atctcttgca gcttcaccac
841 atgtgccagt tagtttacca atccccaccc agacaccctt ctgtcccact cccctcttc
901 ctccacatag tgaattcttt ctcaccacat tcatatctat agatttgtaa tagcattcag
961 taaatcgtat tatagttcag cggcctccat tttttttttt tttttttttt tagtagagac
1021 ggggtttcat catgttggtc aggtctggtc caaactcctg acctcagggt atccatctgc
1081 ctcggtctcc caaagtgtgt gaattatagg tgtgagctac tgcgccagc ctccaatttt
1141 tttgattgct cactccacta tgaacattgt gtgagcacac cctcctccca gttttgggt
1201 atttatccat tgtttatatg cactcctgtc agcagtggat ctcaaccaag gtgcatgtc
1261 acatcatctg gggaaatggt gggagatctt ttaaaaatac ggatatgtgg cctacttcac
1321 aggaatttta ttttaataac tgaagataga gatgggcact agtggtcttt taaaaccctt
1381 aggtgagttg agagccagag ttgagagtca caggcttaga gacgtttacc tgtcatcctc
1441 atgacctccc taaagatcac tttgaac

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L3 ANSWER 97 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC):          HSA308381      GenBank (R)
GenBank ACC. NO. (GBN): AJ308381
GenBank VERSION (VER): AJ308381.1  GI:18369772
CAS REGISTRY NO. (RN): 387812-74-0
SEQUENCE LENGTH (SQL): 736
MOLECULE TYPE (CI):   DNA; linear
DIVISION CODE (CI):   Primates
DATE (DATE):          23 Jan 2002
DEFINITION (DEF):     Homo sapiens partial CHT1 gene for ***high***
                      ***affinity*** ***choline*** ***transporter***
                      , exon 6.
                      ***human***
SOURCE:
  ORGANISM (ORGN):     Homo sapiens
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                      Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                      Hominidae; Homo
NUCLEIC ACID COUNT (NA): 191 a 148 c 197 g 200 t
REFERENCE:
  1 (sites)
  AUTHOR (AU):         Wieland,A.; Bonisch,H.; Bruss,M.
  TITLE (TI):          Molecular cloning of the ***human*** and murine
                      high affinity choline transporters and
                      characterization of the ***human*** gene structure
  JOURNAL (SO):        Unpublished
REFERENCE:
  2 (bases 1 to 736)
  AUTHOR (AU):         Bruess,M.
  TITLE (TI):          Direct Submission
  JOURNAL (SO):        Submitted (23-JAN-2001) Bruess M., University of Bonn,
                      Pharmacology and Toxicology, Reuterstr. 2b, D-53113
                      Bonn, GERMANY

```

## FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..736	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
gene	1..736	/gene="CHT1"
intron	<1..34	/gene="CHT1"

exon 35..178 /gene="CHT1"  
 /number=6  
 /usedin=AJ308378:CHT1-CDS  
 /usedin=AJ308377:CHT1-mRNA  
 intron 179..>736 /gene="CHT1"  
 /number=6

SEQUENCE (SEQ):  
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 121 gctgggaact gttgactcat ctgaagtcta ctcttggcct gatagttttc tgttgttggg  
 181 aagtaatgct cttacctgaa gaatgtgatt taattgttcc tgaaatcaaa tttgttttca  
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 481 aggcaaaacc ttgtaaaggc tttattttgt gttttgaatt aaggcatgaa acccaactta  
 541 tgaataagt ctctcattca ctcttgaatt acagagtaag tgaattagta gtgctagagg  
 601 ccctaagtga ggcaggttgg aaagggacat gtcactcagg aaagatgcca agagagaggc  
 661 cctcaggagc cagaggaagc ttgaaaacag gcagaacttt gggcaaaagg tgcaggcact  
 721 ttgcaggagg acatgg

L3 ANSWER 98 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308380 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ308380  
 GenBank VERSION (VER): AJ308380.1 GI:18369771  
 CAS REGISTRY NO. (RN): 387812-73-9  
 SEQUENCE LENGTH (SQL): 1308  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 23 Jan 2002  
 DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
 \*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 , exon 5.  
 \*\*\*human\*\*\*  
 SOURCE:  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 415 a 234 c 224 g 435 t  
 REFERENCE:  
 1 (sites)  
 AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and  
 characterization of the \*\*\*human\*\*\* gene structure  
 JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 1308)  
 AUTHOR (AU): Bruess,M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
 Bonn, GERMANY

Feature Key	Location	Qualifier
source	1..1308	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q11-13"
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intron	<1..578	/gene="CHT1"
exon	579..727	/number=4 /gene="CHT1" /number=5 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
intron	728..>1308	/gene="CHT1" /number=5

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 61 cgaatttgta gccaggagc aataggccat accatgtagc ctagggtgtg agtagttaca  
 121 ccatcaagat ttgtgagtga gtacatactg tgaagtgcac aacagtgaaa tcacctaaca

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241 tcagaggttcc agatagtga attattttga gtctctgtga tgtattttaa tttctcaggt
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361 caaaccagta atttcagaaa gaaaaagtat gtatctcact gaatttatta agatatacaa
421 atttcaatat aaaaattaac tttagggtgt ttcattccact gcatttcata tgacagagag
481 aaaaatgttg tttatcactg aacttttcatt atgtcccttat acaaagagca gaatctgtct
541 gggcaccttg accacagaac tctcttggtt gtttgacagga gccaccatca gcgtgatcat
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661 ggtgggaggg ctctattctg tggcctacac tgatgtcgtt cagctctttt gcatttttgt
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L3 ANSWER 99 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA308379 GenBank (R)  
GenBank ACC. NO. (GBN): AJ308379  
GenBank VERSION (VER): AJ308379.1 GI:18369728  
CAS REGISTRY NO. (RN): 387812-40-0  
SEQUENCE LENGTH (SQL): 2326  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Primates  
DATE (DATE): 23 Jan 2002  
DEFINITION (DEF): Homo sapiens partial CHT1 gene for \*\*\*high\*\*\*  
\*\*\*affinity\*\*\* \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
, exons 3-4.  
\*\*\*human\*\*\*

SOURCE:  
ORGANISM (ORGN): Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 785 a 405 c 397 g 739 t  
REFERENCE: 1 (sites)

AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and  
characterization of the \*\*\*human\*\*\* gene structure

JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 2326)  
AUTHOR (AU): Bruess,M.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (23-JAN-2001) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuterstr. 2b, D-53113  
Bonn, GERMANY

FEATURES (FEAT):	Location	Qualifier
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gene	1..2326	/gene="CHT1"
exon	879..992	/gene="CHT1" /number=3 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
intron	993..1744	/gene="CHT1" /number=3
exon	1745..1900	/gene="CHT1" /number=4 /usedin=AJ308378:CHT1-CDS /usedin=AJ308377:CHT1-mRNA
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SEQUENCE (SEQ):

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421 ataaaaacat caatacaagt aaaatggaag ggcctcgaaa taaagaaaat ttacccttg
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L3 ANSWER 100 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AJ414146 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ414146 AL590842  
 GenBank VERSION (VER): AJ414146.1 GI:15979072  
 CAS REGISTRY NO. (RN): 361328-59-8  
 SEQUENCE LENGTH (SQL): 210050  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 21 Nov 2002  
 DEFINITION (DEF): *Yersinia pestis* strain C092 complete genome; segment 6/20.

SOURCE: *Yersinia pestis* C092  
 ORGANISM (ORGN): *Yersinia pestis* C092  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Enterobacteriaceae; *Yersinia*

NUCLEIC ACID COUNT (NA): 53724 a 46781 c 53011 g 56534 t

COMMENT:

Notes:

Details of *Y. pestis* sequencing at the Sanger Centre are available on the World Wide Web.

(URL, [http://www.sanger.ac.uk/Projects/Y\\_pestis/](http://www.sanger.ac.uk/Projects/Y_pestis/)).

REFERENCE:

1 (bases 1 to 210050)  
 AUTHOR (AU): Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Brooks, K.; Cerdeno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Feltwell, T.; Hamlin, N.; Holroyd, S.; Jagels, K.; Leather, S.; Karlyshev, A.V.; Moule, S.; Oyston, P.C.F.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.  
 TITLE (TI): Genome sequence of *Yersinia pestis*, the causative agent of plague  
 JOURNAL (SO): Nature, 413 (6855), 523-527 (2001)  
 OTHER SOURCE (OS): CA 135:314279

AUTHOR (AU): Parkhill, J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (04-OCT-2001) Submitted on behalf of the  
 Yersinia sequencing team, Sanger Centre, Wellcome Trust  
 Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:  
 parkhill@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..210050	/organism="Yersinia pestis C092" /strain="C092" /db-xref="taxon:214092" /note="biovar: Orientalis"
gene	829..11946	/gene="yapH" /note="synonym: YPO1004"
CDS	829..11946	/gene="yapH" /note="Previously sequenced as Yersinia pestis YapH protein TR:CAC14227 (EMBL:AJ277631) (3705 aa) fasta scores: E(): 0, 99.6% id in 3705 aa. Similar in regions to Escherichia coli YchA protein TR:Q9JMS3 (EMBL:AP001918) (1371 aa) fasta scores: E(): 0, 39.1% id in 1405 aa, and to Escherichia coli adhesin Aida-I precursor SW:AIDA-ECOLI (Q03155) (1286 aa) fasta scores: E(): 0, 29.2% id in 1286 aa. Contains a possible N-terminal signal sequence." /codon-start=1 /transl-table=11 /product="putative autotransporter protein" /protein-id="CAC89847.1" /db-xref="GI:15979073" /db-xref="SPTREMBL:Q8ZHA1" /translation="MNTIFKVIWNASLNVVVVS ELAKGRIKTKSSRNLISEGVLPKF EQSMVSKLFRKNLLALSLGSI VFLSTGPVFAADI TVSTQAELSAALSNGTYDKIILGA DITLIGSLTVNMTSNQVVIDGQKFGLTVNNTTN YGLVVSSSGTTLTLQNMSKIDSAN YYSMVVLNGANTAVNVIYNNIDFLGSSQLIYMGA YGAATNSIMTFGDILNDVVVNDRA QEIGE VNKLAFTGRFHVHTGTGSSVTSFVSTGGAN NTSTMDFASGADV KIDRTGSTGDL TSTGVNAFAYTFADGASFELIANQNVFSGTTTNR GLEIGSYNSIDGFGSGVKIVLQSR SDGSIISGNIDNATTNAAGINNANSGDANVIYN LGTGSILKATNTGILATKNANNAS DIYIRSAGDITAATGISATHNGTGTVKIKNDGTI TSTTAGIAISSASIKEISVDNTDG TITATAGTGVNVLASAILNLFGGTINTSATANGI TFAGTEGGHTLTDLTINLLGTGIA LSNVAGVNLTLNVTNLNTLNGTALNSLTGLTLVD SLNGRNTINIEGAGIGIAATNTEL NTFDAEALDINVNGAGIGIQATGGGVNLSASNLI INVANTLGTALQITDGIDNTTTIG NEIQLNAENATAINFLGSSSKTLNNGTIKGSVI FAGVADHI INNNGTLDGTLTTGAG NDTLVLDSSSQSNDVINLGDGNNSVTIQNGATVS SIITGNGNDTFTINGMSVGSSTYL SLDAGTGLNTLNFNASTDELAATSLQGFTNINL VDSHITLVSDDNIGSGMVNIDSSS ELLFGSTFDGILHATLGAGTGSAIVNNSANVSLE QASMFAGTWQVNQGGALTASNSNQ LGSAKIGLDGTLNLDNIALFNHVLGTNGTLNVAK NLATTA FDFGSTVGGAFSGIVNLT KTTFALSADNAAALASATLKLSDDSVTTVGT TDR TLHGLDLSGGT LIFDGAVPQSQTS GVVTVTDLALNSGTVNITGSGSWDNTDPLATNVS ILEQDRAGSTLELINATNVTGDID ALDLLVNGTAITSGTQGVQSAIQGGSTVANAIH

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VTQTL SLEESLQERALLVSFASNM



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gene      complement(12049..13929 /gene="YPO1005"
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CDS       complement(12049..13929 /gene="YPO1005"
)
/Note="Similar to neighbouring
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to Salmonella typhimurium
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fasta scores: E(): 0, 39.0% id in
644 aa, and to Shigella flexneri
65.4 kDa antigen IpaH 4.5
SW:IPA4-SHIFL (P18009) (574 aa)
fasta scores: E(): 0, 40.4% id in
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EQQNRLAGDWANIETEANSAAFSVFLHRLATTQN
ANNIPEFKQQIAAWLLQLADSPTL
REQTFLIAQEASATCEDRITLTHNDMQAVMLHE
VEKGKYDEKLPELMARGREMFRL
QLENIAREKVKILKTLNVNSVDDIEVYLAYQVKL
LNSLQLSSVNKEMRFFGVSHVTAD
DLLSAETRVKTAENQDFSRWLSQWSPWKS VVQRI
EPERYAAAVEKQYHALENIYPDKL
AAELAANGMTGDVDANRIVGKRINDELMGEIDMA
LTHEVLSAKGASSLLDNLWMEYLI SP"
misc-feature complement(13099..13164 /gene="YPO1005"
)
/Note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
9.30, E-value 44"
misc-feature complement(13219..13290 /gene="YPO1005"
)
/Note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
12.80, E-value 8.4"
misc-feature complement(13294..13353 /gene="YPO1005"
)
/Note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
10.40, E-value 30"
misc-feature complement(13468..13539 /gene="YPO1005"
)

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misc-feature complement(13543..13602) /note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
17.30, E-value 0.36"
/ gene="YPO1005"

gene complement(14492..15367) /note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
12.90, E-value 7.8"
/ gene="YPO1006"

CDS complement(14492..15367) /gene="YPO1006"

/ note="Similar to neighbouring
CDSs YPO1005 and YPO1007. Similar
to regions of Salmonella
typhimurium secreted protein h2
TR:Q9RPH0 (EMBL:AF160727) (788 aa)
fasta scores: E(): 2.5e-24, 41.9%
id in 272 aa, and to regions of
Yersinia pestis outer membrane
protein YopM TR:O68701
(EMBL:AF053946) (409 aa) fasta
scores: E(): 7e-23, 40.5% id in
259 aa"
/ codon-start=1
/ transl-table=11
/ product="putative antigenic
leucine-rich repeat protein"
/ protein-id="CAC89849.1"
/ db-xref="GI:15979075"
/ db-xref="SPTREMBL:Q8ZH99"
/ translation="MYLSNITSNVSMNPNGPDRE
IHADRPAATALTPADYHAIWEKWE
NDPRTVAGEQRGQAVARMKECLENNALNLSSL
DLTSLPDTLPCCNELNIIICNNLTE
LPTTLPDNLQTLKASYNQLRTLPLNPASLLSLK
VHMNELERLPEPLPEGLKTLDVGC
NTSLQLPSRLPPVLESIDISNCNLTELPTLPNSL
KELDAHGNQLRILPDTLPISLLRL
NVAYNQLTALPENLPGSLRCIYTEYNQLSQLPDL
AHLRQNCNICLDGNPLSPSTLLAL
LRLSTKPNYQGPRIS"
misc-feature complement(14657..14728) /gene="YPO1006"

/ note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
15.40, E-value 1.3"
misc-feature complement(14732..14791) /gene="YPO1006"

/ note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
9.30, E-value 43"
misc-feature complement(14981..15040) /gene="YPO1006"

/ note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
11.30, E-value 22"
misc-feature complement(15095..15163) /gene="YPO1006"

/ note="Pfam match to entry PF00560
LRR, Leucine Rich Repeat, score
9.40, E-value 43"
gene complement(15575..17392) /gene="YPO1007"

CDS complement(15575..17392) /gene="YPO1007"

/ note="Similar to neighbouring
CDSs YPO1005 and YPO1006. Similar
to Salmonella typhimurium
leucine-rich repeat protein SlrP
TR:Q9XCV2 (EMBL:AF127079) (765 aa)
fasta scores: E(): 0, 36.9% id in
642 aa, and to Shigella flexneri
65.4 kDa antigen IpaH
SW:IPA4-SHIFL (P18009) (574 aa)

```

569 aa, and to Salmonella typhimurium secreted protein H2  
 TR:Q9RPH0 (EMBL:AF160727) (788 aa)  
 fasta scores: E(): 0, 40.3% id in 608 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="putative antigenic leucine-rich repeat protein"  
 /protein-id="CAC89850.1"  
 /db-xref="GI:15979076"  
 /db-xref="SPTREMBL:Q8ZH98"  
 /translation="MNLSNITSNESMPNIEPDRE  
 IHSARTSTAALTPADYYAIWEKWE  
 NDPRTVAGEQRGQAVARMKECLENNTERLDLDEL  
 GLTSLPDTLPCCNKLNIENKLTE  
 LPTTLPDNLQTLNAAFNLRLTPNTLPASLLSLN  
 VYGNELERLPESLPEGLKKLDVGR  
 NESLQRPNRLPPNLESLGMANCRLTELPTLPNSL  
 EKLEVDNNQLHTLPDTLPALLSSL  
 LVSSNRLTALPENLPGSLRDIYAKDNQLSQLPDL  
 AHLPPQNCISIRLDGNPFSTSTLQAL  
 QHLYINLDYQGPRI SCRELDNLPPVSLRNIVATW  
 VPPEQQKSLAEDWAKIEKETNSGD  
 FNVFLCRLATTQNVKNIPEFKQQA AAWLLQLAGS  
 FTLREQTFLLIAQEASATCEDRITL  
 THNDMQKAVMLHEVEKGKYDEKLPELIARGREMF  
 RLEQLENIAREKVTKLTLNVHSV  
 DDIEVYLAYQVKLRGSLELSSVNKEMRFFGVSDV  
 TTDDLLSAETRVKTAENQDFPRWL  
 SQWSPWKS VVQRIEPERYAAAVEKQYHALENIYP  
 DKLAELAANGMTGDVDANRIVGK  
 RINDEIMEEIDMALTHEVLSAKGASSLLDNLWME  
 SLISF"

misc-feature	complement(16625..16690 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 13.70, E-value 4.6"
misc-feature	complement(16757..16816 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 10.80, E-value 26"
misc-feature	complement(16931..17002 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 17.30, E-value 0.36"
misc-feature	complement(17006..17065 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 9.90, E-value 36"
misc-feature	complement(17117..17188 )	/gene="YPO1007"  /note="Pfam match to entry PF00560 LRR, Leucine Rich Repeat, score 10.00, E-value 34"
gene	18111..19667	/gene="YPO1008"
CDS	18111..19667	/gene="YPO1008"

/note="Similar to Vibrio cholerae  
 hypothetical protein VC0863  
 TR:Q9KTN8 (EMBL:AE004171) (519 aa)  
 fasta scores: E(): 0, 47.5% id in  
 512 aa, and to Neisseria  
 gonorrhoeae putative efflux pump  
 component MtrF TR:Q9RNX2  
 (EMBL:AF176820) (522 aa) fasta  
 scores: E(): 0, 37.2% id in 524  
 aa, and to Escherichia coli  
 arsenical pump membrane protein  
 ArsB SW:ARB1-ECOLI (P08691) (429  
 aa) fasta scores: E(): 1.1, 26.1%  
 id in 111 aa"

		/transl-table=11
		/product="putative integral
		membrane efflux protein"
		/protein-id="CAC89851.1"
		/db-xref="GI:15979077"
		/db-xref="SPTREMBL:Q8ZH97"
		/translation="MSDVKPKQNDRQTGILNAIER
		IGNAMPDITMLFIYALGVCWALSF
		GLSFINFDFYFHPLTGDQIKVTNMLAPVELVTFIT
		TMVKNFINFPPLAITIVATLGIGI
		AEGSGFIQVMLKKMLNVTPQRILTPAVVFIGVVS
		HVASDSAYVILMPVAAMMFYASGR
		HPLAGIAAAAFAGLAGGFSASYTPSIIDPIMQGFT
		OGAAHIIDPSYNVNVLCNYFLSFG
		STFGVILVCWFITDKIVEPRLKSMPLNSDLSGL
		QSNNELQKVTPQESKAFKRAGLVM
		LLMLIGLAAALYPENSLRSPDGSLTRPDAPIMQ
		AIVPLLFFMFAIPGLIYGFSSGTF
		KSTKDVLTASMENITRSLVSFLVFSFFCAQFLYSF
		SHSNIGTLMATSGADFLRTLAMPA
		GFTILGVILLSCALDIIITSASSKWSILAPILVP
		MLMAVGISPELTQASFRVSSTVNI
		STPMFAFYPLIIMYCROYCSKTGVGTLCAMMLPY
		TLGLTVVLTMLLYLFWGLDIPLGF
		QSGYTYPATQ"
misc-feature	18198..18257	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18300..18368	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18381..18449	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18492..18560	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18597..18665	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18735..18803	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	18921..18974	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19032..19100	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19161..19229	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19272..19340	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19359..19412	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19440..19508	/gene="YPO1008"
		/note="one of 13 probable
		transmembrane helices predicted
		for YPO1008 by TMHMM2.0"
misc-feature	19545..19613	/gene="YPO1008"
		/note="one of 13 probable

gene 19745..20977  
CDS 19745..20977

for YPO1008 by TMHMM2.0"  
/gene="YPO1009"  
/gene="YPO1009"  
/note="Similar to Bacillus  
subtilis Peptidase T PepT  
SW:PEPT-BACSU (P55179) (410 aa)  
fasta scores: E(): 0, 39.6% id in  
396 aa, and to Escherichia coli  
Peptidase T PepT SW:PEPT-ECOLI  
(P29745) (408 aa) fasta scores:  
E(): 0, 38.2% id in 408 aa"  
/codon-start=1  
/transl-table=11  
/product="probable peptidase"  
/protein-id="CAC89852.1"  
/db-xref="GI:15979078"  
/db-xref="SWISS-PROT:Q8ZH96"  
/translation="MTIALSEQLTNRFFRYLAWS  
SQSDAASPTLPSTEGQHKMAQMLA  
EELRQLGLEIDILIDEHATVTARKPGNQPTAPRIG  
FITHIDTVDVGLSPDIHPQRLRFT  
GSDLCLNAEQGIYLRRTAEHPILRYQGEEIIFSD  
GTSVLGADNKAAVTVVMTLLENLT  
ADDCHGDIVVAFVFPDEEIGLRGAKALDLARFDVD  
FAYTIDCCELGEVVYENFNAASAE  
IDIIGVTAHPMSAKNVLINPIRVAYDIISEFSPQ  
ETPEHTEGREGYVWFTDMTANPNS  
AKLKIAIRDFDNVSFAARKAYIGEVVAKVSAQYP  
RAKISYSVTDVYSNISNSIGEDKR  
AIDLIFSSMAELNIEPKVIPMRGGTDGAALSTQG  
LLTPNYFTGAHNFHSPFEFLPISS  
FVKSYQLTRTICLSAACA"

misc-feature 19781..20011

/gene="YPO1009"  
/note="Pfam match to entry PF01546  
Peptidase-M20, Peptidase family  
M20/M25/M40, score 19.30, E-value  
0.00013"

misc-feature 20171..20425

/gene="YPO1009"  
/note="Pfam match to entry PF01546  
Peptidase-M20, Peptidase family  
M20/M25/M40, score 15.90, E-value  
0.0012"

misc-feature 20549..20818

/gene="YPO1009"  
/note="Pfam match to entry PF01546  
Peptidase-M20, Peptidase family  
M20/M25/M40, score 15.90, E-value  
0.0013"

gene 21365..23437  
CDS 21365..23437

/gene="YPO1011"  
/gene="YPO1011"  
/note="Similar to Azospirillum  
irakense putative outer membrane  
salicin receptor salC TR:Q9LAE4  
(EMBL:AF143227) (726 aa) fasta  
scores: E(): 0, 25.3% id in 730  
aa, and to Escherichia coli  
probable TonB-dependent receptor  
YncD SW:YncD-ECOLI (P76115) (700  
aa) fasta scores: E(): 2.1e-15,  
22.9% id in 721 aa"  
/codon-start=1  
/transl-table=11  
/product="putative TonB-dependent  
outer membrane receptor"  
/protein-id="CAC89853.1"  
/db-xref="GI:15979079"  
/db-xref="SPTREMBL:Q8ZH95"  
/translation="MMVFYRKFFTVTVLISLPCL  
AWSQSHNNSKDELDTITVVAQKIN  
QQQOKTPISISVLTGFDLERENIENIYESIMRIP  
NVYIMVKAGNPSDAGFFTMRGTTTPG  
MEGIQSVGFFIDGVYANTFDTELLDVDRIEVLRG  
PQATLYGRNTESGVINVITKDPEF  
SPEYKIGLSYGNYNRTQVTTVLGGSINDSEQFSY  
RAALKYLYGNGYFKRDYDGKNNVD  
NLNDFSGRFKLRWQPMDDGWDVMTTFDIQNRNG

		SDVDAYKGQVNAVYTFDDIDFTSVSAYVDERKVD NQDLDFTRLISISELLMNRKTKQFS QEFRLNSKYSQPFNLIGSYFYQDDENEIDFRY LPYNLAQLRKSDIKTNNYAVFGNV NYYLLNDVELVAGARYDYEKKKLNFLMDNGFNPNY QPYSHDNNSNSFGAFLPKVGLNYY ITGDAMLYTSIARGYKSGGFNTLGPQSSRAYNAE YMTTYEAGVKTEWFDRTVRWNTSL FWNDMKDQQVEVAYYPISSVNSGKSLSRGLESE LAWRITRGLTVSANVGYTDAYFKN FPTEIKVDNNYIPVNYKGNRPANSPGYTYSIGAD YNFLNGYFVNATYNVKGSTYLDNA NSKKQPAYGLLDLTAGYENKDYGVNVWIKNILDE TYVTRAFKMDDGIWYGRAGEPINF GVNFNVKF"
misc-feature	21365..21487	/gene="YPO1011" /note="PS00430 TonB-dependent receptor proteins signature 1."
misc-feature	23117..23434	/gene="YPO1011" /note="Pfam match to entry PF00593 TonB-boxC, TonB dependent receptor C-terminal region, score 28.70, E-value 1.3e-06"
gene	23618..26928	/gene="YPO1012"
CDS	23618..26928	/pseudo /gene="YPO1012" /note="This CDS is disrupted by the insertion of IS100 element. Similar to regions of polyketide synthases/peptide synthetases eg. Bacillus subtilis MycA TR:Q9R9J1 (EMBL:AF184956) (3971 aa) fasta scores: E(): 0, 29.5% id in 1112 aa, Streptomyces coelicolor polyketide synthase SC3f7.12 TR:O54155 (EMBL:AL021409) (2297 aa) fasta scores: E(): 0, 31.1% id in 1199 aa and Sorangium cellulosum polyketide synthase EpoC TR:Q9L8C7 (EMBL:AF210843) (7257 aa) fasta scores: E(): 0, 39.3% id in 499 aa." /pseudo /codon-start=1 /transl-table=11 /product="putative peptide/polyketide synthase subunit (pseudogene)"
misc-feature	23705..25051	/gene="YPO1012" /note="Pfam match to entry PF00501 AMP-binding, AMP-binding enzyme, score -62.80, E-value 6.5e-12"
misc-feature	25382..25576	/pseudo /gene="YPO1012" /note="Pfam match to entry PF00550 pp-binding, Phosphopantetheine attachment site, score 29.50, E-value 1.5e-06"
misc-feature	25637..26854	/pseudo /gene="YPO1012" /note="Pfam match to entry PF00109 ketoacyl-synt, Beta-ketoacyl synthase, score 419.00, E-value 4.3e-122"
misc-feature	26081..26131	/pseudo /gene="YPO1012" /note="PS00606 Beta-ketoacyl synthases active site."
misc-feature	26929..28882	/pseudo /note="insertion sequence, IS100"
misc-feature	26929..26956	/note="IS100 inverted repeat"
gene	27015..28037	/gene="YPO1013" /note="synonyms: y1093, ypmt1"
CDS	27015..28037	/gene="YPO1013" /note="Similar to Escherichia coli transposase for insertion sequence"

(P15025) (390 aa) fasta scores: E(): 3e-27, 33.1% id in 329 aa. Identical to the previously sequenced Yersinia pestis, Yersinia pseudotuberculosis, and Escherichia coli pesticin plasmid insertion sequence transposase Y1055 TR:P74993 (EMBL:U59875) (340 aa) fasta scores: E(): 0, 100.0% id in 340 aa"

/codon-start=1  
/transl-table=11  
/product="transposase for insertion sequence IS100"  
/protein-id="CAC89855.1"  
/db-xref="GI:15979080"  
/db-xref="SPTREMBL:P74993"  
/translation="MVTFTVMEIKILHKQGMSS  
RAIARELGISRNTVKRYLQAKSEP  
PKYTTPRPAVASLLDEYRDYIRQRIADAHYPKIPA  
TVIAREIRDQGYRGMTILRAFIR  
SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS  
PLHVFVAVLGYSRMLYIEFTDNMR  
YDTLETCHRNAFRFFGGVPREVLYDNMKTVVLR  
DAYQTGQHRFHPSLWQFGKEMGFS  
PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL  
RPMGITVDVETANRHGLRWLHDVA  
NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD  
VHLDENLVNFDKHPHPLSIYDS FCRGVA"

misc-feature 27039..27122 /gene="YPO1013"  
/note="Pfam match to entry PF00239 recombinase, Site-specific recombinases, score 25.70, E-value 4.7e-06"

misc-feature 27066..27131 /gene="YPO1013"  
/note="Predicted helix-turn-helix motif with score 2147 (+6.50 SD) at aa 18-39, sequence MSSRAIARELGISRNTVKRYLQ"

misc-feature 27360..27893 /gene="YPO1013"  
/note="Pfam match to entry PF00665 rve, Integrase core domain, score 81.90, E-value 1.6e-22"

gene 28034..28816 /gene="YPO1014"  
/note="synonym: ypmt1.57c"

CDS 28034..28816 /gene="YPO1014"  
/note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa."

/codon-start=1  
/transl-table=11  
/product="insertion sequence IS100, ATP-binding protein"  
/protein-id="CAC89856.1"  
/db-xref="GI:15979081"  
/db-xref="SPTREMBL:Q9R3L5"  
/translation="MMELQHQRMLMALAGQLQLE  
SLISAAPALSQQAVDQEWSYMDFL  
EHLLHEEKLARHQRKQAMYTRMAAFPAVKTFEEY  
DFTFATGAPQKQLQSLRSLSFIER  
NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF  
TTAADLLLQLSTAQRQGRYKTTLO  
RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR  
YEKSAMILTSNLPFGQWDQTFAGD  
AALTSAMLDRIHHSHVQIKGESYRLRQKRKAG  
VIAEANPE"

		/note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	28361..28384	/gene="YPO1014" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	complement(28855..28882)	/note="IS100 inverted repeat"
gene	28881..29060	/gene="YPO1014a"
CDS	28881..29060	/partial /gene="YPO1014a" /note="Similar to the C-terminal regions of Escherichia coli prepilin peptidase dependent protein A PpdA SW:PPDA-ECOLI (P33554) (156 aa) fasta scores: E(): 0.00089, 41.304% id in 46 aa, and Escherichia coli O157:H7 prepilin peptidase dependent protein A ECS3683 TR:BAB37106 (EMBL:AP002563) (156 aa) fasta scores: E(): 0.00089, 41.304% id in 46 aa. Probable gene remnant resulting from insertion of the upstream IS element and recombination." /codon-start=1 /transl-table=11 /product="prepilin peptidase (partial)" /protein-id="CAC89857.1" /db-xref="GI:15979082" /db-xref="SPTREMBL:Q8ZH94" /translation="QITLPLQKEMGFYGVNRTAQ AGNIILSSPAGRIRLVISSRGRIR LCSEQQSMAGIHLCL"
gene	29051..29659	/gene="YPO1015"
CDS	29051..29659	/gene="YPO1015" /note="Similar to Escherichia coli prepilin peptidase dependent protein B SW:PPDB-ECOLI (P08371) (187 aa) fasta scores: E(): 5e-17, 30.4% id in 191 aa, and N-terminus of Pseudomonas aeruginosa general secretion pathway protein J precursor SW:GSPJ-PSEAE (Q00517) (237 aa) fasta scores: E(): 0.19, 39.3% id in 61 aa" /codon-start=1 /transl-table=11 /product="putative prepilin peptidase dependent protein" /protein-id="CAC89858.1" /db-xref="GI:15979083" /db-xref="SPTREMBL:Q8ZH93" /translation="MPLVVNVLSTPLNAQPTRTA GFTLPPEMMLALSFGSLIALSTAQV LPKLSQQISVLQOHYRLELVMNQAMGAMEKDLRR AGFCHGKCGEAITIEHYLGETAH SCLIVAYDLNCNGRWEGAKHQESEYFGYRLRNKA LESQRGELNCHGRGWEEKLFDPRDV TVTHFSVTPLSGQLFKLRLVGHKTGNPAIHHQVT YLIRGNV"
misc-feature	29108..29170	/gene="YPO1015" /note="PS00409 Prokaryotic N-terminal methylation site."
gene	29656..30126	/gene="YPO1016"
CDS	29656..30126	/gene="YPO1016" /note="No significant database matches" /codon-start=1 /transl-table=11 /product="putative membrane protein"



		/db-xref="GI:15979084"
		/db-xref="SPTREMBL:Q8ZH92"
		/translation="MTQVFQRGSSSTLAAMVTLFS LGLFWLSAIHRQLDNIQQITGEEQ RYLRAYNQAESSLNWGVSRWALRIPWRVGSAAW CMAHQELGLKACVKRSSLAGFFIL KGESLPLGSLPPLMLYQRVKLKAVTGSSGNYQLI DTPHGWLDPCPKDAQFCLD"
misc-feature	29683..29742	/gene="YPO1016" /note="1 probable transmembrane helix predicted for YPO1016 by TMHMM2.0"
gene	30114..30524	/gene="YPO1017"
CDS	30114..30524	/gene="YPO1017" /note="Weakly similar to Escherichia coli prepilin peptidase dependent protein C precursor PpdC SW:PPDC-ECOLI (P08372) (107 aa) fasta scores: E(): 0.42, 23.7% id in 114 aa, and to Pseudomonas aeruginosa PilV TR:Q57003 (EMBL:L36117) (185 aa) fasta scores: E(): 0.91, 32.8% id in 58 aa" /codon-start=1 /transl-table=11 /product="putative prepilin peptidase dependent protein" /protein-id="CAC89860.1" /db-xref="GI:15979085" /db-xref="SPTREMBL:Q8ZH91" /translation="MPRLITKHAYGQTISVETGG FNLRLHGRGFSLLLEVLIAALFFSIS LLGLLQYHQALLOGFASSWQQRQAWSWLHQYMES QSGTDPEERWAPEVKPGWHYRQFI DRIEGDCREFSVKLITRQDSPVELSRWFCSTEMI "
misc-feature	30192..30254	/gene="YPO1017" /note="PS00409 Prokaryotic N-terminal methylation site."
misc-feature	30198..30266	/gene="YPO1017" /note="1 probable transmembrane helix predicted for YPO1017 by TMHMM2.0"
gene	30659..34030	/gene="recC"
CDS	30659..34030	/note="synonym: YPO1018" /gene="recC" /EC-number="3.1.11.5" /note="Similar to Escherichia coli exodeoxyribonuclease V gamma chain RecC SW:EX5C-ECOLI (P07648) (1122 aa) fasta scores: E(): 0, 63.5% id in 1123 aa, and to Vibrio cholerae exodeoxyribonuclease V, 125 kDa subunit VC2322 TR:Q9KPP4 (EMBL:AE004302) (1148 aa) fasta scores: E(): 0, 45.8% id in 1130 aa" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease V gamma chain" /protein-id="CAC89861.1" /db-xref="GI:15979086" /db-xref="SPTREMBL:Q8ZH90" /translation="MFTVYHSNQLDLLKALTAL IEREPLDNPFOQEVVLVQSPGMAQ WLQMQLAQQFSIAANIVFPLPATFIWDMFTRVLP DIPKESAFSKEAMTWKLMWLLPDL LENPLFSPMKRYLSDDGDRRKIHQLAARVADLFD QYLIVYRPEWLESWERGQLIEGLDD AQWQALLWVELTRYTRQLEQPEWHRANLYQRFI HQLLKSDVCPQGLPKRVFICGISA LPPIYLQALQALGKHIDIHLMFTNPCRYFWGDIQ DYTFLLAKLQSRKRRHYRESIELSL"

MYLLSQIDEIQEVHAFVDIEPDNL  
LHGIQHDMLELEDHAVIGTTPETLARSQKRRLD  
LDDRSLSFHVCHSPQREVEVLQDH  
LLGLLAADPELTPRDIIVMVVDIDSYTPYIQAAP  
GNAPSERYLPFAISDRKASQAHPA  
LHAFITLLDLPQSRFTAEQVLALLEVPALATKFG  
ITEDGLRRLRQWVGESGIRWGLDD  
DNVRELSLPATGQHTWRFGLTRMLLGYAMDSTAG  
DWQGILPYDESSGLAAELAGQLAD  
MLMHL SQWRQQLGQPRELSEWLPICRQLLDTFFD  
QDNDTEAALVLIQQWQKVIGYGI  
AAQYPDVVPLNLLRDELAARLDNERISQRFLAGP  
INFCTLMPMRSIPFKVVCLLGMND  
GVYPRTLPPQGFDLMAKKVRRGDRSRDDDRYLF  
LEALLSAQQQLYISYIGRSIQDNS  
KRYPSVLVSELIEYVAQSYHLPGDEKLSADDSAQ  
RVTQHLLCWHARMPFSAENFIKNS  
ELQSYAAEWLPSAESKGHAHPNFNQPLQAEPLAE  
ITLDELVRFYRHPVRAFFQLRLGV  
NFVIEETELPDEEPFTLDNLSRYQFNTQLLNALI  
NEDDINSVFARARAAGVLPYGSFG  
ELYWESQQDEMVP LAEQIRSERKENHSIELNIEF  
ADITVTGWIHQVQDDGLVRWRPSI  
LTAVDGLLLWLEHLVYCSAGGEGESRIYGRKGTA  
WRYAPMAADEARPYLQQLIKGYQQ  
GLCEPLMLLSKSGWAWLSQCFDRESGQILWDEET  
QGKARMKLLQVWQGDQRTGEGED  
HYIQRVCRMDNQHLDIILHETERYLLPIARHNK  
A"

/gene="ptrA"  
/note="synonyms: ptr, YPO1019"  
/gene="ptrA"  
/EC-number="3.4.24.55"  
/note="Similar to Escherichia coli  
protease III precursor PtrA  
SW:PTRA-ECOLI (P05458) (962 aa)  
fasta scores: E(): 0, 63.0% id in  
947 aa, and to Vibrio cholerae  
peptidase, insulinase family  
VC2072 TR:Q9KQC8 (EMBL:AE004281)  
(939 aa) fasta scores: E(): 0,  
28.0% id in 919 aa"  
/codon-start=1  
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/product="protease III precursor"  
/protein-id="CAC89862.1"  
/db-xref="GI:15979087"  
/db-xref="SPTREMBL:Q8ZH89"  
/translation="MHKQLARIVGIVFFLGLLAP  
SSWAAIPAWQPLAETIYKSEHDLR  
KYQAIKLSNGMTVLLVSDTQAPKSLAALALPVGS  
LEDPDNQLGLAHYLEHMLMGSKH  
FPEPGSFSEFLKKHGGSHNASTASYRTAFYLEIE  
NDALAPAVERLADAIAEPLLDPIN  
ADRERNAVNAELTMARSRDGMRMAQVNAETLNPA  
HPSARFSGGNLETLRDKPDGKLHD  
ELVSFYHRYYSANLMVGVLYSNQSLEQLAQLAAD  
TFGRIPNRDAKVPTITVPVVPDQ  
TGIIIHYPVPAQPRKQIKVDFRIANNSADFRSKTD  
TYISYLSNRSKNTLSDWLQKQGL  
ADAINAGADPMLDRNGGVFSITVSLTDKGLAQRD  
VVVAAIFDYINMLHKEGIKKSYFD  
EIAHVLNLDFRYPSITRDMDYIEWLVDMMLRVPV  
AHTLDAPYLADQYDPKAIASRLAE  
MTPENARIWVFSPEEPHNKVAYFVDAPYQVDKIG  
VQRMKEWQQLGQKIALSLPALNPY  
IPDNFTLIKADKNITRPQNVADQPGLRVFYMP SQ  
YFADEPKADITVAFRNPHALNSAR  
HQVLFALTDYLAGLSLDQLSYQASIGGISFSTAP  
NNGLYVNAGGFTQRM PQLLTSLSV  
GYASFPTPEEQLVQAKSWYREQLDVAEK GKAYEL  
AIQPAKLLSNVPYSERSERRKLLD  
SISVQDVLTYRDDLLKQSAIEVLAVGNMTAEQVT  
ELTESLKKQLNLIGTTWWVGEDVI  
IEKTQLANMERVGSSSDAALAAVYVPTGYTEIAG

gene 34112..37000  
CDS 34112..37000

misc-feature 34274..34693

misc-feature 34340..34411

gene 36997..40659

CDS 36997..40659

LGYAVFSFPM SVGHQWGIGFLLQSN SKEPNYLYQ  
RYLAFYPQAEKRLREMKPDDFEQY  
KQGLVNQQLLQRPQTLDEEAERYRKDFNLNNFAFD  
SREKMIAQVKQLTANELADFFQQA  
VIKPGGLALLSQVKGQQAGGFAPVEGWTTTPTT  
SALQATLPQKVLAP"  
/gene="ptrA"  
/note="Pfam match to entry PF00675  
Peptidase-M16, Insulinase  
(Peptidase family M16), score  
166.30, E-value 5e-46"  
/gene="ptrA"  
/note="PS00143 Insulinase family,  
zinc-binding region signature."  
/gene="recB"  
/note="synonyms: rorA, YPO1020"  
/gene="recB"  
/EC-number="3.1.11.5"  
/note="Similar to Escherichia coli  
exodeoxyribonuclease V beta chain  
RecB SW:EX5B-ECOLI (P08394) (1180  
aa) fasta scores: E(): 0, 62.0% id  
in 1190 aa, and to Vibrio cholerae  
exodeoxyribonuclease V, 135 kDa  
subunit VC2320 TR:Q9KPP6  
(EMBL:AE004302) (1208 aa) fasta  
scores: E(): 0, 48.0% id in 1203  
aa"  
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beta chain"  
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/db-xref="SPTREMBL:Q8ZH88"  
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LGGDAAFRRPLMVEEILVVTFTTEATEELRGRIR  
DNIHGLRIACVRGVSDDPMYQALL  
AEITDWAVAAAQLLAAERQMDEAAIYTIHGFCQR  
MLANNAFESGILFEQTLVQDELPL  
WRQACADFWRRHCYPLPLVIARAVSQEWSGPEAL  
LSDLSAYLQGETPKFRQAPGDDDET  
ILSRHQHVVTQIDALKAEWRLAAPELEALISRSG  
VDKRSYSSKHLPNWLEKVGWLWAEQ  
ETEDYQLPKLEKFRQSVLLEKTKKGAAPQHTLF  
SAIDSIFEQPLTLRDLILARAISE  
IRFSVQQEKRQRAELGFDDLLSKLDAALQQSGGE  
LLAQSIIRTRYPVAMIDEFQDTPQ  
QYRIFHTVYGGQEACALLIGDPKQAIYAFRGAD  
IFTYIRARSEVSAHYTLETNWRSS  
FPMVQSVNRLFSLVNTPFLFEQIPFINVAAAKKN  
HDLSEFIKGEKQPALHFWLQPGDG  
VGVSEYQQVMARQCAAQIRDWLTAGQQQAELLT  
TKGPKPVQASDITILVRSRAEAL  
IRDALSALAIPSVYLSNRDSVFETTEAKDLLWLL  
QAVLAPEQERALSAMATGILGLD  
ARMLDALNHDERAWDALVDEFDHYRQHWQRRGVL  
PMLREMMARRHLAENLLATPGGER  
RLTDLLHLGELLQEAASQLDSEHALIRWLAQQIA  
QPNPQSDSQQLRLES DRHLVRVVT  
IHKSKGLEYPVWLVPFIGNFRQQQNVLYHDRHSF  
EALLDLNADEESQALAEERLAED  
LRLLYVALTRSVYHCSVGIAPLIKGGRKKQGESH  
MHRSA LGYLVQHGPDAHVLSEK  
LTELARSSNGDICVSPVEPPDDKPWQPQPEALPE  
LTARHFTRKMQDYWRVTSYSGLQQ  
SGSTKKLYGSATGDVSQALGAPLQVLLPRLDIDA  
VGEQAVVTEDDHLTPHTFPRGAAP  
GTFLHDLLEPLDFSQPIELAWLSERLQQQGFSEQ  
WAPVLHQWLNDIVQTPLTDTGATL  
AGLSPERKQAELOFYLPIDSLRAEVLDRLIKQY  
DPLSRQCPVLDFFQVVRGMLKGFID  
LVFCWQQGYLLDYKSNWLGEDSRAYTVEAMTQA  
MAEHRYDLQYQLYTLALHRYLRHR

misc-feature	37006..39120	PEOKLIEEMDRLFSGTIGSNATAS DKSGSNVIHSGERASR" /gene="recB" /note="Pfam match to entry PF00580 UvrD-helicase, UvrD/REP helicase, score 367.30, E-value 1.6e-106"
misc-feature	37066..37089	/gene="recB" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	40656..42614	/gene="recD" /note="synonym: YPO1021"
CDS	40656..42614	/gene="recD" /EC-number="3.1.11.5" /note="Similar to Escherichia coli exodeoxyribonuclease V alpha chain RecD SW:EX5A-ECOLI (P04993) (608 aa) fasta scores: E(): 0, 56.7% id in 638 aa, and to Vibrio cholerae exodeoxyribonuclease V, 67 kDa subunit VC2319 TR:Q9KPP7 (EMBL:AE004302) (706 aa) fasta scores: E(): 0, 45.3% id in 727 aa" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease V alpha chain" /protein-id="CAC89864.1" /db-xref="GI:15979089" /db-xref="SPTREMBL:Q8ZH87" /translation="MMTLLAQAAARDLLRPLDVQ FSRMIAGDDDDPRLQLAAAILSAEV GAGHVCLPLRYLQPELLFGGRQPDLSLALWQAAG SPDKAQWLQALQNAPVVS DGSQPT PLVLQOERLYLQRMWQYEGDVVQFIASDSVFINR DSDFMSTKGIATSVDESLLRETLD ALFGCAGSEVDWQKVAAVAATTRISVISGGPGT GKTTTVAKLLTALIRLSQGQRLRI KLAAPTGKAAARLTESLGKAIHQFFLTDDERKLF PDQASTLHRLLGVPNSQRLRYHR GNPLNLDVLVVD EASMDLPMMARLIAALPAKAK VIFLGDRDQLASVEAGAVLGDICR FAELGYSEQRAQQLTQLTGYLLTNNALTSNVLTN KALANKAQPD EYSDSANVRDSL LLRKS YRFDEKSGIGQLALAVNAGEYRQALSVLN SAYS DVERFPLADEEDYQVLL EAC AVGYQH YLERVAALAPAAEVLA AFGRYQLLCALR SGPFGV SGLNERIEQVLHRKGFII RPSG PSGRWYVGRPVMIELNDSALGLFNGDIGIA LHDNEGELRVYFQLPDGNIKSVQP SRLPSHETAYAMTVHKSQGFSEFEHTALVLPNTFM PVLTR ELVYTAITRARQHLTLYCS DAVLSHAIRTPTLRLSGLVDRLNTLNRQ" /gene="recD" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	41223..41246	/gene="recD"
misc-feature	42384..42524	/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement(42769..44094 )	/gene="recD" /note="Pfam match to entry PF01443 Viral-helicase1, Viral (Superfamily 1) RNA helicase, score 29.70, E-value 6.5e-08"
CDS	complement(42769..44094 )	/gene="argA" /note="synonym: YPO1022" /gene="argA" /EC-number="2.3.1.1" /note="Similar to Escherichia coli amino-acid acetyltransferase ArgA SW:ARGA-ECOLI (P08205) (443 aa) fasta scores: E(): 0, 87.3% id in 441 aa, and to Vibrio cholerae N-acetylglutamate synthase VC2316 TR:Q9KPQ0 (EMBL:AE004301) (456 aa) fasta scores: E(): 0, 65.8% id in

```

/codon-start=1
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acetyltransferase"
/protein-id="CAC89865.1"
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/db-xref="SPTREMBL:Q8ZH86"
/translation="MKERSTELVQGRHSVPYIN
AHRGKTFVVMLGGEAIEHENFSSI
VNDIGLLHSLGIRLVVVYGARPOIDSNLADHNYE
PIYHKHTRVTDARTLEMVKQAAGL
LQLDITARLSMSLNNTPLQGAHINVSGNFIIAQ
PLGVDDGVDYCHSGRIRRIDEEAI
HRQLDNGAIVLLGPVAVSVTGESFNLTSEEVATQ
LAIKLKAEKMIGFCSSQGVTDSEG
NIISELFPNDAQKRIEDLEQDGDYNSGTVRFLRG
AVKACRSGVRRSHLLSYQEDGALI
QELFSRDGIGTQIVMESAEQVRRATINDIGGILE
LIRPLEQQGILVRRSREQLEMEID
KFTTIERDNLTIACAALYPFPDEHIGEMACVAVH
PDYRSSSRGEMLLNRITNQARQMG
LKKLFVLTTRSIHWFOERGFTPAEVDVLPIQKQE
LYNYQRRSKILLADL"
misc-feature      complement(42856..43074) /gene="argA"
)
/note="Pfam match to entry PF00583
Acetyltransf, Acetyltransferase
(GNAT) family, score 42.00,
E-value 1.3e-08"
misc-feature      complement(43387..44022) /gene="argA"
)
/note="Pfam match to entry PF00696
aakinase, Amino acid kinase
family, score 65.00, E-value
1.6e-15"
gene              44330..45580 /gene="YPO1023"
CDS               44330..45580 /gene="YPO1023"
)
/EC-number="3.5.1.28"
/note="Similar to Escherichia coli
N-acetylmuramoyl-L-alanine amidase
AmiC precursor SW:AMIC-ECOLI
(Q46929) (417 aa) fasta scores:
E(): 0, 70.4% id in 419 aa, and to
Neisseria meningitidis
N-acetylmuramoyl-L-alanine amidase
AmiC or NMA2028 TR:Q9JT18
(EMBL:AL162757) (416 aa) fasta
scores: E(): 0, 49.9% id in 421
aa"
/codon-start=1
/transl-table=11
/product="N-acetylmuramoyl-L-alani
ne amidase AmiC precursor"
/protein-id="CAC89866.1"
/db-xref="GI:15979091"
/db-xref="SPTREMBL:Q8ZH85"
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WMLSISRVGFAASSHIVAVRVWPS
STYTRVTLESNTPLKYRQFALTHPDRIVVDIEGV
QLNSVLKEISRQVQSADPYLKQAR
VGQFDKNTVRLVLELKQISIPQLFTLKPFAEFRN
RLVVDLYPAEGGTS AEDDPLLALL
EDYNKGNVDRTLPPETPKAGKAGRDRPIIIMLDP
GHGGEDPGAIGKNKTKEKDIVLQI
ARRLRALIQKEANMRVFMTRNEDVFIPLKVRVAK
ARKLRADLFISIHADAFTNRAASG
SSVFALSTKGATSTAARFLAQTONEADQIGGVSK
SGDPYLDHTIIDLLQTATINDSLK
FGKEVLSRMSKINKLHKNRVDQAGFAVLKAPDIP
SILVETAFISNLEEERKLRTSRFQ
QQIAESIFAGIKAYFANGGAMARL"
misc-feature      45077..45553 /gene="YPO1023"
)
/note="Pfam match to entry PF01520
Amidase-3,
N-acetylmuramoyl-L-alanine

```

tRNA	complement(45810..45886)	1.4e-67" /product="tRNA-Met"  /note="tRNA Met anticodon CAT, Cove score 86.07"
tRNA	complement(46010..46086)	/product="tRNA-Met"  /note="tRNA Met anticodon CAT, Cove score 86.07"
gene CDS	46302..47474 46302..47474	/gene="YPO1025" /gene="YPO1025" /EC-number="3.2.1.-" /note="Similar to Escherichia coli membrane-bound lytic murein transglycosylase A precursor SW:MLTA-ECOLI (P46885) (365 aa) fasta scores: E(): 0, 69.9% id in 366 aa, and to Vibrio cholerae membrane-bound lytic murein transglycosylase A precursor TR:Q9KPQ4 (EMBL:AE004301) (368 aa) fasta scores: E(): 0, 46.0% id in 359 aa" /codon-start=1 /transl-table=11 /product="membrane-bound lytic murein transglycosylase A precursor" /protein-id="CAC89867.1" /db-xref="GI:15979092" /db-xref="SPTREMBL:Q8ZH84" /translation="MTSRWGKYLLSGIMIAVLG CQSRPTDRGQQYKDGRLQSLLELV NEPNAAGKPVNAKDYSQVKVINQSSPGLYNRNS DTFNAVQNWMLAGADTSKLSLFLG NAYQMEGVDFNFGNVQFTGYITPVLQARYTPQGEF RHPLYRMPAKGKRRLPDRAAIYAG ALDNRNLIIAYTNSLVDNFMMEVQSGSYVDYGDG RPLTFFGYAGKNGHAYRSIGKVL DRGEVARADMSMQAIRQWAENHSEAEVRELLEQN PSFVFFKPVMPYAPVKGASAVPLIA KASVASDKSLIPPGTTLLAEVPLLDQGGKFTGKY QMRLMVALDVGGAIKGQHFDIYQG IGHEAGQAAGFYNHYGRVWVLKNAQSSGPLFTAY KGGTQSEPTSNDSSLLVNNQDR" /gene="YPO1025" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	46332..46364	
gene CDS	47617..48444 47617..48444	/gene="YPO1026" /gene="YPO1026" /note="Similar to Escherichia coli hypothetical protein YgdL SW:YGDLE-ECOLI (Q46927) (268 aa) fasta scores: E(): 0, 80.5% id in 267 aa, and to Vibrio cholerae HesA/MoeB/ThiF family protein VC2311 TR:Q9KPQ5 (EMBL:AE004301) (273 aa) fasta scores: E(): 0, 65.8% id in 263 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89868.1" /db-xref="GI:15979093" /db-xref="SPTREMBL:Q8ZH83" /translation="MSTAYSEAYQQRFGGIARLY GQALALFSQAHVCVIGIGGVGSW AAEALARTGIGAITLIDMDVVCVTNTNRQIHALLR HNIGQAKTEVMAERILAINPECHV TCIDDFITADNVAELLNKNFSYVIDAIDSVRPKA ALLSYCRRYKIPVVTGGAGGQID PTRIAVVDLAKTIQDPLAAKLRLKSDFNVVKN SKGKLIGIDCVFSSEPLVYPQADGS

misc-feature 47701..48114 VSHVLKKMMAKAAARQHESAATAS"  
 /gene="YPO1026"  
 /note="Pfam match to entry PF00899  
 ThiF-family, ThiF family, score  
 183.20, E-value 4.2e-51"  
 misc-feature 48319..48387 /gene="YPO1026"  
 /note="1 probable transmembrane  
 helix predicted for YPO1026 by  
 TMHMM2.0"  
 gene complement(48480..48923 /gene="YPO1027"  
 )  
 CDS complement(48480..48923 /gene="YPO1027"  
 )  
 /note="Similar to Escherichia coli  
 hypothetical protein YgdK  
 SW:YGDK-ECOLI (Q46926) (147 aa)  
 fasta scores: E(): 5.7e-30, 59.0%  
 id in 139 aa, and to Vibrio  
 cholerae hypothetical protein  
 VC2310 TR:Q9KPQ6 (EMBL:AE004301)  
 (144 aa) fasta scores: E():  
 3.5e-19, 43.1% id in 144 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
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 /db-xref="GI:15979094"  
 /db-xref="SPTREMBL:Q8ZH82"  
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 FSAHKQWEDRYRQLILLAKQLPPL  
 QEAWKKNELELTGCENRVWLGHQHLDPDGLTHFYG  
 DSEGRIVRGLLAVILTAVEGKTPQ  
 QVLAADPLALFEQLGLRQQLSTSRANGLQALAQG  
 VQTIAAKYAER"  
 gene complement(49058..50377 /gene="YPO1028"  
 )  
 CDS complement(49058..50377 /gene="YPO1028"  
 )  
 /note="Similar to Escherichia coli  
 ORF-O401 TR:Q46925 (EMBL:U29581)  
 (401 aa) fasta scores: E(): 0,  
 67.1% id in 401 aa, and to Vibrio  
 cholerae aminotransferase, class V  
 VC2309 TR:Q9KPQ7 (EMBL:AE004301)  
 (404 aa) fasta scores: E(): 0,  
 51.5% id in 396 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="putative  
 aminotransferase class V"  
 /protein-id="CAC89870.1"  
 /db-xref="GI:15979095"  
 /db-xref="SPTREMBL:Q8ZH81"  
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 TMIKAKKFRGHSQDANNSMKVFNP  
 MDFRREFPALSDKLTLYLDSAATALKPRAMIDATQ  
 QFYQQDSATVHRSQHQSALSLTVR  
 FENTRQQVADFINSSAENIIWTRGTTEAINLIA  
 QSYARPRLOPEDEIIVSEAEHHAN  
 LIPWLMVAEQTGAKIVKLPLGLDHLPLDQLPQL  
 LNEKTRILALGQMSNVTGGSPDLA  
 QAIRLAHQYDCVVVDGAQGIVHYPADVQALDID  
 FYAFSSHKLYGPTGIGVLYGKTEL  
 LEEMPAWQGGGKMLTHASFGGFTPHEVPYRFEAG  
 TPNIAGVIGLSAVLKWLEHIDLEE  
 AEVYSQGLATMAENKLAQLPGFHSYRCQQSSLLA  
 FTFDGVHHSDDLVALLAEQGIALRA  
 GQHCAQPLMAALGVNGSLRASFAFYNTPDVEML  
 CSALGKALELLRD"  
 misc-feature complement(49100..50176 /gene="YPO1028"  
 )  
 /note="Pfam match to entry PF00266  
 aminotran-5, Aminotransferases  
 class-V, score 5.20, E-value

misc-feature complement(49568..49627 /gene="YPO1028"  
 )  
 /note="PS00595 Aminotransferases  
 class-V pyridoxal-phosphate  
 attachment site."  
 gene 50923..51840 /gene="gcvA"  
 /note="synonym: YPO1029"  
 CDS 50923..51840 /gene="gcvA"  
 /note="Similar to Escherichia coli  
 glycine cleavage system  
 transcriptional activator GcvA  
 SW:GCVA-ECOLI (P32064) (305 aa)  
 fasta scores: E(): 0, 88.2% id in  
 304 aa, and to Vibrio cholerae  
 transcriptional regulator, LysR  
 family VC0896 TR:Q9KTK6  
 (EMBL:AE004173) (306 aa) fasta  
 scores: E(): 0, 69.3% id in 296  
 aa"  
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 transcriptional activator"  
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 /db-xref="SPTREMBL:Q8ZH80"  
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 SINEATRKLQARSAGALTVSLPP  
 SFAIQWLVPRLSGFNAAYPGIDVRIQAVDREEDK  
 LADDVDVAIFYGRGNWSGLRTERL  
 YAEFLLPVCAPSLLTGENGLKVPSDLNHTLLHD  
 TSRRDWLAYTRQLGVPOINVQOGP  
 IFSHSAMVVQAAVHGQGIALLVNNVMAQSEIEAGR  
 LVCPFNDVLVSKNAFYLVCHDSQA  
 ELGKIAAFRQWILARAASEQEKLRFYEN"  
 misc-feature 50944..51357 /gene="gcvA"  
 /note="Pfam match to entry PF00126  
 HTH-1, Bacterial regulatory  
 helix-turn-helix protein, lysR  
 family, score 185.90, E-value  
 6.3e-52"  
 misc-feature 50983..51048 /gene="gcvA"  
 /note="Predicted helix-turn-helix  
 motif with score 1894 (+5.64 SD)  
 at aa 21-42, sequence  
 LSFTKAAEELFVTQAAVSHQIK"  
 misc-feature 50986..51078 /gene="gcvA"  
 /note="PS00044 Bacterial  
 regulatory proteins, lysR family  
 signature."  
 gene 52006..52401 /gene="YPO1030"  
 CDS 52006..52401 /gene="YPO1030"  
 /note="Similar to Escherichia coli  
 hypothetical protein YgdD  
 SW:YGDD-ECOLI (P32065) (131 aa)  
 fasta scores: E(): 0, 71.8% id in  
 131 aa"  
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 protein"  
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 /db-xref="GI:15979097"  
 /db-xref="SPTREMBL:Q8ZH79"  
 /translation="MNSRLMLIFSALSGFFYVAF  
 GAFGAHVLSTSLGLNEMAWIRTGL  
 EYQGFHTLVILILAVAMQRQVSLWFWYWSGALLAL  
 GTLLFSGSLYCLALSHLRLWIYIT  
 PVGGVCFLAGWILMLIGALRLRKRAERHE"  
 misc-feature 52018..52086 /gene="YPO1030"  
 /note="one of 4 probable  
 transmembrane helices predicted  
 for YPO1030 by TMHMM2.0"



misc-feature	52201..52269	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1030"
misc-feature	52297..52365	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1030"
gene CDS	52394..53500 52394..53500	/note="one of 4 probable transmembrane helices predicted for YPO1030 by TMHMM2.0" /gene="YPO1031" /gene="YPO1031" /note="Similar to Escherichia coli hypothetical protein YgdE SW:YGDE-ECOLI (P32066) (366 aa) fasta scores: E(): 0, 78.1% id in 365 aa, and to Haemophilus influenzae hypothetical protein HI1195 SW:YGDE-HAEIN (P45100) (363 aa) fasta scores: E(): 0, 60.9% id in 358 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89873.1" /db-xref="GI:15979098" /db-xref="SPTREMBL:Q8ZH78" /translation="MNNKIALYCRSGFEKECAAE ITEKAAQLEIFGFARVKENSGYVL FECYQLEDADRLIREIPREFIFARQMMVVGELL KDLPPEDRVSPIVGMLVGVIEKAG ELRVEVADTNESKELLKFCRKLTVPLRSALREQK ILSARENAHRPVVHVFFIAPGCCY VGYSYSNNNSPFYMGIPRLKFPDAPSRSTLKE EAFHVFIPADEWEERLASGMHAVD LGACPGGWYQLVQSRMMIQAVDNGLMAQSLMDT GOVTHHRADGFKYEPTRSNIYWL CDMVEKPTKVTQLITKWLNVNGWCREAIFNLKLPM KKRYEEVVQNLA MMDEQLKENGIN ADIIHAKQLYHDREEVTVHVRRRIWSGAPGRRDERY " /gene="xni"
gene	complement(53751..54506)	
CDS	complement(53751..54506)	/note="synonyms: exo, YPO1032" /gene="xni"  /EC-number="3.1.11.-" /note="Similar to Escherichia coli exodeoxyribonuclease IX Xni or Exo SW:EX9-ECOLI (P38506) (281 aa) fasta scores: E(): 0, 71.7% id in 247 aa, and to Vibrio cholerae exodeoxyribonuclease IX VC0898 TR:Q9KTK4 (EMBL:AE004173) (283 aa) fasta scores: E(): 0, 53.9% id in 254 aa" /codon-start=1 /transl-table=11 /product="exodeoxyribonuclease IX" /protein-id="CAC89874.1" /db-xref="GI:15979099" /db-xref="SPTREMBL:Q8ZH77" /translation="MQIHLLIVDALNLIRRIHAV QGSPCVKACQHALQQLIQHSQPSH AVAVFDEDDRSDSWRHQCLPDYKAGRSPMPDNLQ QEMPLIRQAFNELGVACWHS PGNE ADDLAATLVVKVAGAGHQVTIVSTDKGYCQLLAP NIQIRDYFQKRWLDMPFVKQEFV LPRQLPDYWGLAGISSSKIPGVAGVGA KTATLLL QQADTLEVLYQNLESIPEKWRKKL QQHQQMAFTCKQIATLKTDLLLSGNLQQLRLKK" /gene="xni"
misc-feature	complement(53754..54500)	

```

5-3-exonuclease, 5'-3'
exonuclease, score 123.20, E-value
4.9e-33"
gene      complement(54766..56130 /gene="YPO1033"
)
CDS      complement(54766..56130 /gene="YPO1033"
)
/note="Similar to Escherichia coli
hypothetical protein YgdH
SW:YGDH-ECOLI (P37350) (454 aa)
fasta scores: E(): 0, 82.6% id in
454 aa, and to Vibrio cholerae
hypothetical protein VC0899
TR:Q9KTK3 (EMBL:AE004173) (457 aa)
fasta scores: E(): 0, 69.9% id in
455 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAC89875.1"
/db-xref="GI:15979100"
/db-xref="SPTREMBL:Q8ZH76"
/translation="MITHVSPLGSMDLLSQLEVD
MLKRTASSDLRLFRNCSLAVLNS
GSLTDNSKELLSRNETFDINVLRERGVKLELVN
PPEHAFVDGKIIRSLQANLFAVLR
DILFVNGQIVSASNFQHLNMESSSHLTNLVFSIL
RNARALHIDEEPNMVVCWGGHSIN
ETELYLYARKVGSQGLRELNICTGCGPGAMEAPM
KGAAVGHAQQHYKKGRFIGMTEPS
IIAAEPPNPLVNELVIMPDIEKRLEAFVRIAHGI
IIFPGGVGTAEELLYLLGILMNPE
NSEQVLPLILTGPKEADYFKVVDEFIMNTLGDG
ARKYYQIIIDDPDEVARQMKKAMP
LVKEYRRNTGDAYSFNWSIRIEPDLQHPFEPNHE
NMANLDLSHNQPPEKLAAALRRAF
SGIVAGNVKEVGIQAIEAHGPFKLHGDPQLMKQM
DRLLQDFIAQHRMKLPGSVYTPCY EICS"
gene      complement(56283..57128 /gene="YPO1034"
)
CDS      complement(56283..57128 /gene="YPO1034"
)
/note="Similar to Escherichia coli
hypothetical protein Yqcd
SW:YQCD-ECOLI (Q46920) (282 aa)
fasta scores: E(): 0, 75.9% id in
282 aa, and to Vibrio cholerae
hypothetical protein VC0902
TR:Q9KTK0 (EMBL:AE004174) (287 aa)
fasta scores: E(): 0, 64.2% id in
282 aa"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="CAC89876.1"
/db-xref="GI:15979101"
/db-xref="SPTREMBL:Q8ZH75"
/translation="MSSYQNHKALAEITLTKPTA
YCDYYDATLLQAVPRSMNREPLGL
YPDNLFPFHGADIWTLYELSWLNSNGLPQVAVGEI
SLNADSINLIESKSFKLYLNSFNQ
TIFADKESVRMTLQRDLAACAQGNVSVALYDLDE
ITGQPISNFNGECLDKQDIRIDSY
EFNADYLQGAAGKDHVEESLVSHLLKSNCLITHQ
PDWGSVQIHYRGPQIDHEALLRYL
VSFRHHNEFHEQCVERIFNDIMRFCQPETLTVYA
RYTRRGGLDINPWRSTDFVPLTG RLARQ"
gene      57266..57811
)
CDS      57266..57811
)
/note="synonyms: ydr, YPO1035"
/gene="syd"
/note="Similar to Escherichia coli
Syd protein SW:SYDP-ECOLI (P43526)
(181 aa) fasta scores: E(): 0,

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		cholerae Syd protein VC0903 TR:Q9KTJ9 (EMBL:AE004174) (198 aa) fasta scores: E(): 0, 50.0% id in 176 aa" /codon-start=1 /transl-table=11 /product="Syd protein" /protein-id="CAC89877.1" /db-xref="GI:15979102" /db-xref="SPTREMBL:Q8ZH74" /translation="MNISTALRSFTQRYIDLWQQ QTGHLPAASKELYGVSPSPCIVETGE DQVFWQPQAFLEATLTNIERALEIQLHPDIHDF YTQQYAGDMMADLGNHRFTLLQVW SEDDFIRLQENLIGHLVTQKRLKLSPTLFLATTS SEMTMASLCNVSGNVVLEQFGSDK RTLLASTLSHFLDALRPVLPE"
gene	58074..58355	/gene="csrB"
misc-RNA	58074..58355	/gene="csrB"
		/note="Similar to Escherichia coli regulatory RNA csrB, 62% identity in 283 nt overlap"
misc-feature	58356..59067	/note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	58501..58959	/gene="tnp"
		/note="synonym: YPO1036"
CDS	58501..58959	/gene="tnp"
		/note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC89878.1" /db-xref="GI:15979103" /db-xref="SPTREMBL:Q9X9F5" /translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRRAIGSILRKL CEWKNVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKKGKSSMLLYEQFGDLKFKYRN REFWCRGYYVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	58555..58866	/gene="tnp"
		/note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	59213..59545	/gene="YPO1037"
CDS	59213..59545	/gene="YPO1037"
		/note="Similar to Escherichia coli hypothetical protein YqcC SW:YQCC-ECOLI (Q46919) (109 aa) fasta scores: E(): 1.3e-15, 41.3% id in 109 aa, and to the N-terminal region of Erwinia carotovora exoenzyme regulation regulon ORF1 SW:YQCB-ERWCA (Q47417) (376 aa) fasta scores: E(): 1.8e-16, 67.1% id in 70 aa. Note that the Erwinia carotovora paralogue is fused to the downstream gene" /codon-start=1 /transl-table=11 /product="conserved hypothetical

gene 59545..60318  
CDS 59545..60318

/protein-id="CAC89879.1"  
/db-xref="GI:15979104"  
/db-xref="SPTREMBL:Q8ZH73"  
/translation="MSTENKVRQSLQDIEFAMRE  
TDLWQTVPPPEAEAFESNEPFSIDT  
MAAEQWLQWVFLPRMYALLELNGPFPTRFAITPY  
FEEALSGDGRPDYSALLAQLRCLD·DLLNKESE"  
/gene="YPO1038"

/gene="YPO1038"  
/note="Similar to Escherichia coli  
hypothetical protein YqcB  
SW:YQCB-ECOLI (Q46918) (260 aa)  
fasta scores: E(): 0, 69.3% id in  
257 aa, and to the C-terminal  
region of Erwinia carotovora  
exoenzyme regulation regulon ORF1  
SW:YQCB-ERWCA (Q47417) (376 aa)  
fasta scores: E(): 0, 76.3% id in  
257 aa. Note that the Erwinia  
carotovora paralogue is fused to  
the upstream gene"  
/codon-start=1  
/transl-table=11  
/product="Conserved hypothetical  
protein"

misc-feature 59572..60054

/protein-id="CAC89880.1"  
/db-xref="GI:15979105"  
/db-xref="SPTREMBL:Q8ZH72"  
/translation="MLEIIYQDEHIVAVNKPAGW  
LVHRSWLDNRNETVFVMQTVRDQIG  
QHVVTVHRLDRPTSGVLLMALSSDVARMLSLQFE  
QHQIQKTYHAVVRGYVLEGGTVDY  
AMAEELDKIADKFAKSDKAPQPSVSHYEALAQVE  
VPLAIGRYETARYSLVALKPETGR  
KHQLRRHMAHIRHPPIIGDSTHGDLRQNRGVAQHF  
GCSRLMLHASHLHLNHPVTGEALT  
LTARWDEPWQGLMSQFGWSGIAPHLERVEFPLTA  
SQDNE"  
/gene="YPO1038"  
/note="Pfam match to entry PF00849  
PseudoU-synth-2, RNA  
pseudouridylate synthase, score  
176.90, E-value 3.4e-49"

misc-feature 59692..59736

gene 60346..60795  
CDS 60346..60795

/gene="YPO1038"  
/note="PS01129 Rlu family of  
pseudouridine synthase signature."  
/gene="YPO1039"  
/gene="YPO1039"  
/note="Similar to Escherichia coli  
hypothetical protein TR:Q46917  
(EMBL:U29581) (149 aa) fasta  
scores: E(): 0, 66.2% id in 148  
aa, and to Erwinia carotovora  
SCRI193 TR:Q47418 (EMBL:X79474)  
(151 aa) fasta scores: E(): 0,  
68.9% id in 148 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"

gene complement(60885..61274  
)  
CDS complement(60885..61274  
)

/protein-id="CAC89881.1"  
/db-xref="GI:15979106"  
/db-xref="SPTREMBL:Q8ZH71"  
/translation="MAQVGIFVGTVYGNALLVAE  
EAENILKDQGHEVKLFDEGTLEDW  
QHRYRQHYVLVITSTTGQGDFFDSIASLFAVVRDQ  
VGFQPELRYGVIALGDSSYDNFCG  
AGRTFDELLQEQGATRIGERLEIDAIEHSEPEAI  
SAPWVEQWGRLLQ"  
/gene="YPO1040"  
/note="Similar to Escherichia coli  
hypothetical protein YaeH"

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gene      complement(61398..62222)
)
CDS       complement(61398..62222)
)
          /note="synonym: YPO1041"
          /gene="dapD"
          /EC-number="2.3.1.117"
          /note="Similar to Escherichia coli
          2,3,4,5-tetrahydropyridine-2-carbo
          xylate N-succinyltransferase dapD
          SW:DAPD-ECOLI (P03948) (274 aa)
          fasta scores: E(): 0, 92.3% id in
          274 aa, and to Mycobacterium bovis
          2,3,4,5-tetrahydropyridine-2-carbo
          xylate N-succinyltransferase dapD
          SW:DAPD-MYCBO (P56220) (274 aa)
          fasta scores: E(): 0, 93.8% id in
          274 aa"
          /codon-start=1
          /transl-table=11
          /product="2,3,4,5-tetrahydropyridi
          ne-2-carboxylate
          N-succinyltransferase"
          /protein-id="CAC89883.1"
          /db-xref="GI:15979108"
          /db-xref="SPTREMBL:Q8ZH69"
          /translation="MQQLQNVIETAFERRADITP
          ANVDTVTREATHVIDLLDTGALR
          VAEKIDGQWVTHQWLKKAVLLSFRINDNQVMEGA
          ETRYDYDKVPMKFAGYDEARFQREG
          FRVVPATVRKGAFIARNTVLMPSYVNIGAFVDE
          GTMVDTWATVGSCAQIGKNVHLSG
          GVGIGGVLEPLQANPTIIEDNCFVGARSEVVEGV
          IVEEGSVISMGVFIGQSTRIYDRE
          TGEVHYGRVPAGSVVVSIGNLPSKDGSSLYCAVI
          VKKVDAKTRSKVGINELLRTID"
          /gene="dapD"
          /note="Pfam match to entry PF00132
          hexapep, Bacterial transferase
          hexapeptide (four repeats), score
          11.30, E-value 23"
          /gene="dapD"
          /note="Pfam match to entry PF00132
          hexapep, Bacterial transferase
          hexapeptide (four repeats), score
          10.60, E-value 28"
          /gene="dapD"
          /note="Pfam match to entry PF00132
          hexapep, Bacterial transferase
          hexapeptide (four repeats), score
          13.30, E-value 6"
          /gene="dapD"
          /note="PS00101 Hexapeptide-repeat
          containing-transferases"

```

misc-feature complement(61779..61832 /gene="dapD"  
 )  
 /note="Pfam match to entry PF00132  
 hexapep, Bacterial transferase  
 hexapeptide (four repeats), score  
 5.50, E-value 1.4e+02"

misc-feature complement(61848..61901 /gene="dapD"  
 )  
 /note="Pfam match to entry PF00132  
 hexapep, Bacterial transferase  
 hexapeptide (four repeats), score  
 3.20, E-value 2.8e+02"

gene complement(62397..65135 /gene="glnD"  
 )  
 /note="synonym: YPO1042"

CDS complement(62397..65135 /gene="glnD"  
 )  
 /EC-number="2.7.7.59"  
 /note="Similar to Escherichia coli  
 [protein-PII] uridylyltransferase  
 GlnD SW:GLND-ECOLI (P27249) (890  
 aa) fasta scores: E(): 0, 76.5% id  
 in 880 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="[protein-PII]  
 uridylyltransferase"  
 /protein-id="CAC89884.1"  
 /db-xref="GI:15979109"  
 /db-xref="SWISS-PROT:Q8ZH68"  
 /translation="MTSRHRRLFYGLRSSSGKHM  
 SDNHTTEHSLSLTLTPTISEQPALP  
 STYLDSDIHCPIKQRLDAFORWQAEAFNSGTSA  
 EVLIAARSDYIDHLLQRLWTFYGF  
 DKVPETALVAVGGYGRGELHPLSDIDVLVLSKQR  
 LNDEQAQRVGQLITLLWDLKLEVG  
 HSVRTLEECLLEGLADLTATNMIESRLICGDVA  
 LFLQMQKHIFSDSFWPSPOFFHAK  
 VVEQQERHKRYHGTSYNLEPDIKSSPGGLRDIHT  
 LLWVARRHFGATSLSEMVDGFLT  
 NAERNELNESQSFLWRIRFALHLVLTRYDNRLLF  
 DRQLSVAQLLRYEGEGNEPVEHMM  
 KDFYRMTRRVSELNNMLLQLFDEAILALDANEKP  
 RPLDEEFQLRGDLIDLRDENLFVR  
 QPEAIMRMFYLMVRNQDIKGIYSTTVRRLRHARR  
 HLKAPLCHIPEARLKFMAILRHGP  
 AVSRALLPMHRHSVLWAYMPQWGSIVGQMQFDLF  
 HAYTVDEHTIRVLLKIESFADEDT  
 RPRHPLCVELYPRLPQPELLLLAALFHDIAGRG  
 GDHSILGAHDAVEFAEQHGLNSRE  
 SQLVAWLVRCHLLMSVTAQRRDIQDPAVIQQFSA  
 EVQSETRLRYLVSLTVADICATNE  
 NLWNSWKQSLRLRELYFATEKQLRRGMQNSPDLRE  
 RVRHHRLQALALLRMDNIDEEALH  
 RIWSRCRADYFLRHSPNQLAWHARHLLHEDSTKP  
 LVLVSRQATRGGTEIFIWSPDRPS  
 LFAAVVGELDRRNLVHDAQIFTNRDGMAMDTFI  
 VLEPDGSPLAQDRHPIISHALQQA  
 INRSDYQHPPRVRLSPKLRHFSVPTEANFLPTH  
 NERRTYLELIALDQPGLLARVGKI  
 FADLGLSLHSARITTIGERVEDLFVLADKDRRAL  
 SLETRRELAQRLADTLNPNDKL"

misc-feature complement(62403..62627 /gene="glnD"  
 )  
 /note="Pfam match to entry PF01842  
 ACT, ACT domain, score 43.20,  
 E-value 6e-09"

misc-feature complement(63267..63671 /gene="glnD"  
 )  
 /note="Pfam match to entry PF01966  
 HD, HD domain, score 75.50,  
 E-value 1.1e-18"

misc-feature complement(64566..64883 /gene="glnD"  
 )  
 /note="Pfam match to entry PF01909"

gene complement(65138..65929) Nucleotidyltransferase domain,  
score 39.90, E-value 5.8e-08  
/gene="ampM"

CDS complement(65138..65929) /note="synonyms: b0168, map,  
YPO1043"  
/gene="ampM"  
/EC-number="3.4.11.18"  
/note="Similar to Escherichia coli  
methionine aminopeptidase  
SW:AMPM-ECOLI (P07906) (264 aa)  
fasta scores: E(): 0, 84.0% id in  
263 aa"  
/codon-start=1  
/transl-table=11  
/product="methionine  
aminopeptidase"  
/protein-id="CAC89885.1"  
/db-xref="GI:15979110"  
/db-xref="SPTREMBL:Q8ZH67"  
/translation="MAISIKTPEDIQKMRVAGRL  
AAEVLEIIIEPYVKPGVTTGELDRI  
CHDHITNHQQAISACLGYPKSVCSVNEVIC  
HGIPSDEKVLKEGDIVNIDVTVIK  
DGFHGDTSKMFIVGKPTILGERLCRVTQESLYLA  
IKMVKPGIRLRTLKGAIQKFVEAE  
NFSVVREYCGHGIGEGFHEEPQVLHYDADDGGVV  
LQAGMAFTIEPMVNAGDYRIRTMK  
DGWTVKTKDRNLSAQYEHTIVVTDNGCEIMTLRK  
DDTIPNIITHE"  
/gene="ampM"

misc-feature complement(65192..65920) /note="Pfam match to entry PF00557  
Peptidase-M24, metallopeptidase  
family M24, score 336.80, E-value  
2.4e-97"

misc-feature complement(65372..65428) /gene="ampM"  
/note="PS00680 Methionine  
aminopeptidase subfamily 1  
signature."

gene 66364..67089 /gene="rpsB"  
/note="synonym: YPO1044"

CDS 66364..67089 /gene="rpsB"  
/note="Similar to Escherichia coli  
30S ribosomal protein S2 RpsB  
SW:RS2-ECOLI (P02351) (240 aa)  
fasta scores: E(): 0, 93.8% id in  
240 aa"  
/codon-start=1  
/transl-table=11  
/product="30S ribosomal protein  
S2"  
/protein-id="CAC89886.1"  
/db-xref="GI:15979111"  
/db-xref="SWISS-PROT:Q8ZH66"  
/translation="MATVSMRDMLQAGVHFGHQT  
RYWNPCKMKPFIFGARNKVHIINLE  
KTVPMFNEALAEITKISSRKKGKILFVGTKRAASE  
AVKEAANNCDQFFVNRWLGGMLT  
NWKTVRQSIKRLKDLEIQSQDGTDFDKLTKEALM  
RTRELNKLENSLGGIKDMGGLPDA  
LFVVDADHEHIAIKEANNLGIPVFSIVDTNSDPD  
GVDFIIPGNDDAIRAVKLYLGAVA  
TAVREGRSQDLAVQAEESFVEAE"  
/gene="rpsB"

misc-feature 66379..66414 /note="PS00962 Ribosomal protein  
S2 signature 1."

misc-feature 66388..67038 /gene="rpsB"  
/note="Pfam match to entry PF00318  
Ribosomal-S2, Ribosomal protein  
S2, score 435.90, E-value  
3.5e-127"

misc-feature 66835..66909 /gene="rpsB"

gene	67217..68074	S2 signature 2."
CDS	67217..68074	/gene="tsf" /note="synonym: YPO1045" /gene="tsf" /note="Similar to Escherichia coli elongation factor Ts Tsf SW:EFTS-ECOLI (P02997) (282 aa) fasta scores: E(): 0, 78.4% id in 282 aa" /codon-start=1 /transl-table=11 /product="elongation factor Ts" /protein-id="CAC89887.1" /db-xref="GI:15979112" /db-xref="SWISS-PROT:Q8ZH65" /translation="MVAITAALVKELRERTAAGM MECKKALVEANGDIELAIDNMRKS GQAKAAKAGRIAAEGIIILAKVSADGKYGVILEL NCETDFVAKDAGFKAFGEVINAA LAEKIADIDVLKAKFEEQRANLVAKIGENINIRR VAVLEGDILGTYLHGARIGVMVAA TGADDEELVKHIAMHIAASKPEYVKPDDVPAEVVA REHQIQLDIAIESGKPREIAEKMV EGRMRKFTGEVSLTGQNFVMDPSKTVGDLLKENN ADVNNFIRFEVGEIEKVETDFAA EVAAMSKQS"
misc-feature	67223..67342	/gene="tsf" /note="Pfam match to entry PF02094 TS-N, TS-N domain, score 71.00, E-value 2.6e-17"
misc-feature	67385..68011	/gene="tsf" /note="Pfam match to entry PF00889 EF-TS, Elongation factor TS, score 356.30, E-value 3.2e-103"
misc-feature	67445..67477	/gene="tsf" /note="PS01127 Elongation factor Ts signature 2."
gene	68283..69008	/gene="pyrH"
CDS	68283..69008	/note="synonyms: smbA, YPO1046" /gene="pyrH" /EC-number="2.7.4.-" /note="Similar to Escherichia coli uridylylate kinase PyrH SW:PYRH-ECOLI (P29464) (240 aa) fasta scores: E(): 0, 90.8% id in 240 aa" /codon-start=1 /transl-table=11 /product="uridylylate kinase" /protein-id="CAC89888.1" /db-xref="GI:15979113" /db-xref="SWISS-PROT:Q8ZH64" /translation="MATNAKPVYQRIILLKLSGEA LQGAEGFGIDASVLDMAQEVKEL VELGIQVGVVIGGNLFRGAGLAQAGMNRVVGHD MGMLATVMNGLAMRDALHRAVYVNA RLMSAIPLNGVCDNYSWAEAISLLRHNRRVVF GTGNPFFTTDSAACLRGIEIEADV VLKATKVDGVYSADPVKNPDATLYEQLTYQDVLE QELKVMDLAAFTLARDHNLPIRVF NMNKP GALRRVVMGENEGT LIAK"
misc-feature	68310..68861	/gene="pyrH" /note="Pfam match to entry PF00696 aakinase, Amino acid kinase family, score 148.00, E-value 1.7e-40"
gene	69144..69701	/gene="frr"
CDS	69144..69701	/note="synonyms: b0172, rrf, YPO1047" /gene="frr" /note="Similar to Escherichia coli ribosome recycling factor SW:RRF-ECOLI (P16174) (185 aa) fasta scores: E(): 0, 80.5% id in 185 aa"



		<pre> /transl-table=11 /product="ribosome recycling factor" /protein-id="CAC89889.1" /db-xref="GI:15979114" /db-xref="SWISS-PROT:Q8ZH63" /translation="MINEIRKDAEVRMEKCLEAF QNHISKIRTGRASPSILDGIQVEY YGTATPLRQLANIVVEDSRTLALTVFDRSLSAAV EKAIMTSDLGLNPSSAGTVIRVPL PALTEERRKDLIKVVRAEAEQGRVSIRNVRRDAN DKVKALLKDKEISEDEDRRSQDDV QKLTDAYIKKVDAALAVKEAELMDF" </pre>
misc-feature	69198..69692	<pre> /gene="frr" /note="Pfam match to entry PF01765 RRF, Ribosome recycling factor, score 336.80, E-value 2.4e-97" </pre>
gene	69915..71111	<pre> /gene="dxr" /note="synonyms: b0173, YPO1048" </pre>
CDS	69915..71111	<pre> /gene="dxr" /EC-number="1.1.1.-" /note="Similar to Escherichia coli 1-deoxy-D-xylulose 5-phosphate reductoisomerase SW:DXR-ECOLI (P45568) (398 aa) fasta scores: E(): 0, 72.2% id in 396 aa" /codon-start=1 /transl-table=11 /product="1-deoxy-D-xylulose 5-phosphate reductoisomerase" /protein-id="CAC89890.1" /db-xref="GI:15979115" /db-xref="SWISS-PROT:Q8ZH62" /translation="MKQLTILGSTGSIGNSTLSV VRANPELFKVTALVAGRNVREMAQ QCLEFSPRYAAMSDEHSAKSLRLLLAEQGSDTEV YSGETAACELAALDDVDQVMAAIV GIAGLPSTLAAIRAGKQVLLANKESLITCGKLFM DEVKRSRAQLLPIDSEHNAIFQSL PERIQRQLGYSSLNENGVSRIILTGSGGPFRETP LSQFSDVTPDQACAHPNWSMGRKI SVDSATMMNKGLEYIEARWLFNASAEQIEVVLHP QSVIHSMVRYHDGSILAQMGTDPDM RTPIAHAMAYPMRVSSGVAPLDFCKVGALTFTTP DYQRYPCLKLAIDACNAGQAATTA LNAANEISVMAFLDSKIRFTDIEVINRTVVEGLL LSEPTSVEEVLVIDRKARDVAAQV IAKLNN" </pre>
gene	71335..72093	<pre> /gene="upps" /note="synonyms: rth, YPO1049" </pre>
CDS	71335..72093	<pre> /gene="upps" /EC-number="2.5.1.31" /note="Similar to Escherichia coli undecaprenyl pyrophosphate synthetase SW:UPPS-ECOLI (Q47675) (253 aa) fasta scores: E(): 0, 78.8% id in 245 aa" /codon-start=1 /transl-table=11 /product="undecaprenyl pyrophosphate synthetase" /protein-id="CAC89891.1" /db-xref="GI:15979116" /db-xref="SPTREMBL:Q8ZH61" /translation="MSPVKEDRANLSRSPRHVA IIMDGNGRWAKNKGKLRVFGHKAG VKSVRRRAVSFAAKHNLDALTLYAFSSSENWNRPDQ EVTALMELFVRALDSEVKSLHKHN VRLSIIGDISRFSGRLQERIRRSEKLTANNDGLK LNIAANYGGRWDIIQGVRLAEQV QKGELQPTDISEESLNSYICLHEQSQVDLVIRTG GEHRISNFWLLWQIAYAEELYFTDVL WPDFDENVFEGALNAFAQRERRFGGTTPIDATAS " </pre>
misc-feature	71398..72063	<pre> /gene="upps" /note="Pfam match to entry PF01255" </pre>

misc-feature	71896..71949	undecaprenyl diphosphate synthase, score 454.70, E-value 8e-133" /gene="uppS" /note="PS01066 Undecaprenyl pyrophosphate synthetase family signature."
gene	72103..72951	/gene="cdsA"
CDS	72103..72951	/note="synonyms: cds, YPO1050" /gene="cdsA" /EC-number="2.7.7.41" /note="Similar to Escherichia coli phosphatidate cytidyltransferase cdsA or cds SW:CDSA-ECOLI (P06466) (249 aa) fasta scores: E(): 0, 75.2% id in 246 aa" /codon-start=1 /transl-table=11 /product="phosphatidate cytidyltransferase" /protein-id="CAC89892.1" /db-xref="GI:15979117" /db-xref="SPTREMBL:Q8ZH60" /translation="MLKYRLITALILIPVVIGAL FLLPPVGFAIVTLVVCMLAAWEWG QLAGFASRTQRIWLAILCGFLLVAMLLSLPEYQH SPHHLLVSTPLWLWSMGWWVAALML VLTYPRSAVSWRNSRLLRIIFGILTIIPFFWGMF ALRQYGYEQNHNTGAWWLLYVMLL VWGADSGAYMFGKLFQKHKLAPKVSFGKTWEGLI GGLLTSA LISLLFGRYAPLDIVPE KLLICSVVAALASVLGDLTESMFKREAGIKDSGH LIPGHGGILDRIDSLTAAVPVFAC LMLLVF"
misc-feature	72106..72945	/gene="cdsA" /note="Pfam match to entry PF01148 Cytidyltransferase, Phosphatidate cytidyltransferase, score 155.80, E-value 7.5e-43"
misc-feature	72121..72225	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72268..72324	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72343..72411	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72454..72513	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72550..72618	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72676..72735	/gene="cdsA" /note="one of 6 probable transmembrane helices predicted for YPO1050 by TMHMM2.0"
misc-feature	72817..72897	/gene="cdsA" /note="PS01315 Phosphatidate cytidyltransferase signature."
gene	72980..74335	/gene="YPO1051"
CDS	72980..74335	/gene="YPO1051" /note="Similar to Escherichia coli hypothetical 49.1 kDa protein in cdsA-hlpA intergenic region SW:YAEI-ECOLI (P37764) (450 aa) fasta scores: E(): 0, 77.6% id in 451 aa, and to Neisseria meningitidis putative integral membrane protein NMA0084 TR:Q9JX32 (EMBL:AL162752) (446 aa) fasta

		aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAC89893.1" /db-xref="GI:15979118" /db-xref="SWISS-PROT:Q8ZH59" /translation="MMSILWSLAAAFIVALGILIT VHEFGHFWVARRCGVRVERFSIGF GKALWRRRTDRQGTEYVIALIPLGGYVKMLDERVE AVAPELRHQSFNNKTVLQRAAIVS AGPIANFLFAIVAYWLVTIIGVPSVRPVIGDISP QSIAAQANISSGMELKSVDDGIETP DWDSVRLALISRIGDKQMVGVPFGSDNVVEKT LDLRQWQFEPDKQDPVVALGIIPR GPQIESVLAEVQPGSAAQKAGLQAGDRIVKVNGQ LLDRWQTFVLQVRDNPQGPLVLDI ERESTPLSLTLIPDTKSVGENRSEGFAGVVPKVI PLPDEYKTIRQYGPFTAVYQAGDK TWQLMRLTVSMLGKLITGDVKLNNLSGPISIAQG AGLSAEYGLVYYLMFLALISVNLG IINLFPLPVLDDGHHLLFLAIEKLKGGPVSERVQD FSYRIGSILLVLLMGLALFNDFSR L"
misc-feature	72992..73060	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	73034..73063	/gene="YPO1051" /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature."
misc-feature	73271..73339	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	73574..73816	/gene="YPO1051" /note="Pfam match to entry PF00595 PDZ, PDZ domain (Also known as DHR or GLGF)., score 46.40, E-value 6.2e-10"
misc-feature	74108..74176	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
misc-feature	74258..74317	/gene="YPO1051" /note="one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0 one of 4 probable transmembrane helices predicted for YPO1051 by TMHMM2.0"
gene CDS	74372..76759 74372..76759	/gene="YPO1052" /gene="YPO1052" /note="Similar to Photorhabdus luminescens outer membrane antigen Oma TR:Q9S341 (EMBL:AJ236920) (797 aa) fasta scores: E(): 0, 80.4% id in 797 aa, and to Haemophilus influenzae protective surface antigen D15 precursor SW:D151-HAEIN (P46024) (797 aa) fasta scores: E(): 0, 44.3% id in 804 aa" /codon-start=1 /transl-table=11 /product="putative surface antigen" /protein-id="CAC89894.1" /db-xref="GI:15979119" /db-xref="SPTREMBL:Q8ZH58" /translation="MAMKKLLIASLLFGSATVYG ADGFVVDNIHFEGLRVAVGAALL NMPVRVGDIVSDDDIGKTIRALFATGNFEDVRVL RDGNTLIVQVKERPTIASITFSGN KAVKEDMLKQNLEASGVRVGEALDRTTISNIEKG

NRVDLKLVFTEGVSAKIQQINIVGNHSFTTDELI  
 SRFQLRDEVPWWNVVGDRKYQKQK  
 LAGDLETLSFYLDRGYARFNIDSTQVSLTPDKK  
 GIYVTINITEGPQFKLNSVIVSGN  
 LAGHQSEAELTKIEPGELFNGSKVTRMEDDIKK  
 MLGRYGYAYPRVVTQPEINDDDKT  
 VKLHINVDAGNRFYVRHIRFEGNDTSKDSVLRRE  
 MRQMEGAWLGNDQVEAGKERLNLRL  
 GYFETVDVETQRVPGAADLVDVTKVKERNTGSL  
 NFGIGYGTESGVSFQVGVQQDNWL  
 GTGNTVGVINGTKNDYQTYAEFTLMDPYFTVDGVS  
 LGGRIFYNDFKADNADLSGYTNSS  
 YGADGTLGFPIENNSLRVGVGVVHNDLSDMLPQ  
 VAMWRYLESVGERPGYDREGFTT  
 DDFTLNLGWTYNNLDRGFFPTSGVKSSVNTKITV  
 PGSDNEFYKVTFDTSAYQPLNEDR  
 SWVLLGRGRLGYGDGIGSKEMPFYENFYAGGSST  
 VRGFRSNNIGPKAAYYANGGATVT  
 NSTDAVGGNAMAVASIELITPTPFISEKYSNSVR  
 TSIFIDSGTVWDTNWENTAKTRAA  
 GIPDYGKASNIRVSAGVALQWMSPLGPLVFSYAK  
 PVKDYEGDKSEQQFNIGKTW"  
 /gene="YPO1052"  
 /note="Pfam match to entry PF01103  
 Bac-surface-Ag, Bacterial surface  
 antigen, score 1444.20, E-value 0"  
 /gene="YPO1052"  
 /note="1 probable transmembrane  
 helix predicted for YPO1052 by  
 TMHMM2.0"  
 /gene="ompH"  
 /note="synonym: YPO1053"  
 /gene="ompH"  
 /note="Similar to Yersinia  
 enterocolitica cationic 19 kDa  
 outer membrane protein precursor  
 OmpH SW:OMPH-YEREN (P31519) (164  
 aa) fasta scores: E(): 0, 93.3% id  
 in 165 aa, and to Escherichia coli  
 histone-like protein Hlp-1  
 precursor SW:HLP-ECOLI (P11457)  
 (161 aa) fasta scores: E():  
 1.3e-30, 67.1% id in 167 aa"  
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 TMKASDRTKLENEVMKQRETFSTK  
 AQAFEQDNRRRQAEERNKILSRIQDAVKS VATKG  
 GYDVVIDANAVAYADSSKDITADV LKQVK"  
 /gene="lpxD"  
 /note="synonyms: firA, omsA,  
 YPO1054"  
 /gene="lpxD"  
 /EC-number="2.3.1.-"  
 /note="Similar to Escherichia coli  
 UDP-3-o-[3-hydroxymyristoyl]  
 glucosamine N-acyltransferase  
 SW:LPXD-ECOLI (P21645) (340 aa)  
 fasta scores: E(): 0, 82.6% id in  
 339 aa, and to Yersinia  
 enterocolitica  
 UDP-3-o-[3-hydroxymyristoyl]  
 glucosamine N-acyltransferase  
 SW:LPXD-YEREN (P32203) (339 aa)  
 fasta scores: E(): 0, 95.3% id in  
 339 aa"  
 /codon-start=1  
 /transl-table=11

misc-feature 74378..76756

misc-feature 74390..74449

gene 76917..77414

CDS 76917..77414

gene 77418..78440

CDS 77418..78440

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o5l] glucosamine
N-acyltransferase"
/protein-id="CAC89896.1"
/db-xref="GI:15979121"
/db-xref="SWISS-PROT:P58611"
/translation="MPSIRLADLAQQLDAQVHGD
GDLVITGIASMHSAPPEQITFLSN
SRYREQLASCNAGAVVLTEADLPFCKVAALVVEN
PYFTYARMAQIMDTTPQPAQDIAP
SAVISPOATLGEVSVGANAVIESGVVLGDNVVI
GAGCFIGKNTHIGAGSRLWANVSI
YHEVVIGQNCLIQSGTVIGADGFGYANDRGNWVK
IPQLGSVHIGDRVEIGACTTIDRG
ALDNTIIGNGVIIDNQCQIAHNVVIGDNTAVAGG
VIMAGSLKVGRYCMIGGASVINGH
MEICDKVTITGMGMVMPITEPGLYSSGIPLQPN
KMWRKTAALVMNIDGINKRLKAVE RKIDKE"
misc-feature      77715..77801
                    /gene="lpxD"
                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      77742..77795
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    13.90, E-value 3.9"
misc-feature      77796..77849
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    22.20, E-value 0.012"
misc-feature      77805..77891
                    /gene="lpxD"
                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      77850..77903
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    16.70, E-value 0.54"
misc-feature      77904..77957
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    18.50, E-value 0.15"
misc-feature      78015..78068
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    13.90, E-value 3.8"
misc-feature      78081..78134
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    19.10, E-value 0.1"
misc-feature      78090..78176
                    /gene="lpxD"
                    /note="PS00101 Hexapeptide-repeat
                    containing-transferases
                    signature."
misc-feature      78135..78188
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    12.90, E-value 7.7"
misc-feature      78207..78260
                    /gene="lpxD"
                    /note="Pfam match to entry PF00132
                    hexapep, Bacterial transferase
                    hexapeptide (four repeats), score
                    6.50, E-value 1e+02"
gene              78598..79143
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                    /note="synonyms: sefA, YP01055"
CDS               78598..79143
                    /gene="fabZ"
                    /EC-number="4.2.1.-"
                    /note="Similar to Escherichia coli
                    FabZ SW:FABZ-ECOLI (P21774) (151

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		in 151 aa, and to Yersinia enterocolitica FabZ SW:FABZ-YEREN (P32205) (201 aa) fasta scores: E(): 0, 90.1% id in 181 aa"
		/codon-start=1
		/transl-table=11
		/product="(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (EC 4.2.1.-)"
		/protein-id="CAC89897.1"
		/db-xref="GI:15979122"
		/db-xref="SWISS-PROT:Q8ZH57"
		/translation="MTTDTHTLHIEEILDLLPHRFPFLLVDRVLDFFEEGKFLRAVKNVSENEPFFQGHFPGKPIFPGVLILEAMAQATGILAFKSRGKLEPGELYFFAGIDEARFKRPVVPQDQMIMEVEFVKERRGLTRFTGVAKVDGEIVCTATMMCARSKPAAPAESVVVKPDVVKPDVVKPDVVNPVVKES"
misc-feature	78619..79017	/gene="fabZ"
		/note="Pfam match to entry PF01377 Thioester-dehyd, Thioester dehydrase, score 286.40, E-value 3.5e-82"
gene	79147..79935	/gene="lpxA"
		/note="synonym: YPO1056"
CDS	79147..79935	/gene="lpxA"
		/EC-number="2.3.1.129"
		/note="Similar to Escherichia coli acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase LpxA SW:LPXA-ECOLI (P10440) (262 aa) fasta scores: E(): 0, 81.3% id in 262 aa, and to Yersinia enterocolitica acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase LpxA SW:LPXA-YEREN (P32201) (262 aa) fasta scores: E(): 0, 90.1% id in 262 aa"
		/codon-start=1
		/transl-table=11
		/product="acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase"
		/protein-id="CAC89898.1"
		/db-xref="GI:15979123"
		/db-xref="SWISS-PROT:Q8ZH56"
		/translation="MIDKTAFIHPSSIVEEGAIIGAGVYIGPFCIVGSQVEIGAGTELKSHVVVNGITKIGCDNQIYQFASIGEANQDLKYAGEPTRVEVGDRNRIRESVTIHRGT TQGGGVTKVGCNLLMVNTHVAHDCVIGNRCILANNAALGGHVEIDDYAIIGGMTAIHQFCVIGAHVMVGGCSGITQDVPPFVIAQGNHATPFGINIEGLKRRGFDKESLHAIRSA YKLLYRSGRTLDEVKPEIAELAEQYPVVKAFNDF FARSTRGIIR"
misc-feature	79195..79248	/gene="lpxA"
		/note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 21.70, E-value 0.017"
misc-feature	79204..79290	/gene="lpxA"
		/note="PS00101 Hexapeptide-repeat containing-transferases signature."
misc-feature	79249..79302	/gene="lpxA"
		/note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 11.10, E-value 24"
misc-feature	79303..79356	/gene="lpxA"

misc-feature	79393..79446	hexapep, Bacterial transférse hexapeptide (four repeats), score 8.50, E-value 54" /gene="lpxA" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 7.90, E-value 65" /gene="lpxA" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 0.80, E-value 5.9e+02" /gene="lpxA" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 14.40, E-value 2.7" /gene="lpxA" /note="Pfam match to entry PF00132 hexapep, Bacterial transferase hexapeptide (four repeats), score 17.80, E-value 0.26" /gene="lpxA" /note="PS00101 Hexapeptide-repeat containing-transferases signature." /gene="lpxB" /note="synonyms: pgsB, YPO1057" /gene="lpxB" /EC-number="2.4.1.182" /note="Similar to Escherichia coli lipid-A-disaccharide synthase LpxB SW:LPXB-ECOLI (P10441) (382 aa) fasta scores: E(): 0, 82.2% id in 377 aa" /codon-start=1 /transl-table=11 /product="lipid-A-disaccharide synthase" /protein-id="CAC89899.1" /db-xref="GI:15979124" /db-xref="SWISS-PROT:Q8ZH55" /translation="MQNSPLTADCSLNAGRPLTI GLVAGETSGDILGAGLIRALKVQV PNARFVGAVGPLMQAEGCEAWYEMEELAVMGVVE VLERLPRLKIRKDLTQRFSELSP DVFVGIDAPDFNITLEGRLKQRGIRTIHYVSPSV WAWRQKRVFKIGKATDMVLAFLPF EKAFYDRFNVPFCRFIGTMDAMPLVPDQQAARA ELGIAPNATCLALLPGSRHSEVEM LSADFLRTAVILRDKLPNLEVVPVPLVNSKRREQF ERIKAEIAPDLSVHLLDGKARVAM IASDAALLASGTAALCMLAKCPMVVGYRMKPF FWLAERLVKTPYVSLPNLLAGEEL VTELLQQECQPQKLKAGALLPLLQGGSEIAALKER FLVLHQSIKRCGADEQAQAQAVLELA DR"
gene	79939..81123	/gene="rnhB"
CDS	79939..81123	/note="synonyms: b0183, YPO1058" /gene="rnhB" /EC-number="3.1.26.4" /note="Similar to Escherichia coli ribonuclease hII SW:RNH2-ECOLI (P10442) (198 aa) fasta scores: E(): 0, 84.5% id in 193 aa" /codon-start=1 /transl-table=11 /product="ribonuclease HII" /protein-id="CAC89900.1" /db-xref="GI:15979125" /db-xref="SPTREMBL:Q8ZH54" /translation="MSETFIYPQANLIAGVDEVG RGPLVGAVVTAAVILDPNRPIVGL ADSKKLSEKRRLSLYDEITEKALSWSLGRAEPEE IDQLNILHATMLAMQRAVSGSLHIV
gene	81120..81716	
CDS	81120..81716	

		SILAKVTRDREMTELDLLFPEYGF AQHKGYPYTAFLHLEKLAALGATVHHRRSFGPVKRV LGLV"
misc-feature	81159..81692	/gene="rnhB" /note="Pfam match to entry PF01351 RNase-HII, Ribonuclease HII, score 305.80, E-value 5.1e-88"
gene	81846..85361	/gene="dnaE" /note="synonyms: polC, YPO1059"
CDS	81846..85361	/gene="dnaE" /EC-number="2.7.7.7" /note="Similar to Escherichia coli DNA polymerase III, alpha chain DnaE SW:DP3A-ECOLI (P10443) (1160 aa) fasta scores: E(): 0, 89.0% id in 1160 aa" /codon-start=1 /transl-table=11 /product="DNA polymerase III, alpha chain" /protein-id="CAC89901.1" /db-xref="GI:15979126" /db-xref="SPTREMBL:Q8ZH53" /translation="MIQSTHFWYLDMAEPRFVHL RVHSDYSMIDGLAKIGPLVKRAAA LGMPALAITDFTNLCGLVKFYGSAHGAGIKPIIG ADFYVQSEILGDELAHLTVLARNN EGYQNLTLTLLISEAYQRGYGAAGPIIDRDWLIKHK EGLILLSGGRMGDVGKFLLRGNQV QVDQCLAFYQEHFPDCYYLELIRTGRPDEENYLH AAVALATERGLPVVATNDVRFIDE SDFDAHEIRVAIHGFTLVDPKRPKNYSPOQFMR DEEQMCELFADIPEALINSVEIAK RCNVTIRLGEYFLPQFPTGEMSTEDFLVEKAKQG LEERLEFLFPDPEVRLQKRPEYDE RLDIELKVINQMGPFGYFLIVMEFIQWSKDNGVP VGPGRGSGAGSLVAYALKITDIDP LEFDLLFERFLNPERVSMDFDVFDCMEKRDLVI EHVAEMYGRDAVSQIITFGTMAAK AVIRDVGRVLGHPYGFVDRISKLIPLDPGMTLEK AFAAEPLAEIYEADDEVRALIDM ARKLEGVTRNAGKHAGGVVIAPTKITDFAPLYCD AEGNNPVTQFDKNDVEYAGLVKFD FLGLRTLTIINWALEMINARRAKTGLEPIDIASI PLEDKKSFDMLQRSETTAVFQLES RGMKDLIKRLKPDCEFMIALVALFRPGPLQSGM VDNFIDRKHGREAISYPDIEWQHE SLKPVLEPTYGIILYQEQVMQIAQVLSGYSLGGA DMLRRAMGKKNPAAEMAKQRSVPED GAKNQGIDGELAIKIFDLVEKFAGYGFNKSHSAA YALVSYQTLWLKAHYPAEFMAAVM TADMDNTDKVVGVLVDECWRMGLKILPPDINSGLY HFHVNDGGEIVYGIGAIGVGEGP IEAILEARKEGGYFKELFDLCARVDTKKLNKRIL EKLIMSGAFDRLGPHRAALMSSLG DALKAADQHAKEAIGQVDMFGVLADAPEQVEQS YANVPPWQEQVLDGERETLGLYL TGHPITQYLKEIERYAGGMRLKDMHPTDRGKMTT AVGLVIAARVMVTKRGNRIGICTL DDRSGRLEVMLFTDALEKYQHLLEKDRIILIATGQ VSFDDFSGGLKMTARELMDISEAR EKYASGLAISLTDRQIDDQLLNRLRQSLEPHRAG TIPVHLYYQREDARARLRFGATWR VTPTDRLLIDLRTLVLGNEQVELEFD"
misc-feature	81897..82094	/gene="dnaE" /note="Pfam match to entry PF02231 PHP-N, PHP domain N-terminal region, score 115.50, E-value 1e-30"
misc-feature	84873..85097	/gene="dnaE" /note="Pfam match to entry PF01336 tRNA-anti, tRNA synthetase anti-codon binding domain, score 43.00, E-value 6.7e-09"
gene	85374..86333	/gene="accA"



CDS

85374..86333

```
/gene="accA"  
/EC-number="6.4.1.2"  
/note="Similar to Escherichia coli  
acetyl-coenzyme A carboxylase  
carboxyl transferase subunit alpha  
AccA SW:ACCA-ECOLI (P30867) (318  
aa) fasta scores: E(): 0, 90.5% id  
in 317 aa"  
/codon-start=1  
/transl-table=11  
/product="acetyl-coenzyme A  
carboxylase carboxyl transferase  
subunit alpha"  
/protein-id="CAC89902.1"  
/db-xref="GI:15979127"  
/db-xref="SPTREMBL:Q8ZH52"  
/translation="MSLNFLDFEQPIAELEAKID  
SLTAVSRQDEKLDINLDEEVQRLR  
EKSVELTRKIFSDLGAWQIAQLARHPRRPYTLDY  
IANIFTDFEELAGDRAYADDKAIV  
GGIARLDGRPVMII GHQKGRETKEKIRRNFGMPA  
PEGYRKALRLMEMAERFKLPITF  
IDTPGAYPGVGAEERGQSEAIARNLREMSRLNVP  
IVCTVIGEGSGGALAIGVGDKVN  
MLQYSTYSVISPEGCASILWKSADKAPLAAEAMG  
ITAHRLKELKMIDSVIPEPLGGAH  
RDYAAIAISLKAQLLADLNDLDVLNDEELLNRRY  
ORLMNYGYC"
```

gene  
CDS

86517..86915  
86517..86915

```
/gene="YPO1061"  
/gene="YPO1061"  
/note="Similar to Escherichia coli  
hypothetical protein YaeR  
SW:YAE-ECOLI (P52096) (129 aa)  
fasta scores: E(): 0, 71.1% id in  
128 aa, and to Vibrio cholerae  
glyoxylase I family protein  
VCA0890 TR:Q9KL58 (EMBL:AE004416)  
(127 aa) fasta scores: E():  
1.1e-27, 59.2% id in 125 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89903.1"  
/db-xref="GI:15979128"  
/db-xref="SPTREMBL:Q8ZH51"  
/translation="MLAINKIHIAIICSQDYQAS  
KRFYCEVLGFNLISEVYREERDSW  
KADLALHDQYTIELFSFPSPVPRPSRPEACGLRH  
LAFQVDDIDLALKELVVAGVVCEA  
VRIDPYTQSRFTFFNDPDGLPLELYELKAE"
```

gene  
CDS

86917..88299  
86917..88299

```
/gene="YPO1062"  
/gene="YPO1062"  
/note="Similar to Escherichia coli  
putative cell cycle protein MesJ  
SW:MESJ-ECOLI (P52097) (432 aa)  
fasta scores: E(): 0, 55.2% id in  
440 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89904.1"  
/db-xref="GI:15979129"  
/db-xref="SPTREMBL:Q8ZH50"  
/translation="MNLVTSKPNVLLNPLFAQLG  
ENRHVLVGFSGGLDSTVLLHLLVC  
LRQQLIPELNIRATHIHGHNLPQADSWVKHCMQQ  
CDQWKIELKVVRVNIDPRQNGIEA  
AARTARYQAFSANLAAKEVLLTAQHLLDDQCETFL  
LALKRGS GPAGLSAMA AKMPFAHS  
QLLRPLLA FSREILENYAQAQQLQWIEDDSNQDD  
RFDRNFLRLNVLPILNQRWPHFAQ  
ATARSAGLCAEQEQLLELLAENLQQLQGPDRSL  
SIDGLLQASMAKRAAILRRWLASL
```

gene	88536..88853	VRRFRQHLYLMLPLAEITTNYPW ATVKAAPNSSIIPLLPEPLWLPADLGVLRFVSAG GQAVRPAAVGEEISVRFGLQGDIK IVGRHHSRQSKKVWQELGIPWQQRERIPLLYFGE QLIAAAGVFVTOAGQANENEPDWH LDWDKPLRLG"
CDS	88536..88853	/gene="YPO1063" /gene="YPO1063" /note="Similar to Vibrio cholerae cytochrome C554 VC2241 TR:Q9KPx1 (EMBL:AE004296) (107 aa) fasta scores: E(): 1.6e-14, 50.5% id in 105 aa, and to Shewanella violacea soluble cytochrome CB CytCB TR:Q9RHJ5 (EMBL:AB032405) (206 aa) fasta scores: E(): 9.1e-10, 37.7% id in 106 aa, and to Pseudomonas aeruginosa cytochrome C4 precursor PA5490 TR:AAG08875 (EMBL:AE004961) (201 aa) fasta scores: E(): 2.5e-09, 40.4% id in 104 aa" /codon-start=1 /transl-table=11 /product="putative cytochrome" /protein-id="CAC89905.1" /db-xref="GI:15979130" /db-xref="SPTREMBL:Q8ZH49" /translation="MMKLIVSMAVLLSLCSFQVW AKNDIEAGRAKSSSCVACHGMNGK VSVPMYPNLAGQNALYLQQSLEAYKKGSRSGQA EVMRAYVSGLSDEDFSDLAAYYAS LKP"
misc-feature	88602..88847	/gene="YPO1063" /note="Pfam match to entry PF00034 cytochrome-c, Cytochrome c, score 47.20, E-value 3.6e-10"
misc-feature	88638..88655	/gene="YPO1063" /note="PS00190 Cytochrome c family heme-binding site signature."
gene	complement(89118..89378 )	/gene="YPO1064"
CDS	complement(89118..89378 )	/gene="YPO1064"  /note="Similar to Escherichia coli ROF protein SW:ROF-ECOLI (P52098) (84 aa) fasta scores: E(): 1.4e-26, 73.8% id in 84 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89906.1" /db-xref="GI:15979131" /db-xref="SPTREMBL:Q8ZH48" /translation="MSMSEYQPINCDYDNLLEL ACQHHLLITLKLKRGGEIVEGKASD LLLRKKVEYLIVEQEGTMRELRLDHIASFHPEI GTVVVSAS"
gene	complement(89365..89565 )	/gene="YPO1064a"
CDS	complement(89365..89565 )	/gene="YPO1064a"  /note="Similar to Escherichia coli hypothetical protein YaeP SW:YAEF-ECOLI (P52099) (66 aa) fasta scores: E(): 1.5e-18, 74.2% id in 66 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89907.1" /db-xref="GI:15979132" /db-xref="SPTREMBL:Q8ZH47" /translation="MQQYCELVRRFYAEIGSGDL GYVPDALRCVLKALDEVAANDALP"

gene	89807..90355	/gene="YPO1065"
CDS	89807..90355	/gene="YPO1065"
		/note="Similar to Escherichia coli hypothetical protein YaeQ SW:YAEQ-ECOLI (P52100) (181 aa) fasta scores: E(): 0, 61.8% id in 178 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89908.1" /db-xref="GI:15979133" /db-xref="SPTREMBL:Q8ZH46" /translation="MALKATIHKAAINIADMDRN FFQDINLTIAQHPSETDQRMMLRL LAWICHADERLLFTKGLSADDEPEVWRHNDHNGI ELWIELGLPEEKRLRKACNQSKQV VLYAYSERAARKVWWPQVQEKLAGHRNLRVRFLLD EQMAKLAALSNNRMSLQATLQEGT IWLSDVQNNLEISFAEWQNYGQ"
gene	90358..90774	/gene="YPO1066"
CDS	90358..90774	/gene="YPO1066"
		/note="Similar to Escherichia coli hypothetical protein YaeJ SW:YAEJ-ECOLI (P40711) (140 aa) fasta scores: E(): 0, 65.2% id in 135 aa, and to Pseudomonas putida hypothetical protein SW:YAEJ-PSEPU (P45388) (137 aa) fasta scores: E(): 8.6e-31, 65.2% id in 135 aa, and to Streptomyces coelicolor hypothetical protein SCD95A.11 TR:Q9KXW3 (EMBL:AL357432) (145 aa) fasta scores: E(): 7.4e-13, 41.5% id in 135 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89909.1" /db-xref="GI:15979134" /db-xref="SPTREMBL:Q8ZH45" /translation="MLIISNSVTLASGEIELTAI RAQGAGGQHVNKTSTAIHLRFDIK ASSLP EYYKERLLLLNSHLVTAEGVVIKAQEYR SQDMNREAALARLVALIRQAMVVE KARRATKPTKSGKIRRVGKVRKGATKALRGKIH QE"
gene	90814..91542	/gene="cutF"
CDS	90814..91542	/note="synonyms: nlpE, YPO1067" /gene="cutF" /note="Similar to Escherichia coli copper homeostasis protein CutF precursor SW:CUTF-ECOLI (P40710) (236 aa) fasta scores: E(): 0, 48.3% id in 230 aa" /codon-start=1 /transl-table=11 /product="putative copper homeostasis lipoprotein" /protein-id="CAC89910.1" /db-xref="GI:15979135" /db-xref="SPTREMBL:Q8ZH44" /translation="MTSFHIYRTQYGRITVSKLT ITLLLAVALGSLGSCNNRSQPAEQ VLQPMQQSYQGVLPACDCSGLDTSFLDSDGTFI LKEVYLGTKDGDQTFAEYGKWART ADKLVLTLNGQGEKRYFHPVDKSLVMLDQQGLPIK STLNYQLEPSDQPLSKTPMPLSGM YKYFADAAIFTDCTGKAFPVENNIELETGYLNA RRNPGEFVFLTLNGYFDSRPSMEE GRTNKTLIPEGDIQFNANKSCEKK"
misc-feature	90886..90918	/gene="cutF" /note="PS00013 Prokaryotic

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gene      complement(91676..93394) attachment site."
        ) /gene="proS"

CDS      complement(91676..93394) /note="synonyms: drpA, YPO1068"
        ) /gene="proS"
        /EC-number="6.1.1.15"
        /note="Similar to Escherichia coli
        prolyl-tRNA synthetase
        SW:SYP-ECOLI (P16659) (572 aa)
        fasta scores: E(): 0, 84.2% id in
        571 aa"
        /codon-start=1
        /transl-table=11
        /product="prolyl-tRNA synthetase"
        /protein-id="CAC89911.1"
        /db-xref="GI:15979136"
        /db-xref="SPTREMBL:Q8ZH43"
        /translation="MRTSQYLLSTQKETPADAEV
        ISHQLMLRAGMIRKLASGLYTWLP
        TGVRLVKKVENIVREEMNAGAIEVSMPPVQPAD
        LWQESGRWEQYGPPELLRFVDRGER
        PFVLGPTHEEVITDLIRGEINSYQLPLNFFQIQ
        TKFRDEVPRPRFGVMRAREFLMKDA
        YSFHTTQESLQETYDAMYTAYSKIFSRMDLNFA
        VLADTGSIGGSASHEFQVLAESGE
        DDIVFSTGSDYAANIEFAEALAPTEPRAPATEEL
        RIVDTPNAKTIAELVEQFKLPIEK
        TVKTLVHAHEESGHKLVALLVRGDHLNEIKAE
        KLPQVAKPLTFASEEEIRAAIGAG
        PGSLGPVNLSPVIADHSVAVMSDFGAGANIDGK
        HYFGINWERDLALPLVADLRNVVE
        GDISPDGKGTLLQIKRGIEVGHIFQLGTKYSEVMK
        ATVQGEDGRNQVMTMGCYGIGVSR
        VVAAAEQNHDDRGIIWPDIAIAPFQVAILPMNMH
        KSFVRKELAEELYTTLRSHGIDVI
        LDDRKERPGVMFADMELIGVPHNIVIGDRNLDSE
        EVEYKNRRVGEKQMIKTSEIVEFL LSQIKR"

misc-feature complement(91730..93010) /gene="proS"
        ) /note="Pfam match to entry PF00587
        tRNA-synt-2b, tRNA synthetase
        class II (G, H, P, S and T), score
        244.70, E-value 1.3e-69"

misc-feature complement(92918..92980) /gene="proS"
        ) /note="PS00179 Aminoacyl-transfer
        RNA synthetases class-II signature
        1."

gene      complement(93498..94205) /gene="YPO1069"
        )

CDS      complement(93498..94205) /gene="YPO1069"
        ) /note="Similar to Escherichia coli
        hypothetical protein YaeB
        SW:YAEB-ECOLI (P28634) (235 aa)
        fasta scores: E(): 0, 71.1% id in
        235 aa, and to Vibrio cholerae
        hypothetical protein VC0876
        TR:Q9KTM6 (EMBL:AE004172) (231 aa)
        fasta scores: E(): 0, 50.0% id in
        232 aa"
        /codon-start=1
        /transl-table=11
        /product="conserved hypothetical
        protein"
        /protein-id="CAC89912.1"
        /db-xref="GI:15979137"
        /db-xref="SPTREMBL:Q8ZH42"
        /translation="MSTFSFNQIGVIRSPYKEKF
        AVPRQPGLVEDGGGELQLLAPYNQ
        PESVRGLSDFSHLWVIFVFHQTMEGGWRTVRPP
        RLGGNTRMGVFATRSTFRPNPIGM
        SLIELKGVRQCNGEVILALGSLDLVDGTPVIDIK
        PYLPFAESQPQARAGFAQSPADTE

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PRPAYRKDDNESREYAVLLLEFNV
RWRVIGQQTEVLSLDPR"
misc-feature complement(93774..94154 /gene="YPO1069"
)
/note="Pfam match to entry PF01980
UPF0066, Uncharacterised protein
family UPF0066, score 254.10,
E-value 2e-72"
misc-feature complement(93912..93947 /gene="YPO1069"
)
/note="PS01318 Uncharacterized
protein family UPF0066 signature."
gene complement(94202..94609 /gene="rcsF"
)
/note="synonym: YPO1070"
CDS complement(94202..94609 /gene="rcsF"
)
/note="May be involved in
regulation of exopolysaccharide
biosynthesis. Similar to
Escherichia coli RcsF protein rcsF
SW:RCSF-ECOLI (P28633) (133 aa)
fasta scores: E(): 2.1e-27, 63.5%
id in 137 aa"
/codon-start=1
/transl-table=11
/product="putative lipoprotein"
/protein-id="CAC89913.1"
/db-xref="GI:15979138"
/db-xref="SPTREMBL:Q8ZH41"
/translation="MRALPLCLLALSLTGCTLLP
SKPSTTDNPIKQPPPVIERSPATA
PRPAPVKLYKSAEELVGKPFRLGGEVSGESCQST
VQDSPPSISTARKRMQIRASYMKA
NAVLLHECEIQSGVPGCYQQAVCQGSALNVSSK"
misc-feature complement(94562..94594 /gene="rcsF"
)
/note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
gene complement(94727..95542 /gene="YPO1071"
)
CDS complement(94727..95542 /gene="YPO1071"
)
/note="Similar to Escherichia coli
putative lipoprotein YaeC
precursor SW:YAE-ECOLI (P28635)
(271 aa) fasta scores: E(): 0,
90.4% id in 271 aa, and to Vibrio
cholerae lipoprotein VC0905
TR:Q9KTJ7 (EMBL:AE004174) (275 aa)
fasta scores: E(): 0, 68.3% id in
271 aa"
/codon-start=1
/transl-table=11
/product="putative lipoprotein"
/protein-id="CAC89914.1"
/db-xref="GI:15979139"
/db-xref="SWISS-PROT:Q8ZH40"
/translation="MSLKFKSIAAISALIGTLTL
VGCPTKAPNHIKVGIVVGAEEQ
VAEVAQKVAKKYGKLDVELVTFNDYVLPNEALSK
GDIDLNAFQHKPYLDQKIDRGYK
LVSVGNSFVYPIAGYSKKIKSLDELQPGSQVALP
NDPTNLGRSLLLQLQSVGLIKLKD
VGLLPVLDVVENPKNLKLVELEAPQLPRSLDDQ
QIALAIINTTYASQIGLTPAKDGL
FVEDKESPYVNLIVAREDNKDAENVKKFVQAYQS
DEVYDAANKAFNGGAVKGW"
misc-feature complement(95474..95506 /gene="YPO1071"
)
/note="PS00013 Prokaryotic
membrane lipoprotein lipid
attachment site."
gene complement(95606..96259 /gene="YPO1072"
)

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CDS      complement(95606..96259 /gene="YPO1072"
)
        /note="Similar to Escherichia coli
        hypothetical ABC transporter
        permease protein YaeE
        SW:YAE-ECOLI (P31547) (217 aa)
        fasta scores: E(): 0, 90.8% id in
        217 aa, and to Vibrio cholerae ABC
        transporter, permease protein
        VC0906 TR:Q9KTJ6 (EMBL:AE004174)
        (225 aa) fasta scores: E(): 0,
        54.3% id in 210 aa"
        /codon-start=1
        /transl-table=11
        /product="ABC transporter permease
        protein"
        /protein-id="CAC89915.1"
        /db-xref="GI:15979140"
        /db-xref="SWISS-PROT:Q8ZH39"
        /translation="MSEAMMWLMARGVWETLMMT
        FVSGFFGFVLGLPVGVLLYVTRPG
        QIIANNKIYRTLSGVVNIFRSIPFIILLVWMIPF
        TRMIVGTSIGLQAAIVPLTVGAAP
        FIARMVENALLEIPSGLVEAARAMGATPMQIIKK
        VLLPEALPGLVNAATITLITLVGY
        SAMGGAVGAGGLGQIGYQYGYIGYNATVMNTVLV
        LLVILVYLIQLSGDRIVKAVTHK"

misc-feature complement(95651..95716 /gene="YPO1072"
)

misc-feature complement(95717..95929 /gene="YPO1072"
)
        /note="one of 5 probable
        transmembrane helices predicted
        for YPO1072 by TMHMM2.0"

misc-feature complement(95762..95827 /gene="YPO1072"
)
        /note="Pfam match to entry PF00528
        BPD-transp,
        Binding-protein-dependent
        transport systems inner membrane
        component, score 66.00, E-value
        8.1e-16"

misc-feature complement(95840..95926 /gene="YPO1072"
)
        /note="one of 5 probable
        transmembrane helices predicted
        for YPO1072 by TMHMM2.0"

misc-feature complement(95948..96013 /gene="YPO1072"
)
        /note="PS00402
        Binding-protein-dependent
        transport systems inner membrane
        comp. sign."

misc-feature complement(96029..96094 /gene="YPO1072"
)
        /note="one of 5 probable
        transmembrane helices predicted
        for YPO1072 by TMHMM2.0"

misc-feature complement(96134..96199 /gene="YPO1072"
)
        /note="one of 5 probable
        transmembrane helices predicted
        for YPO1072 by TMHMM2.0"

gene      complement(96252..97283 /gene="abc"
)
        /note="synonym: YPO1073"

CDS      complement(96252..97283 /gene="abc"
)
        /note="Similar to Escherichia coli
        ATP-binding protein Abc
        SW:ABC-ECOLI (P30750) (343 aa)
        fasta scores: E(): 0, 80.2% id in

```

		/codon-start=1 /transl-table=11 /product="ABC transporter ATP-binding protein" /protein-id="CAC89916.1" /db-xref="GI:15979141" /db-xref="SWISS-PROT:Q8ZH38" /translation="MIKLTHISKVFQQGSRTITA LSDVSLHVPAGQIYGVIGASGAGK STLIRCANMLERPTSGQVLVDDQDLTTLSEGQLT RARRQIGMIFQHFNLLSSRTVYGN IALPLELDNTSRADIKKRVNELLDLVGLTDKQDA YPANLSGGQKQORVAIARALASNP VLLCDEATSALDPATTRSILELLKDINRRLGLTI LLITHEMDVVKRICDQVAVISEGK LIEKDSVSEVFSHPKTPLAQQFIQSTLHL DIPED YAKRMSPEPTVDHVP LLKLEFTGK SVDAPLISQAVRRFNIDIGILSSQMDYAGGVKFG VMLAELHGDVQDGLAAIKFLQDHH VKVEVLGYV" /gene="abc"
misc-feature	complement(96633..97193)	/Note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 258.10, E-value 1.2e-73" /gene="abc"
misc-feature	complement(96819..96863)	/Note="PS00211 ABC transporters family signature." /gene="abc"
misc-feature	complement(97149..97172)	/Note="PS00017 ATP/GTP-binding site motif A (P-loop)." /gene="YPO1074" /gene="YPO1074" /Note="Similar to Escherichia coli hypothetical protein YaeD SW:YAED-ECOLI (P31546) (191 aa) fasta scores: E(): 0, 80.3% id in 188 aa, and to Escherichia coli O157:H7 phosphatase YaeD TR:BAA93568 (EMBL:AB035926) (191 aa) fasta scores: E(): 0, 80.3% id in 188 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89917.1" /db-xref="GI:15979142" /db-xref="SPTREMBL:Q8ZH37" /translation="MTQSVPAIFLDRDGTVNVDH GYVHEIDNFQFIDGVIDACRELKE MGFALVLVTNQSGIARGMFTEEQFLSLTEWMDWS LADRGVDLDGIYFCPHHPDGSVAE FSETCECRKPLPGMLLQAQNELNIDMAASYMVG KIEDMQAALAANIGTKVLVVRTGKP VTAEGEAAADWVLNLSLADLPKAIKARYK"
gene CDS	97470..98036 97470..98036	
gene rRNA	98505..99993 98505..99993	/gene="16S-rRNA" /gene="16S-rRNA" /Note="match to 16S-rRNA 1..1489 (EMBL:YPE16SA)"
tRNA	100157..100232	/product="tRNA-Glu" /Note="tRNA Glu anticodon TTC, Cove score 56.95"
gene rRNA	100485..103391 100485..103391	/gene="23S-rRNA" /gene="23S-rRNA" /Note="match to 23S-rRNA 1..2906 (Y. enterocolitica 23S EMBL:U77925)"
gene rRNA	103391..103624 103391..103624	/gene="5S-rRNA" /gene="5S-rRNA" /Note="match to 5SrRNA 1..234 blast score 1131 percent identity 98 (incl. 23S-5S spacer)"

gene	104177..104980	/note="tRNA Asp anticodon GTC, Cove score 90.47"
CDS	104177..104980	/gene="YPO1075" /gene="YPO1075" /note="Similar to Escherichia coli hypothetical oxidoreductase in aspU-mltD intergenic region YafB SW:YAFB-ECOLI (P30863) (267 aa) fasta scores: E(): 0, 74.9% id in 267 aa, and to Corynebacterium sp 2,5-diketo-D-gluconic acid reductase TR:P06632 (EMBL:M12799) (278 aa) fasta scores: E(): 6.3e-31, 41.6% id in 255 aa" /codon-start=1 /transl-table=11 /product="putative aldo/keto reductase" /protein-id="CAC89918.1" /db-xref="GI:15979143" /db-xref="SWISS-PROT:Q8ZH36" /translation="MSIPVFGLGTFRLQDQIVID SVSQALTGLGYRAIDTAQIYENEAP VGQAIQESGINRDELFITTKIWIANLSKDKLIPS LRESIQKLKTDYVDLTLIHWPSPN DEVSVAEFMSSELLKAKGLGLTRQIGISNFTIDLM KQAIAAVGAEEIATNQIELSPLLQ NRNVVDFAKQNGIAVTSYMTLAYGKALAEPIKT IAEQHGATPAQVILSWAMQLGYGV IPSSTKAANLASNLLAQKLCLNAADMALIALTLDR NERLVSPDGLAPKWD"
misc-feature	104177..104941	/gene="YPO1075" /note="Pfam match to entry PF00248 aldo-ket-red, Aldo/keto reductase family, score 357.70, E-value 1.3e-103"
misc-feature	104261..104314	/gene="YPO1075" /note="PS00798 Aldo/keto reductase family signature 1."
misc-feature	104516..104569	/gene="YPO1075" /note="PS00062 Aldo/keto reductase family signature 2."
gene	105015..105479	/gene="YPO1076"
CDS	105015..105479	/gene="YPO1076" /note="no significant database hits" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAC89919.1" /db-xref="GI:15979144" /db-xref="SPTREMBL:Q8ZH35" /translation="MRWFFILVHPDGAETGSVKS VRMDMELPPSMCAVIVGTNLMRAY QRVGEQRVDNSIVKKHGNEAMDQLSLRPDNGS QVESAGQGNCEASIGTERMDTLLP FNRGGRGDWNSWIGGDKENCVACYGGSGKGRIYE ORCLLEEVFYRKGLIYQQ"
gene	105840..106622	/gene="YPO1077"
CDS	105840..106622	/gene="YPO1077" /note="Similar to Escherichia coli hypothetical protein YafD SW:YAFD-ECOLI (P30865) (259 aa) fasta scores: E(): 0, 75.2% id in 254 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89920.1" /db-xref="GI:15979145" /db-xref="SPTREMBL:Q8ZH34" /translation="MPKRTYAMRYVAGQPVEQIF PGAQKQLDKGLPLGEPLPTAELLR VVVWNIFKQQRAGWLPVLKELGRDTQLMLLQEAQ"



		PQHPSGVMTLAAAHVPVYCCPLREREP LLRLSKSA LVTVPYPIHDGRLLMVVNIHAVNFS LGVDVYSKQLDPIGDQIASHRGPVILAGDFNAWS RQRINALQHFAQDAGLQEV EFRVD HRSRAFGRLDFIFYRGLTVIDASVLVTRASDHN PLIVEFQP"
gene	complement(106664..108091)	/gene="mldD"
CDS	complement(106664..108091)	/note="synonyms: dniR, YPO1078" /gene="mldD"  /EC-number="3.2.1.-" /note="Similar to Escherichia coli membrane-bound lytic murein transglycosylase D precursor MldD SW:MLTD-ECOLI (P23931) (452 aa) fasta scores: E(): 0, 63.4% id in 470 aa" /codon-start=1 /transl-table=11 /product="membrane-bound lytic murein transglycosylase D precursor" /protein-id="CAC89921.1" /db-xref="GI:15979146" /db-xref="SPTREMBL:Q8ZH33" /translation="MIARLLSNHIDTHMKT KAIL LASVLLVGCQTSKQDAQAP EQHAQ SLSSAGQASEAGEYTNSTREGSARWLESESSYAQ QDLWNFIKDELKMKVPENSRIREQ KQKYLKNKSYLHDVTLRAEPYMYLIVEQIKKRKM PMELVLLPIVESAFDPHATSSANA AGLWQIVPSTGRNYGLKQNQWYDGRRDVVASTKA ALDILERLNKMFNGDWLLTVAAYN SGEGRVMQAIKANKAKGKPTDFWALS LPRETSIY VPKMLALGDLLKNSKKYGITLPET DKDRALARVDVDQQIELTQAAEMAGMSLT KLKSF NSGYKRVNVTAPDGHGPRYIMLPKA HAEQLKDSLADTDITAVQPTKLATNSTKSASSSQ YKVRPGDTLSTIAKRLNIKTS DLQ SWNNLRKSTLKVGTQLQLASNTTSKSITYQVRK GDSFASIAKRHGVNTDDVMRWNSV VSKANNLQPLGLKLT L FVNDKSTPEA"
misc-feature	complement(106694..106828)	/gene="mldD"
misc-feature	complement(106856..106987)	/note="Pfam match to entry PF01476 LysM, Putative peptidoglycan binding domain, score 44.10, E-value 3.2e-09" /gene="mldD"
misc-feature	complement(107372..107722)	/note="Pfam match to entry PF01476 LysM, Putative peptidoglycan binding domain, score 62.30, E-value 1e-14" /gene="mldD"
misc-feature	complement(107579..107665)	/note="Pfam match to entry PF01464 SLT, Transglycosylase SLT domain, score 122.70, E-value 6.7e-33" /gene="mldD"
misc-feature	complement(108005..108037)	/note="PS00922 Prokaryotic transglycosylases signature." /gene="mldD"
gene	complement(108124..108879)	/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /gene="gloB"
CDS	complement(108124..108879)	/note="synonym: YPO1079" /gene="gloB"  /EC-number="3.1.2.6"

probable hydroxyacylglutathione  
hydrolase GloB SW:GLO2-ECOLI  
(Q47677) (251 aa) fasta scores:  
E(): 0, 57.4% id in 251 aa, and to  
Arabidopsis thaliana  
hydroxyacylglutathione hydrolase,  
mitochondrial precursor Glx2-1  
SW:GL2M-ARATH (O24495) (331 aa)  
fasta scores: E(): 2.9e-32, 39.0%  
id in 236 aa"  
/codon-start=1  
/transl-table=11  
/product="putative  
hydroxyacylglutathione hydrolase"  
/protein-id="CAC89922.1"  
/db-xref="GI:15979147"  
/db-xref="SPTREMBL:Q8ZH32"  
/translation="MNLISIPAFQDNYIWLLANR  
QKHCIVDPGESAPVLATLAQGQY  
VPQAILLTHHHNDHVGGVADLRHHFPDIPVYGPO  
ETAKKGATVIVNDGDSLTIAGQNY  
TIIAVPGHTLGHIAYYSSPYLFCGDTLFSAGCGR  
LLEGTPEQMYASIQRLAQLPDETL  
ICCAHEYTLNLKFAHAILPADQDIATYQQQIEQ  
LRSKNLPSLPVKLQFERKINVFLR  
CNDIDLQRKIGTTSPDLSLVSVFCELSRKDSF"  
/gene="gloB"

misc-feature complement(108385..1088  
61)  
/note="Pfam match to entry PF00753  
lactamase-B,  
Metallo-beta-lactamase  
superfamily, score 162.10, E-value  
9.3e-45"

gene 108924..109643  
CDS 108924..109643  
/gene="YPO1080"  
/gene="YPO1080"  
/note="Similar to Escherichia coli  
hypothetical protein YafS  
SW:YAFS-ECOLI (P75672) (240 aa)  
fasta scores: E(): 0, 63.6% id in  
236 aa, and to Vibrio cholerae  
hypothetical protein VC2235  
TR:Q9KPX7 (EMBL:AE004295) (245 aa)  
fasta scores: E(): 0, 44.2% id in  
233 aa"  
/codon-start=1  
/transl-table=11  
/product="conserved hypothetical  
protein"  
/protein-id="CAC89923.1"  
/db-xref="GI:15979148"  
/db-xref="SPTREMBL:Q8ZH31"  
/translation="MKPAQIRQNIETPASWAELP  
WGEYYRAALEQQQLQPWWPKFFGFH  
LLKVGHLISAEIASDKCAIAHQVNVGEWGKNMQVL  
ASPYQLPFAEKSVDACLLSHTLAY  
AANPHRILREVDRVLIDDGWLVISGFNPFSLLGL  
GKLVPVLRQRPYISRMFTQMRL  
DWLSLLNVEVHLSCFHVLPFNKNGGHFISTHLP  
ALGCVNLIIARKRTVPLTFNPMKF  
GVRKPWFSSRAVGATKSYRDQP"  
/gene="rnhA"

gene complement(109698..1101  
62)  
/note="synonyms: dasF, herA, rnh,  
sdrA, YPO1081"

CDS complement(109698..1101  
62)  
/gene="rnhA"  
/EC-number="3.1.26.4"  
/note="Similar to Escherichia coli  
ribonuclease HI SW:RNH-ECOLI  
(P00647) (155 aa) fasta scores:  
E(): 0, 84.8% id in 151 aa"  
/codon-start=1  
/transl-table=11  
/product="ribonuclease HI"  
/protein-id="CAC89924.1"

		/db-xref="SWISS-PROT:Q8ZH30" /translation="MTKQVEIFTDGSC LGNPGPG GYGAILRYKQHEKTFSAGYYLTTN NRMELMAAIVALEALTSPCEVTLSQYVRQGI TQWIHNWKKRGWKTADRKPVRNVD LWQRLDLAIQSHTIQWEWVKGHAGHPENERCDEL ARQGANSPTLDDTGYNPD" /gene="rnhA"
misc-feature	complement(109737..110159)	/note="Pfam match to entry PF00075 rnaseH, RNase H, score 227.00, E-value 2.8e-64" /gene="dnaQ"
gene	110232..110996	/note="synonyms: mutD, YPO1082" /gene="dnaQ"
CDS	110232..110996	/EC-number="2.7.7.7" /note="Similar to Escherichia coli DNA polymerase III, epsilon chain SW:DP3E-ECOLI (P03007) (243 aa) fasta scores: E(): 0, 75.9% id in 237 aa" /codon-start=1 /transl-table=11 /product="DNA polymerase III, epsilon chain" /protein-id="CAC89925.1" /db-xref="GI:15979150" /db-xref="SPTREMBL:Q8ZH29" /translation="MIITPTRQIVLDTETTGMNK LGVHYEGHRIIEIGAVEVINRRRLT GRNFHVYVKPDRLVDPEAYGVHGISDEFLADKPT FADITPEFLDFIRGAELVIHNAAF DIGFMDYEFRLQDDIPKTETFTCTITDSLLMARR LFPGKRNNLDALCDRYQIDNTKRT LHGALLDAEILADEVYLAMTGGQTSLTFSMEGEVS QNNASEDIQRITRPASALKIIYAT EDELANHESRLDFVMKKGGSC LWRMPLEAEETK AE" /gene="dnaQ"
misc-feature	110253..110780	/note="Pfam match to entry PF00929 Exonuclease, Exonuclease, score 171.30, E-value 1.6e-47" /product="tRNA-Asp" /note="tRNA Asp anticodon GTC, Cove score 94.51" /gene="YPO1083"
tRNA	111109..111185	
gene	complement(111242..112726)	/gene="YPO1083"
CDS	complement(111242..112726)	/note="Similar to Pseudomonas aeruginosa probable permease TR:AAG03865 (EMBL:AE004485) (575 aa) fasta scores: E(): 0, 39.1% id in 465 aa, and to Streptomyces coelicolor putative transmembrane transporter SC1A6.06 TR:O69811 (EMBL:AL023496) (522 aa) fasta scores: E(): 0, 32.6% id in 481 aa" /codon-start=1 /transl-table=11 /product="putative permease" /protein-id="CAC89926.1" /db-xref="GI:15979151" /db-xref="SPTREMBL:Q8ZH28" /translation="MPNNEKISASSINPHYSKPL TNEDLAPTRKQNWGWYNIFSFWMT DVHSMGGYVVAASFFALGLSSWQVLLSLLVGICI VQICANLVAKPSQIAGVPYAVICR QSFGVFGANIPAVIRGLIAVAWYGIQTYLAGNAF MLVMLKFFPSLIPLAQSQWLGLST LGWICFSIMWVLQAMVFWHGMNAIKRFIDFAGPA VYVVMLSLALWIVYQTGWSNISFT LASKILSPSEQVWQMLTATALVVS YFAGPLL NFG DFSRYGKSMQEIIRGNRWGLPFNF

GVAIALGLLTMIATIGINIVANF  
VSPAFDNFNCSPQRINFRTGGMIAAVGSVLLTPW  
NLFQSPIIHYTLVDVLGAFMGPLF  
GILIADFYLIKRGQLYVDDLNFNASSSGRYWYRGG  
FNPKAIMALLPAVAIGLMIIFIPN  
LQOISSFSWFIGAFLGGSIYRFIARNDPNNAALFIRPEIGKD"

misc-feature	complement (111305..111370)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111341..112648)	/gene="YPO1083"  /note="Pfam match to entry PF02133 Transp-cyt-pur, Permeases for cytosine/purines, uracil, thiamine, allantoin, score 272.50, E-value 1.8e-78"
misc-feature	complement (111383..111448)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111536..111601)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111614..111679)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111719..111784)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111845..111910)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (111971..112036)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112091..112156)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112196..112261)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112307..112372)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112466..112531)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
misc-feature	complement (112547..112612)	/gene="YPO1083"  /note="one of 12 probable transmembrane helices predicted for YPO1083 by TMHMM2.0"
gene	113065..113283	/gene="YPO1084"

CDS	113065..113283	/gene="YPO1084" /note="Appears to have been interrupted by the insertion of downstream IS100. Similar to N-terminus of Pseudomonas aeruginosa hypothetical protein TR:AAG04906 (EMBL:AE004580) (308 aa) fasta scores: E(): 6.7e-13, 56.5% id in 69 aa, and to N-terminus of Schizosaccharomyces pombe hypothetical 36.2 kDa protein C19G12.03 in chromosome I SPAC19G12.03 TR:O13842 (EMBL:Z97209) (320 aa) fasta scores: E(): 3.6e-06, 44.4% id in 63 aa" /pseudo /codon-start=1 /transl-table=11 /product="conserved hypothetical protein (pseudogene)"
misc-feature	complement(113283..115236)	/note="insertion sequence, IS100"
misc-feature	113283..113310	/note="IS100 inverted repeat"
gene	complement(113349..114131)	/gene="YPO1085" /note="synonym: ypmt1.57c"
CDS	complement(113349..114131)	/gene="YPO1085"  /note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa." /codon-start=1 /transl-table=11 /product="insertion sequence IS100, ATP-binding protein" /protein-id="CAC89928.1" /db-xref="GI:15979152" /db-xref="SPTREMBL:Q9R3L5" /translation="MMELQHQRMLALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLHEEKLARHQRKQAMYTRMAAFPAVKTFEEY DFTFATGAPQKQLQSLRSLSFIER NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF TTAADLLQLSTAQRQGRYKTTLQ RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR YEKSAMILTSNLPFGQWDQTFAGD AALTSAMLDRIHHSHVQIKGESYRLRQKRKAG VIAEANPE"
misc-feature	complement(113424..113963)	/gene="YPO1085"  /note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	complement(113781..113804)	/gene="YPO1085"  /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement(114128..115150)	/gene="YPO1086"
CDS	complement(114128..115150)	/note="synonyms: y1093, ypmt1" /gene="YPO1086"  /note="Similar to Escherichia coli transposase for insertion sequence"

(P15025) (390 aa) fasta scores:  
E(): 3e-27, 33.1% id in 329 aa.  
Identical to the previously  
sequenced *Yersinia pestis*,  
*Yersinia pseudotuberculosis*, and  
*Escherichia coli* pesticin plasmid  
insertion sequence transposase  
Y1055 TR:P74993 (EMBL:U59875) (340  
aa) fasta scores: E(): 0, 100.0%  
id in 340 aa"  
/codon-start=1  
/transl-table=11  
/product="transposase for  
insertion sequence IS100"  
/protein-id="CAC89929.1"  
/db-xref="GI:15979153"  
/db-xref="SPTREMBL:P74993"  
/translation="MVTFETVMEIKILHKQGMSS  
RAIARELGISRNTVKRYLQAKSEP  
PKYTTPPAVASLLDEYRDYIRQRIADAHYPYKIPA  
TVIAREIRDQGYRGGMTILRAFIR  
SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS  
PLHVFVAVLGYSRMLYIEFTDNMR  
YDTLETCHRNAFRFFGGVPREVLYDNMKTIVVLQR  
DAYQTGQHRFHPSLWQFGKEMGFS  
PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL  
RPMGITVDVETANRHGLRWLHDVA  
NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD  
VHLDENLVNFDKHPLHPLSIYDS FCRGVA"  
/gene="YPO1086"

misc-feature complement(114272..1148  
05) /note="Pfam match to entry PF00665  
rve, Integrase core domain, score  
81.90, E-value 1.6e-22"

misc-feature complement(115034..1150  
99) /gene="YPO1086"  
/note="Predicted helix-turn-helix  
motif with score 2147 (+6.50 SD)  
at aa 18-39, sequence  
MSSRAIARELGISRNTVKRYLQ"

misc-feature complement(115043..1151  
26) /gene="YPO1086"  
/note="Pfam match to entry PF00239  
recombinase, Site-specific  
recombinases, score 25.70, E-value  
4.7e-06"

misc-feature complement(115209..1152  
36) /note="IS100 inverted repeat"

gene complement(115239..1153  
40) /gene="intA"

CDS complement(115239..1153  
40) /note="synonym: YPO1086a"  
/partial  
/gene="intA"  
/note="Probable gene remnant.  
Similar to N-terminal regions of  
*Escherichia coli* prophage Cp4-57  
integrase IntA SW:INTA-ECOLI  
(P32053) (413 aa) fasta scores:  
E(): 2.8e-05, 61.765% id in 34 aa,  
and *Haemophilus influenzae* Cp4-57  
integrase-like protein TR:Q9L8P3  
(EMBL:AF198256) (408 aa) fasta  
scores: E(): 0.00043, 52.941% id  
in 34 aa. CDS is truncated by the  
insertion of the downstream IS100  
element and subsequent  
recombination events"  
/codon-start=1  
/transl-table=11  
/product="phage integrase  
(partial)"  
/protein-id="CAC89930.1"  
/db-xref="GI:15979154"  
/db-xref="SPTREMBL:Q8ZH27"

gene	115752..116063	KDLTLHDGDGLFLL"
CDS	115752..116063	/gene="YPO1087"
		/gene="YPO1087"
		/note="Similar to plasmid proteins. Similar to Xylella fastidiosa hypothetical protein XFA0045 TR:Q9PHG3 (EMBL:AE003851) (106 aa) fasta scores: E(): 3e-14, 54.2% id in 72 aa, and to Pseudomonas alcaligenes hypothetical 11.2 kDa protein TR:Q9XAX7 (EMBL:U88088) (99 aa) fasta scores: E(): 4e-06, 50.0% id in 54 aa"
		/codon-start=1
		/transl-table=11
		/product="putative prophage protein"
		/protein-id="CAC89931.1"
		/db-xref="GI:15979155"
		/db-xref="SPTREMBL:Q8ZH26"
		/translation="MMKTIKHYLTPEGRDLYMEY LKSLRDSIAKAKISSRVNRIASGN FGDHKPCREGVWELRIDQPGYRVYYSLVAVKSC CCFWAVISARRMPTSIRLLCVLKI I"
gene	116071..116391	/gene="YPO1088"
CDS	116071..116391	/gene="YPO1088"
		/note="Similar to Xylella fastidiosa hypothetical protein XFA0046 TR:Q9PHG2 (EMBL:AE003851) (108 aa) fasta scores: E(): 4.3e-10, 40.0% id in 95 aa, and to Pseudomonas alcaligenes hypothetical 10.3 kDa protein TR:Q9XAX6 (EMBL:U88088) (96 aa) fasta scores: E(): 2e-05, 36.6% id in 82 aa"
		/codon-start=1
		/transl-table=11
		/product="putative DNA-binding prophage protein"
		/protein-id="CAC89932.1"
		/db-xref="GI:15979156"
		/db-xref="SPTREMBL:Q8ZH25"
		/translation="MIMAKARLHDDAMVQLLMED PEFAQVYLHQALLDIDEEGGQEAF LMALRHVVEARGGMASVAKKAGVSRETLYRTLSP SGNPTLKTLLSVVSATGFQFSHLA SITA"
misc-feature	116236..116301	/gene="YPO1088"
		/note="Predicted helix-turn-helix motif with score 1826 (+5.41 SD) at aa 56-77, sequence GGMASVAKKAGVSRETLYRTLS"
gene	complement(116740..117828)	/gene="YPO1089"
CDS	complement(116740..117828)	/gene="YPO1089"
		/note="Weakly similar to many from plasmids and bacteriophage. Similar to unidentified replication protein A repA TR:Q03086 (EMBL:M73777) (290 aa) fasta scores: E(): 6.1e-07, 30.7% id in 238 aa, and to uncultured eubacterium plasmid putative DNA helicase repA TR:Q9L3P0 (EMBL:AJ271879) (279 aa) fasta scores: E(): 0.00012, 25.7% id in 237 aa, and to Escherichia coli regulatory protein RepA repA SW:REPJ-ECOLI (P20356) (279 aa) fasta scores: E(): 0.00022, 27.6% id in 192 aa, and to uncultured eubacterium plasmid pIE1115 putative DNA helicase repA"

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aa) fasta scores: E(): 0.00036,
26.7% id in 191 aa, and to
lactococcal bacteriophage bIL170
complete genome e5 TR:O80155
(EMBL:AF009630) (316 aa) fasta
scores: E(): 0.51, 22.2% id in 203
aa"
/codon-start=1
/transl-table=11
/product="putative regulatory
prophage protein"
/protein-id="CAC89933.1"
/db-xref="GI:15979157"
/db-xref="SPTREMBL:Q8ZH24"
/translation="MKTPLILLEREVPVSLTTNLP
LRKGSDDGYNTPQDYNIKGHLPSNT
LASIYGPSGSYKSFLAVSWACHIATGKPWASRRV
TQGSVVYIIVGEGGIGVPRRIRAWG
MEFNNGGTPIESLYRIDCPVFPASPESAIQVIKAA
QDVTEQTGSPVRLIVLDTLARCFCG
GSDENAAKDMGAFIQGCDYIKAETGATVLVIHHS
GKDLDDKGARGSSAFRAALDVEFNV
RREGDGGALVLSCTKMKDSEPTTRAYDLSPLNL
YIDNDGEEVNSLVLCDKGREVSDE
GSPYEAELASIQRLTANHIALWQSIRSRTASGEA
CTKSLVRDDMRGMGFDVAKKFTRW
LDKLETDGLIHIDGENICPNSLSNTARN"
gene      complement(117825..1187 /gene="YPO1090"
84)
CDS      complement(117825..1187 /gene="YPO1090"
84)

/note="Similar to the N-terminal
regions of bacteriophage P4
putative P4-specific DNA primase
alpha SW:PRIM-BPP4 (P10277) (777
aa) fasta scores: E(): 0, 35.8% id
in 324 aa, and Escherichia coli
DNA primase TraC SW:TRC5-ECOLI
(P27190) (1448 aa) fasta scores:
E(): 1.5e-10, 27.8% id in 270 aa.
Possible truncated protein."
/codon-start=1
/transl-table=11
/product="putative prophage DNA
primase"
/protein-id="CAC89934.1"
/db-xref="GI:15979158"
/db-xref="SPTREMBL:Q8ZH23"
/translation="MSRFVSDIIRASQHHWSNIL
SSLAIPIPHLNKKGPCPVCGGKDR
FRFDDKKGRGTWFCNYCGHGDGLDLVTLVRQCDV
IQAAREISRLTDLAPTAPAKERTE
QPLHSDMTQKVTALLAACSQGTSDYLLHKGLNHP
VFLMPANSAKNIGGVHFNVGSMVL
PLVDLSGNTTGALLINRRGEKRLLPKSRIKSSFI
PITHHTLSQTIIITEGFATGLVIS
RFVTATVVA AISATNLTQVAVALRERYPDAQIII
AADNDVTNSDNNPGKQQA EYAALA
VNGLVTLPPPTCGKADWDDYRQQVGTDAARIEFFR
QLYNPREWI"
gene      complement(118777..1193 /gene="YPO1091"
19)
CDS      complement(118777..1193 /gene="YPO1091"
19)

/note="Similar to Shigella
flexneri insertion sequence IS2
DNA TR:Q54157 (EMBL:Z23101) (179
aa) fasta scores: E(): 0.0091,
28.8% id in 132 aa, and to
Bacteriophage P4 ASH protein cI
SW:VASH-BPP4 (P05462) (137 aa)
fasta scores: E(): 0.25, 37.5% id
in 72 aa"
/codon-start=1
/transl-table=11

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protein"
/protein-id="CAC89935.1"
/db-xref="GI:15979159"
/db-xref="SPTREMBL:Q8ZH22"
/translation="MIFYFFLAGALQYNPFAAAK
SVAGISVPKIFLIPSLVIQTWSFI
GMACAHPSMVAQAGAPKGAPVSKKSGNANSVWAT
TQGISVSGGSHYNYFLEAAQWLLP
FTVCTRNTFVPIRGCAMHNSPLTIEEIVDHCHA
LVLAMLEITDPTAKELLLFILAER
LDLLQLMLDEVPAEEANHE"
gene      complement(119512..1204 /gene="YPO1092"
08)
CDS      complement(119512..1204 /gene="YPO1092"
08)

/Note="Similar to Pseudomonas
aeruginosa integrase/recombinase
XerD TR:AAG07125 (EMBL:AE004793)
(298 aa) fasta scores: E(): 0.027,
28.0% id in 239 aa, and to
Chlamydia pneumoniae
integrase/recombinase XerC or
CP0752 TR:Q9Z9F7 (EMBL:AE001587)
(312 aa) fasta scores: E(): 0.16,
23.3% id in 232 aa"
/codon-start=1
/transl-table=11
/product="putative DNA-binding
prophage protein"
/protein-id="CAC89936.1"
/db-xref="GI:15979160"
/db-xref="SPTREMBL:Q8ZH21"
/translation="MFVMSRLSREMKMLAKQAGG
SHKTVHDIRIMDRFSRHLLALNI
QVRDVKHLKAKHIESYITDRFSQGIAIRSLHNEM
AALRTVFRFAGRDKIVLSERLTNK
ALGLGGASRAGSKFAIPEEVYQAALRTAQQQDKG
LACALQLARLLGLRSQEAVQCANS
LKTWQKELEQNRSKLTVVFGTKGGRSRETRILD
EAVKRAVKEAQQIAETRGGKLIDK
PDLKTAMNFWRSHTTRLGLTGHYSPhSLRYAWAQ
DAINYLAAGFSRIEARALTSMDL
GHGDGRGRYVERVYTRKEANYV"
misc-feature complement(120319..1203 /gene="YPO1092"
84)

/Note="Predicted helix-turn-helix
motif with score 1045 (+2.75 SD)
at aa 9-30, sequence
REMKMLAKQAGGSHKTVHDIR"
gene      complement(120421..1207 /gene="YPO1092a"
11)
CDS      complement(120421..1207 /gene="YPO1092a"
11)

/Note="No significant database
matches"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="CAC89937.1"
/db-xref="GI:15979161"
/db-xref="SPTREMBL:Q8ZH20"
/translation="MTPQHKPASAFEISDFTQHV
MHLTPLOQYVRLTAFYKIFEPIPRQ
ANSLGDDLQKQEAAPSASPIPRNTSTAARSGAQV
SFKADNLPFPMRQRNAAS"
gene      complement(120803..1209 /gene="YPO1094"
76)
CDS      complement(120803..1209 /gene="YPO1094"
76)

/Note="No significant database
matches"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="CAC89938.1"

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gene	121207..121434	/db-xref="SPTREMBL:Q8ZH19"
CDS	121207..121434	/translation="MPIGDTVIGYQLSERLASVE QRPLKPVVYHDGAVFAHLNQDASL HQKTPYTSISGAC" /gene="YPO1095" /gene="YPO1095" /note="No significant database matches" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="CAC89939.1" /db-xref="GI:15979163" /db-xref="SPTREMBL:Q8ZH18" /translation="MQVIRIILILETLGAVIDSE FTWGKLRQKLNSGKLLLEAVIRKSN ERGATSLSNLCHLRIFPLASLPKRALHAYSA" /note="Low GC region" /gene="YPO1096"
misc-feature	121566..124482	
gene	complement(121596..1232 66)	/gene="YPO1096"
CDS	complement(121596..1232 66)	/note="No significant database matches" /codon-start=1 /transl-table=11 /product="putative phage protein" /protein-id="CAC89940.1" /db-xref="GI:15979164" /db-xref="SPTREMBL:Q8ZH17" /translation="MKKLILKKIMILSDSGKSAR QFEFGEHLTLITADDDNSVGKSTL AKMIFWTFGCEPIFSEVWRTLDCTSIIIEFEINNA PYIIHRYKNEIKIRHSNGKLHSFP KITGDYSKYFSELVNFNVLLPKKGQLTLETPPPA YYFIPFYIDQKRTWAKPWDSFENL QQYSSWAKPVISYHSGLFKAHFEVEKDIYVIKR ELEEVEKGVTELNNAVIILRQNL DTDNVL PSTEFIFSVIQESEKNKKNLLEERTNLR VEKIRLESQIKLAKGIISELDKDY IFSVENMEDGDIECPTCGTIHENSIAHRTSILID MELAKNQLESLESEVNGIINLLVI KDEEITEQSNKSERSYNNVIESDSNSLISFTNDK FEKRAHEINSKKNITIEIKKSEEK TAKKSQSDILSKEQKSEIKQSFADRLSKYITKLK VNVDISKIKSPLDYKKIYEVGGAA EDARAVLGYYLAIYEQVADSCEEALPPLVIDTPN QQEQASGNYTNIKSISDGINNDR QYVICAMEHKALEQIKTNAQVIKLDARKILLQDQ YEKISKLRNEVIFD" /gene="YPO1097"
gene	complement(123317..1244 05)	
CDS	complement(123317..1244 05)	/gene="YPO1097"  /note="No significant database matches" /codon-start=1 /transl-table=11 /product="putative phage protein" /protein-id="CAC89941.1" /db-xref="GI:15979165" /db-xref="SPTREMBL:Q8ZH16" /translation="MDSEDTS DNPLSEPQRESAG AQS YDRFEYQYHWALCKAFSSYKE SNDFAIFMEYHEDVVYANSIDKNKVKFTFNQIKA NAKKTYTAKVLT KRENGTKPSLLG KLCSSVSDKKYFEKVEKLDFITTS GFNLTKNNKL NLASYKLSSLSSDEASEIIKCLSD ELANFGKFPPQEIIHFTTSDIPLESYYEHTISRIT DSVEEVYPQHLLRTKDIYRILMDS LRIRGKNVFDYENWNDALTKKALTYKDIHTVVTK IVSKGNSDLNFEAIIKYILDDLNLK GTIKAKIIQKINSYSLTLLSPTLAIIKAQKEIQE LLKKNSKKIEIEMSYELLERLIID LSKDTIGLFEDNISISSAIYEMVEATN"

	83)	complement(124484..1256 /gene="YPO1098"	/note="Similar to Escherichia coli prophage CP4-57 integrase SW:INTA-ECOLI (P32053) (413 aa) fasta scores: E(): 0, 57.8% id in 389 aa, and to Vibrio cholerae phage integrase VC0516 TR:Q9KUK2 (EMBL:AE004138) (413 aa) fasta scores: E(): 0, 52.7% id in 393 aa" /codon-start=1 /transl-table=11 /product="putative prophage integrase" /protein-id="CAC89942.1" /db-xref="GI:15979166" /db-xref="SPTREMBL:Q8ZH15" /translation="MARTTRPLTHTEVQKAKATD KDLTLHDGDLGLFLLVKTGKKIWR FRYQLPNSSKRTMISLGAYPALSLADAREIRA EKLQIA EESIFVNVARKWFELKESHVSAAHAKDIWRS IEK DILPSIENIPIQELKARTLIQVLE PIKARGALETVRRLVQRINEIMIYAVNVGLID AN PASGIGNAFERPKKQHMPTIRPEE LPKLMRTIAMSNSLSLPTRCLEWQLLTLIRPA EAA SATAWIEIDLLENKQWCIPAERMKA KRDHIVPLSEQALELLEIMRPISGNRQHVFP SRN DPRNHMNSQTANAALKRIGYGGKL VAHGLRSIASTAMNEAGFNADVIEAALAHSD KNE VRKAYNRSTYLIQRQELMNWWGLE IYTKRSI"
misc-feature	complement(124535..1250 62)	/gene="YPO1098"	/note="Pfam match to entry PF00589 Phage-integrase, Phage integrase family, score 116.60, E-value 4.7e-31"
misc-feature	complement(125799..1265 10)		/note="IS200-like insertion sequence: IS1541. Contains an 'A' at nucleotide position 315."
gene	complement(125907..1263 65)	/gene="tnp"	
CDS	complement(125907..1263 65)	/gene="tnp"	/note="synonym: YPO1099" /note="Similar to Salmonella typhimurium and Salmonella typhi transposase for insertion sequence IS200, TnpA, SW:TNPA-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 93.4% id in 152 aa. Almost identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 99.3% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC89943.1" /db-xref="GI:15979167" /db-xref="SPTREMBL:Q56938" /translation="MRDEKSLAHTRWCKYHIVF APKYRRQVFYREKRRAGSILRKL CEWKNVNILEAEYCVDHIHMLLEIPPKMSVSGFM GYLKKGKSSLMLEYEQFGDLKFKYRN REFWCRGYVDTVGKNTARIQEIYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	complement(126000..1263 11)	/gene="tnp"	/note="Pfam match to entry PF01797"

gene	126588..126951	like, -score 230.20, E-value 3e-65"
misc-RNA	126588..126951	/gene="ssrA"
		/gene="ssrA"
		/note="Similar to Escherichia coli small stable RNA molecule, tmRNA [10Sa RNA] (D12501), 91% identity in 333 nt overlap"
gene	complement(127000..127482)	/gene="smpB"
		/note="synonyms: b2620, smqB, YPO1101"
CDS	complement(127000..127482)	/gene="smpB"
		/note="Similar to Escherichia coli SsrA-binding protein SmpB SW:SMPB-ECOLI (P32052) (159 aa) fasta scores: E(): 0, 84.9% id in 159 aa, and to Vibrio cholerae SsrA-binding protein small protein B TR:Q9KTQ3 (EMBL:AE004170) (161 aa) fasta scores: E(): 0, 67.7% id in 161 aa"
		/codon-start=1
		/transl-table=11
		/product="SsrA-binding protein (small protein B)"
		/protein-id="CAC89944.1"
		/db-xref="GI:15979168"
		/db-xref="SWISS-PROT:Q8ZH14"
		/translation="MTKKKAYKPGSATIAQNKRA RHEYFIEEEFEAGLALQGWEVKSL RAGKANISDSYVMFKNGEAFLEFGATITPLNVAST HVVCEPMRTRKLLLNKRELDLSLFG RVNREGYTVVALSMYWKNAWVKVIGVAKGKKDN DKRDDIRDREWKLDKARIMKHANR "
misc-feature	complement(127243..127449)	/gene="smpB"
		/note="Pfam match to entry PF01668 SmpB, SmpB protein, score 161.50, E-value 1.4e-44"
misc-feature	complement(127351..127389)	/gene="smpB"
		/note="PS01317 Protein smpB signature."
gene	127643..128077	/gene="YPO1102"
CDS	127643..128077	/gene="YPO1102"
		/note="Similar to Escherichia coli hypothetical protein YfjG SW:YFJG-ECOLI (P52121) (158 aa) fasta scores: E(): 0, 79.3% id in 145 aa, and to Vibrio cholerae hypothetical protein VC0849 SW:Y849-VIBCH (P52122) (144 aa) fasta scores: E(): 0, 69.0% id in 142 aa"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAC89945.1"
		/db-xref="GI:15979169"
		/db-xref="SPTREMBL:Q8ZH13"
		/translation="MPQISRSALVPFSVKQMYQL VNDVRSYPEFLPGCTGSRVLDATE NEMIAAVDVAKAGISKTFTRNTLTDNQ SINMQL VDGPFPRKLMGGWHFTPLSADACKV ELHLDFFEFTNKLIELAFGKIFKELAGNMVQAFTQ RAKEVYSA"
gene	128070..128354	/gene="YPO1103"
CDS	128070..128354	/gene="YPO1103"
		/note="Similar to Escherichia coli hypothetical protein YfjF SW:YFJF-ECOLI (P52119) (96 aa) fasta scores: E(): 5.8e-24, 76.4% id in 89 aa, and to Vibrio

		SW:YFJF-VIBCH (P52120) (101 aa) fasta scores: E(): 2.4e-17, 60.9% id in 92 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89946.1" /db-xref="GI:15979170" /db-xref="SWISS-PROT:Q8ZH12" /translation="MPDIRVEVVYALSERQYLRT VSLVVGSTVEDAIKASGLLELRPD IDLEKNKVGIYSRPVKLGDKLNDGDRVEIYRPLI ADPKELRRQRAEQAKK" /gene="YPO1104"
gene	complement(128504..1288	
	54)	
CDS	complement(128504..1288	/gene="YPO1104"
	54)	
		/note="Similar to Escherichia coli small protein A precursor SmpA SW:SMPA-ECOLI (P23089) (113 aa) fasta scores: E(): 0, 78.8% id in 113 aa, and to Vibrio cholerae small protein A homolog precursor SmpA TR:Q9KTQ0 (EMBL:AE004170) (136 aa) fasta scores: E(): 3.1e-12, 36.8% id in 114 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89947.1" /db-xref="GI:15979171" /db-xref="SPTREMBL:Q8ZH11" /translation="MITMRCKMLTAAAVMLAMLT AGCSTLEKVVYRPDINQGNYSPI DASKIHKGMTQQQVAYTLGTPMLQDPFGTQTWFF VFRQQPGHEKITQQTTLTLTFDSSG VLTDIKNEPALTGS" /gene="YPO1104"
misc-feature	complement(128786..1288	
	18)	
		/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site." /gene="YPO1105"
gene	complement(128959..1306	
	38)	
CDS	complement(128959..1306	/gene="YPO1105"
	38)	
		/note="Similar to Escherichia coli DNA repair protein RecN SW:REC�-ECOLI (P05824) (553 aa) fasta scores: E(): 0, 74.3% id in 553 aa, and to Vibrio cholerae DNA repair protein RecN SW:REC�-VIBCH (P52118) (554 aa) fasta scores: E(): 0, 53.7% id in 553 aa" /codon-start=1 /transl-table=11 /product="DNA repair protein RecN" /protein-id="CAC89948.1" /db-xref="GI:15979172" /db-xref="SPTREMBL:Q8ZH10" /translation="MYRGFTMLVQLTISNFAIVR ELEIDFQPGMTAITGETGAGKSIA VDALGLCLGNRSDGSMVRLGATRADICARFSLAD TPSARQWLENNHLLDDNNECLLRA IGADGRSRGFINGTPVPVSQLRELQHLIQIHGQ HAHQLLLKPDHQKQLLDAYANQSS LLAEMKAAAYQIWHQSCRDLALHQQSLERTARQE LLQYQKELNSFSPQAGEYEQIDI EYKRLANSQGQLLSLSQQTLLQLLSDDEQNNILSQL YAAKHQLTELASMDEQFNLLNML EEASIQISEASDEL RHYAEQLDMDPNRLYELEKR LSRQLNLARKHHVAPEELPQFHQQ LLDEQELLSQQENDHEQLSNAVNTHYQQALAIK"

SMPHKGFAIETIFEPEHLSAEGATRIEFCVTTNP  
 GQPLQALVKVASGGELSRIALAIQ  
 VITARKMDTPALIFDEVDVGISGPTAAIVGRLLR  
 QLGESTQVMCVTHLPQVAGCGHQH  
 FFVSKQTDGTETETETHMRLDKKARLQELARLLGG  
 SEVTKNTLANAKELLAA"  
 /gene="YPO1105"  
 /note="PS00017 ATP/GTP-binding  
 site motif A (P-loop)."

misc-feature complement(130513..130536)  
 gene complement(130707..131588)  
 CDS complement(130707..131588)  
 /gene="YPO1106"  
 /note="Similar to Escherichia coli  
 hypothetical protein YfjB  
 SW:YFJB-ECOLI (P37768) (292 aa)  
 fasta scores: E(): 0, 82.9% id in  
 293 aa, and to Vibrio cholerae  
 hypothetical protein VC0853  
 TR:Q9KTP8 (EMBL:AE004170) (294 aa)  
 fasta scores: E(): 0, 59.3% id in  
 290 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="conserved hypothetical  
 protein"  
 /protein-id="CAC89949.1"  
 /db-xref="GI:15979173"  
 /db-xref="SWISS-PROT:Q8ZH09"  
 /translation="MNNRRFDCIGIVGHPRHPAA  
 LATHEILYHWLKARGYAVMVEQQI  
 AHDNLNLTDAITGSLADIGQKADLAVVVGGDGNML  
 GAARVLARYDIKVGIVNRGNLGLF  
 TDLDPDNALQQLSDVLEGEYLSEQRFLLETHVRR  
 TNQQSRISTAINEVVLHPGKVAHM  
 IEFEVYIDDRFAFSQRSDDLIIATPTGSTAYSLS  
 AGGPILTPTLDAIVLVPMFPHTLT  
 ARPLVISSSSSTIRLKFSHITSLEISCD SQIALP  
 IQEGEEVLIRRSDFHLNLIHPKDY  
 SYFNTLSTKLGWSKLFF"  
 /gene="YPO1106"  
 /note="Pfam match to entry PF01513  
 DUF15, Domain of unknown function  
 DUF15, score 397.30, E-value  
 1.5e-115"

misc-feature complement(130746..131522)  
 gene 131712..132290  
 CDS 131712..132290  
 /gene="YPO1107"  
 /note="Similar to Escherichia coli  
 GrpE protein SW:GRPE-ECOLI  
 (P09372) (197 aa) fasta scores:  
 E(): 0, 59.2% id in 179 aa, and to  
 Vibrio cholerae GrpE protein  
 TR:Q9KTP7 (EMBL:AE004170) (200 aa)  
 fasta scores: E(): 2.1e-28, 53.9%  
 id in 167 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="heat shock protein GrpE"  
 /protein-id="CAC89950.1"  
 /db-xref="GI:15979174"  
 /db-xref="SPTREMBL:Q8ZH08"  
 /translation="MSSKEQKTPNEQVSEEMENT  
 AEQQVEATQETGECVDPRAELEV  
 QLSDALQRERESLLRAKAEVENIRRRTEL DVEKA  
 HKFALERFSSELLPVIDNLERALD  
 TADKTNTELISMIEGVELTLKSLLDVAVGKFGIEV  
 VGETHVFPFNPEVHQAMTMLESADH  
 EPNHVMVMQKGYTLNGRLLRPAMVAVSKAKS"  
 /gene="YPO1107"  
 /note="Pfam match to entry PF01025  
 GrpE, GrpE, score 240.00, E-value  
 3.2e-68"

misc-feature 131778..132278  
 misc-feature 132141..132272  
 /gene="YPO1107"

gene	complement(132398..133678)	signature." /gene="gltA"  /note="synonyms: gluT, icdB, YPO1108"
CDS	complement(132398..133678)	/gene="gltA"  /EC-number="4.1.3.7" /note="Similar to Escherichia coli citrate synthase GltA SW:CISY-ECOLI (P00891) (427 aa) fasta scores: E(): 0, 86.7% id in 427 aa, and to Vibrio cholerae citrate synthase VC2092 TR:Q9KQA8 (EMBL:AE004283) (431 aa) fasta scores: E(): 0, 78.0% id in 422 aa" /codon-start=1 /transl-table=11 /product="citrate synthase GltA" /protein-id="CAC89951.1" /db-xref="GI:15979175" /db-xref="SPTREMBL:Q8ZH07" /translation="MADKKATLNLGEAAIELGVL SPTLGTDVIDVRTLGSKGYFTFDP GFTSTASCESKITYIDGDQGILLHRGFPIAQLAK DSTYLEVCYILLYGETPTPEEYKT FKTTTVTRHTMIHEQITRLFHGFRDRSDHPMAVLCG VTGALAAFYHDALDVNNERHREIT AFRLLSKMPTVAAMCYKYSLGQPFVYPRNDLSYA GNFLHMMFSTPCEKYEVPVLER MDRILILHADHEQNASTSTVRTAGSSGANPFACI AAGIASLWGPAGGGANEACLKMLE EIKTVEHIPEFIRRAKDKNDSFRLMGFGHRVYKN YDPRATVMRETCHVLEELKLNS LLEVAMELENIALNDPYFIEKKLYPNVDFYSGII LKAMGIPSSMFTVIFAIARTIGWI AHWNEMHNDGIKIARPRQLYTGTERDFQSQLKK "
misc-feature	complement(132455..133546)	/gene="gltA"  /note="Pfam match to entry PF00285 citrate-synt, Citrate synthase, score 783.50, E-value 4.5e-246"
misc-feature	complement(132737..132775)	/gene="gltA"  /note="PS00480 Citrate synthase signature."
gene	134388..134777	/gene="sdhC" /note="synonyms: cybA, YPO1109"
CDS	134388..134777	/gene="sdhC" /note="Similar to Escherichia coli succinate dehydrogenase cytochrome b556 subunit SdhC SW:DHSC-ECOLI (P10446) (129 aa) fasta scores: E(): 0, 77.2% id in 127 aa, and to Vibrio cholerae succinate dehydrogenase, cytochrome b556 subunit VC2091 TR:Q9KQA9 (EMBL:AE004283) (130 aa) fasta scores: E(): 0, 75.0% id in 124 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase cytochrome b-556 subunit" /protein-id="CAC89952.1" /db-xref="GI:15979176" /db-xref="SPTREMBL:Q8ZH06" /translation="MGKTVKKQRPVNLDLQTIRF PVTAIASILHRVSGVITFVAVGIL LWLLGLSVSSQEGFMAATIMNSFFVKFIFWGIL TALAYHICGGIRHLLMDFGYLEEN LAVGTRSAQVAMGLTLVLSVLAGVLVW"
misc-feature	134403..134756	/gene="sdhC"

misc-feature	134412..134486	Sdh-cyt, Succinate dehydrogenase cytochrome b subunit, score 165.60, E-value 8.3e-46" /gene="sdhC" /note="PS01000 Succinate dehydrogenase cytochrome b subunit signature 1."
misc-feature	134472..134540	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
misc-feature	134601..134669	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
misc-feature	134637..134678	/gene="sdhC" /note="PS01001 Succinate dehydrogenase cytochrome b subunit signature 2."
misc-feature	134712..134771	/gene="sdhC" /note="one of 3 probable transmembrane helices predicted for YPO1109 by TMHMM2.0"
gene	134771..135118	/gene="sdhD" /note="synonym: YPO1110"
CDS	134771..135118	/gene="sdhD" /note="Similar to Escherichia coli succinate dehydrogenase hydrophobic membrane anchor protein SdhD SW:DHSD-ECOLI (P10445) (115 aa) fasta scores: E(): 1.9e-32, 69.3% id in 114 aa, and to Vibrio cholerae succinate dehydrogenase, hydrophobic membrane anchor protein VC2090 TR:Q9KQB0 (EMBL:AE004283) (114 aa) fasta scores: E(): 1.1e-23, 57.4% id in 115 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase hydrophobic membrane anchor protein" /protein-id="CAC89953.1" /db-xref="GI:15979177" /db-xref="SPTREMBL:Q8ZH05" /translation="MVSNASALGRNGVHDWLLLR ASAIVITLYVFYILGFVIVPDIT YEIWRGFFASHITKVFTLLTLLSILAHAWIGLWQ VLTDYIKPLAIRLVQLVTVVITLL VYLLYGTIVVWGA"
misc-feature	134819..134887	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
misc-feature	134945..135013	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
misc-feature	135041..135109	/gene="sdhD" /note="one of 3 probable transmembrane helices predicted for YPO1110 by TMHMM2.0"
gene	135119..136885	/gene="sdhA" /note="synonym: YPO1111"
CDS	135119..136885	/gene="sdhA" /EC-number="1.3.99.1" /note="Similar to Escherichia coli succinate dehydrogenase flavoprotein subunit SdhA SW:DHSA-ECOLI (P10444) (588 aa) fasta scores: E(): 0, 92.0% id in 588 aa, and to Vibrio cholerae succinate dehydrogenase, flavoprotein subunit VC2089"



		fasta scores: E(): 0, 82.3% id in 588 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase flavoprotein subunit" /protein-id="CAC89954.1" /db-xref="GI:15979178" /db-xref="SPTREMBL:Q8ZH04" /translation="MNLPIREFDAVVVGAGGAGM RAALQISQMGLSCALISKVFPTRS HTVSAQGGITVALGNTHEDNWEWHMYDTVKGS DY IGDQDAIEYMCKTGPEAVLELEHM GLPFSRLEDGSIYQRPFGGQSLNFGGGQAARTAA AADRTGHALLHTLYQQNLKNHTTI FSEWYALDLVKNQDGA FVGCTAINIETGEVVYFK ARATILATGGAGRIYQSTTNAHIN TGDGVGMALRAGVPVQDMEMWQFHPTGIAGAGVL VTEGCRGEGGYLLNKHGERFMERY APNAKDLAGR DVVARSIMIEIREGRGCDGPWGP H AKLKLDHLGKDVLESRLPGILELS RTFAHVDPIKEPIPVIPPTCHYMMGGIPTKV TGQA ITVNEKGEDVVIPGLFAVGEIACV SVHGANRLGGNSLLDLVVFGRAAGMHLQESLMEQ GASRDASESDIEASLARMNRWNNT RSGEDPVEIRKALQACMQNNFSVFREGDAMAKGL EELKTIRERLQARLDDTSSEFNT QRIECLELDNLMETAFSTAVSANFRTESRGAHSR FDFPDRDDVNWLCHSLYLPGTESM TRREVMQPKLREAFPPKVR SY" /gene="sdhA" /note="PS00504 Fumarate reductase / succinate dehydrogenase FAD-binding site."
misc-feature	135245..135274	
misc-feature	135440..136438	/gene="sdhA" /note="Pfam match to entry PF00890 FAD-binding-2, FAD binding domain, score 733.90, E-value 7.1e-217"
gene	136935..137651	/gene="sdhB" /note="synonym: YPO1112"
CDS	136935..137651	/gene="sdhB" /EC-number="1.3.99.1" /note="Similar to Escherichia coli succinate dehydrogenase iron-sulfur protein SdhB SW:DHSB-ECOLI (P07014) (238 aa) fasta scores: E(): 0, 90.8% id in 238 aa, and to Vibrio cholerae succinate dehydrogenase, iron-sulfur protein VC2088 TR:Q9KQB2 (EMBL:AE004283) (236 aa) fasta scores: E(): 0, 80.2% id in 237 aa" /codon-start=1 /transl-table=11 /product="succinate dehydrogenase iron-sulfur protein" /protein-id="CAC89955.1" /db-xref="GI:15979179" /db-xref="SPTREMBL:Q8ZH03" /translation="MKLEFSIYRYNPDVDNAPHM QDYTLDAEEGRDMMLLDALIQ LKE KDPTLSFRRSCREGVCGSDGLNMNGKNGLACITP ISALQKGNKKIVIRPLPGLPVVRD LVVDMGQFYTQYEKIKPYLLNDGKNPPAREHLQS PEQRAKLDGLYECILCACCSTSCP SFWWNPDKFVGPAGLLAAYRFLIDSRDTETASRL DDLDDAFSVFRCHSIMNCVSVCPK GLNP TKAIGHIKSM LLQRSA" /gene="sdhB" /note="Pfam match to entry PF00111 fer2, 2Fe-2S iron-sulfur cluster binding domains, score 8.70, E-value 0.96"
misc-feature	136980..137177	/gene="sdhB" /note="Pfam match to entry PF00111 fer2, 2Fe-2S iron-sulfur cluster binding domains, score 8.70, E-value 0.96"
misc-feature	137379..137414	/gene="sdhB"

gene	138007..140814	iron-sulfur binding region signature."
CDS	138007..140814	/gene="sucA" /note="synonym: YPO1113" /gene="sucA" /EC-number="1.2.4.2" /note="Similar to Escherichia coli 2-oxoglutarate dehydrogenase E1 component SucA SW:ODO1-ECOLI (P07015) (933 aa) fasta scores: E(): 0, 87.8% id in 935 aa, and to Vibrio cholerae 2-oxoglutarate dehydrogenase, E1 component VC2087 TR:Q9KQB3 (EMBL:AE004282) (936 aa) fasta scores: E(): 0, 73.8% id in 936 aa" /codon-start=1 /transl-table=11 /product="2-oxoglutarate dehydrogenase E1 component" /protein-id="CAC89956.1" /db-xref="GI:15979180" /db-xref="SPTREMBL:Q8ZH02" /translation="MQNGAMKAWLDSSYLAGANQ SYIEQLYEDFLTDPGSVDDSWRSI FQQLPTTGVPDQLHSQTREYFRRLLAKDSTRYNS SINDPDIDAKQVKVLQLINAFRR GHQHANLDPLGLWKQESVPDLDPsyhnlteADFQ NTFNVGSFAIGKETMKLADLYAAL KQTYCGSVGAEMYHITNTEEKRWIQQRIESVVGK PTFSDAEKRRFLSELTAAGLERY LGAKFPGAKRFSLEGGDSLVTMLKEMIRHAGKNG TREVVLGMAHRGRLNVLINVLGKK PEDLFDEFAGKKHEHLGTGDVKYHQGFSSDVETE GGLVHLALAFNPSHLEIVSPVIG SVRARRDRDLDEARSNMVLPITIHGDAAITGQGVV QETLNMSQARGYEVGGTVRIVINN QIGFTTSNPLDARSTQYCTDIKVMQAPIFHVNA DDPEAVAFVTRLALDFRNTFKRDV MIDLVCYRRHGHNEADEPSATQPVMYQKIKKHPT PRKIYADKLI EQNIASLEDATEMV NLYRDALDHGDCVVEWRP MNLQSF TWSPYLNHE WDEAYPSKVEMKRLQELARRISSA PEAIEMQSRVAKIYSDRALMASGEKPFDWGGAET LAYATLVDEGIPIRLSGEDAGRGT FFHRHAVIHNQKNGSVYVPLSNIHSGQGDFQVWD SVLSEEAVLAFEYGYATAEPRTL IWEAQFGDFANGAQVVIDQFISSGEQKWGRMCGL VMLLPHGYEGQGPEHSSARLERYL QLCAEQNMQVCIPSTPAQVYHMIRRQALRGMRRP LIVMSPKSLRLRHPLATSSSLELAN GSFLPAIGEIDELDPKGIKRVVMCSGKVYYDLLE QRRKNGQTDVAIVRIEQLYPFPHQ AVQSVLEQYAHVHDFVWCQEEPLNQAWYCSQHN FREVIPFGASLRYAGRPASASPAV GYLSVHQKQQQALVNDALNVE"
misc-feature	138625..139599	/gene="sucA" /note="Pfam match to entry PF00676 E1-dehydrog, Dehydrogenase E1 component, score 115.00, E-value 1.5e-30"
gene	140844..142067	/gene="sucB"
CDS	140844..142067	/note="synonym: YPO1114" /gene="sucB" /EC-number="2.3.1.61" /note="Similar to Escherichia coli dihydroliipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex SucB SW:ODO2-ECOLI (P07016) (404 aa) fasta scores: E(): 0, 84.2% id in 406 aa, and to Vibrio cholerae 2-oxoglutarate dehydrogenase, E2 component, dihydroliipoamide"

TR:Q9KQB4 (EMBL:AE004282) (404 aa)  
 fasta scores: E(): 0, 75.1% id in  
 405 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="dihydrolipoamide  
 succinyltransferase component of  
 2-oxoglutarate dehydrogenase  
 complex"  
 /protein-id="CAC89957.1"  
 /db-xref="GI:15979181"  
 /db-xref="SPTREMBL:Q8ZH01"  
 /translation="MSSVDINVPDLPESVADGSV  
 ATWHKKPGDSVVKRDEVLVEIETDK  
 VILEVPASQDGILDAILEDEGATVTSRQVLGRIR  
 PSDSSGKPTEEKSQSTESTPAQRQ  
 TASLEEEESNETLSPAIRRLIAEHDLDATAIKGSG  
 VGGRITREDVDSHLASRKSASAVV  
 ADAKAVAAAAPVLAGRSEKRVPMRLRKRVAERL  
 LEAKNSTAMLTTFNEINMQPIMDL  
 RKQYGEAFEKRHGVRLGFMSFYIKAVVEALKRYP  
 EVNASIDGEDVVYHNYFDVSIASV  
 TPRGLVTPVLRDVTLSMADIEKKIKELAVKGRD  
 GKLKVEELTGGNFTITNGGVFGSL  
 MSTPIINPPQSAILGMHAIKDRPMAVNGQVVILP  
 MMYLALSVDHRLIDGRESVGYLVT  
 VKEMLEDPARLLLDV"

misc-feature 140853..141074

/gene="sucB"  
 /note="Pfam match to entry PF00364  
 biotin-lipoyl, Biotin-requiring  
 enzymes, score 90.40, E-value  
 3.7e-23"

misc-feature 141402..142061

/gene="sucB"  
 /note="Pfam match to entry PF00198  
 2-oxoacid-dh, 2-oxo acid  
 dehydrogenases acyltransferase  
 (catalytic domain), score 364.60,  
 E-value 1e-105"

gene 142180..143346

/gene="sucC"  
 /note="synonyms: b0728, YPO1115"

CDS 142180..143346

/gene="sucC"  
 /EC-number="6.2.1.5"  
 /note="Similar to Escherichia coli  
 succinyl-CoA synthetase beta chain  
 SW:SUC-ECOLI (P07460) (388 aa)  
 fasta scores: E(): 0, 92.8% id in  
 388 aa, and to Vibrio cholerae  
 succinyl-CoA synthase, beta  
 subunit VC2085 TR:Q9KQB5  
 (EMBL:AE004282) (388 aa) fasta  
 scores: E(): 0, 77.1% id in 388  
 aa"

/codon-start=1  
 /transl-table=11  
 /product="succinyl-CoA synthetase  
 beta chain"  
 /protein-id="CAC89958.1"  
 /db-xref="GI:15979182"  
 /db-xref="SWISS-PROT:Q8ZH00"  
 /translation="MNLHEYQAKQLFARYGMPAP  
 TGYACTTPREAEAAASKIGAGPWV  
 VKCQVHAGGRGKAGGVKLVNSKEDIRAFAEQWL  
 KKLVTYQTDANGQPVHQILVEAAT  
 DIDKELYLGAVIDRSSRRVVFMASTEGGVEIEKV  
 AEETPELIHKIALDPLTGPQPYQG  
 RELAFKLGLTGKQVGQFTKIFMGLATLFLERDLA  
 MVEINPLVVTKQGDLCIDGKLGA  
 DGNALFRQPELREMRDPSQEDAREAHAAQWELNY  
 VALDGNIGCMVNGAGLAMGTMDIV  
 KLHGGEPAFLDVGGGATKERVTEAFKIILSDDK  
 VKAVFVNIFGGIVRCDLIADGIIG  
 AVEEVGVNVPVVVRLEGNNALGAKKLADSG  
 LNI  
 IAATSLTDAAQQVVAAGVAK"

misc-feature 142264..142773

/gene="sucC"  
 /note="Pfam match to entry PF02222"

misc-feature	142915..143343	213.20, E-value 4e-60" /gene="sucC" /note="Pfam match to entry PF00549 ligase-CoA, CoA-ligases, score 280.20, E-value 2.6e-80"
misc-feature	142948..143022	/gene="sucC" /note="PS01217 ATP-citrate lyase / succinyl-CoA ligases family signature 3."
gene	143346..144218	/gene="sucD" /note="synonym: YPO1116"
CDS	143346..144218	/gene="sucD" /EC-number="6.2.1.5" /note="Similar to Escherichia coli succinyl-CoA synthetase alpha chain SW:SUCD-ECOLI (P07459) (288 aa) fasta scores: E(): 0, 90.9% id in 287 aa, and to Vibrio cholerae succinyl-CoA synthase, alpha subunit VC2084 TR:Q9KQB6 (EMBL:AE004282) (290 aa) fasta scores: E(): 0, 85.4% id in 287 aa" /codon-start=1 /transl-table=11 /product="succinyl-CoA synthetase alpha chain" /protein-id="CAC89959.1" /db-xref="GI:15979183" /db-xref="SPTREMBL:Q8ZGZ9" /translation="MSILIDKNTKVICQGFTGSQ GTFHSEQAIAYGTKMVGGVTPGKG GTQHLGLPVFNTVREAVETTGATASVIYVPAPFC KDSILEAIDAGIKLIICITEGIPT LDMLVVKVRLEQSDARMIGPNCPGVITPGECKIG IMPGHIHLPGKVGIVSRSGTLTYE AVKQTTDIGFGQSSCVGIGGDPPIPGSNFIDILKL FQEDPQTEVIVMIGEIGGNAEEEA AAYIKEHVTKPVVGYIAGVTAPKKGKRMGHAGAI AGGKGTADDKFAALEAAGVKT VRS LAEIGNAVKAVLPQ"
misc-feature	143742..144185	/gene="sucD" /note="Pfam match to entry PF00549 ligase-CoA, CoA-ligases, score 225.20, E-value 9.4e-64"
misc-feature	143799..143888	/gene="sucD" /note="PS01216 ATP-citrate lyase / succinyl-CoA ligases family signature 1."
misc-feature	144051..144092	/gene="sucD" /note="PS00399 ATP-citrate lyase / succinyl-CoA ligases family active site."
gene	144985..146553	/gene="cydA" /note="synonym: YPO1117"
CDS	144985..146553	/gene="cydA" /EC-number="1.10.3.-" /note="Similar to Escherichia coli cytochrome D ubiquinol oxidase subunit I SW:CYDA-ECOLI (P11026) (522 aa) fasta scores: E(): 0, 86.6% id in 522 aa" /codon-start=1 /transl-table=11 /product="cytochrome D ubiquinol oxidase subunit I" /protein-id="CAC89960.1" /db-xref="GI:15979184" /db-xref="SPTREMBL:Q8ZGZ8" /translation="MFDIVELSRLOFALTAMYHF LFVPLTLGLAFLLAIMESVYVLSG KQIYKDMTKFWGKLFAINFALGVATGLTMEFQFG TNWSYFSHYVGDIFGAPLAIEGLM AFFLESTFVGLFFFGWDRDLTKHQHLAVTWLVALG SNFSALWILVANGWMQNPIASDFN"

GAMFILGISSYYLLKGRDIPFAKR  
 SFAIAASFGLASVLSVIVLGDESGYEMGDVQKTK  
 LAAIEAEWETQPPPAFTLFAIPN  
 QETMENRFAIQIPYALGLIATRLDTPVIGLRDL  
 MSQHEVRIRNGIQAYSLLLEQLRGG  
 NTDPAVRDAFNKAKQDLGYGMLLKRYTENVADAT  
 EEQIQLAAQDSIPRVLPLYFAFRI  
 MVACGFLMLLIIGLAFYNVVRGRIGEKKWLLRAA  
 LYGIPLPWIAVEAGWFVAEYGRQP  
 WAIGEVLPTAVANSSVTAGEILFSMALICGLYTL  
 FLIAEMYLMFKFARLGPSSLKTGR  
 YHFEQPTAPVQEAR"

misc-feature 145003..146517

/gene="cydA"  
 /note="Pfam match to entry PF01654  
 Bac-Ubq-Cox, Bacterial Cytochrome  
 Ubiquinol Oxidase, score 1092.40,  
 E-value 0"

misc-feature 145042..145110

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 145144..145212

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 145270..145338

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 145357..145425

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 145537..145605

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 145639..145698

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 146143..146211

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 146245..146313

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

misc-feature 146380..146448

/gene="cydA"  
 /note="one of 9 probable  
 transmembrane helices predicted  
 for YPO1117 by TMHMM2.0"

gene 146568..147707

/gene="cydB"  
 /note="synonym: YPO1118"

CDS 146568..147707

/gene="cydB"  
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 /note="Similar to Escherichia coli  
 cytochrome D ubiquinol oxidase  
 subunit II SW:CYDB-ECOLI (P11027)  
 (379 aa) fasta scores: E(): 0,  
 78.4% id in 379 aa"  
 /codon-start=1  
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 /product="cytochrome D ubiquinol  
 oxidase subunit II"  
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 /db-xref="GI:15979185"  
 /db-xref="SPTREMBL:Q8ZGZ7"  
 /translation="MFDYEVLRFIWLLIGVLLI  
 GFAVTDGFDMGVIGILLRIIGKNDT  
 ERRIMINSIAPHWDGNQVWLITAGGALFAAWPMV  
 YAAAFSGFYIAMILVLAALFFRPV  
 GFDYRSKLENSRWRNMWDWGIFIGSFVPAVVFGV  
 AFGNLLQGVPFHMNEYMRLFYTGN"

misc-feature 146580..147668

misc-feature 146586..146639

misc-feature 146799..146867

misc-feature 146928..146996

misc-feature 147054..147122

misc-feature 147183..147236

misc-feature 147354..147422

misc-feature 147441..147509

misc-feature 147567..147635

gene 147799..148131  
CDS 147799..148131

misc-feature 147886..147939

misc-feature 147982..148041

misc-feature 148054..148122

ELHLRSRKAQISALVMSVAFLLA  
GIWLVKGIDGFVITSVLDTAESNPMRKEVAHQ  
GAWLINFNKYPILWALPALGVILP  
LFTILLSRFEKGAWAFLFSSLTIACVILTAGVTM  
FPFVMPSSSTMPNVSLTMWDATSSL  
LTLKVMITIVAIIFVPIILLYTSWCYYKMFGRI  
DK  
EFIENNKHSLY"  
/gene="cydB"  
/note="Pfam match to entry PF02322  
Cyto-ox-2, , score 714.90, E-value  
3.7e-211"  
/gene="cydB"  
/note="one of 8 probable  
transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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/note="one of 8 probable  
transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
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/note="one of 8 probable  
transmembrane helices predicted  
for YPO1118 by TMHMM2.0"  
/gene="YPO1119"  
/gene="YPO1119"  
/note="Similar to Escherichia coli  
protein YbgE SW:YBGE-ECOLI  
(P37343) (97 aa) fasta scores:  
E(): 6e-22, 59.6% id in 89 aa, and  
to Vibrio cholerae hypothetical  
protein VC1841 TR:Q9KR06  
(EMBL:AE004260) (105 aa) fasta  
scores: E(): 4.3e-08, 34.5% id in  
84 aa"  
/codon-start=1  
/transl-table=11  
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protein"  
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/db-xref="SPTREMBL:Q8ZGZ6"  
/translation="MKPTQQLKPLTMATTMLSDK  
LYELMDKGPLRALSLVLAFAALFC  
VFWDPTRFAAATSSLEVWQEVFIVWAVCTGVIHG  
VGFRPKQVWLRAFFAPLPAIVILA TGLFYFFA"  
/gene="YPO1119"  
/note="one of 3 probable  
transmembrane helices predicted  
for YPO1119 by TMHMM2.0"  
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/note="one of 3 probable  
transmembrane helices predicted  
for YPO1119 by TMHMM2.0"  
/gene="YPO1119"  
/note="one of 3 probable

gene	148263..148664	for YPO1119 by TMHMM2.0"
CDS	148263..148664	/gene="YPO1120"
		/gene="YPO1120"
		/note="Similar to Escherichia coli hypothetical protein YbgC SW:YBGC-ECOLI (P08999) (134 aa) fasta scores: E(): 0, 72.2% id in 133 aa"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="CAC89963.1"
		/db-xref="GI:15979187"
		/db-xref="SPTREMBL:Q8ZGZ5"
		/translation="MSNTLFRWPVRVYFEDTDAG GMVYHARYVAFYERARTEMLRQRN FHQQQLLSEHVAFVRSMTVEYLAAPARLDDMLEV QSEVTAMRGASLTFAQRILDSHGN LLSSAEVLIACIDPHQMKPRALPKSIVAEFK"
gene	148664..149350	/gene="tolQ"
		/note="synonym: YPO1121"
CDS	148664..149350	/gene="tolQ"
		/note="Similar to Escherichia coli TolQ protein SW:TOLQ-ECOLI (P05828) (230 aa) fasta scores: E(): 0, 89.4% id in 227 aa"
		/codon-start=1
		/transl-table=11
		/product="TolQ colicin import protein"
		/protein-id="CAC89964.1"
		/db-xref="GI:15979188"
		/db-xref="SPTREMBL:Q8ZGZ4"
		/translation="MADMNILDLEFLQASLFVKLI MLVLMGFSIASWAIITQTRILNA ATRDAEAFEDKFWSGIELSRLYQESQARRDTLSG SEQIFHSGFKEFARLHRANSHAPE AVIDGASRAMRISMNRELEALETHIPFLGTVGSI SPYIGLFGTVWGIMHAFISLGAVK QATLQMVAPGIAEALIAATAIGLFAAIPAVMAYNR LNQHVNKLEQNYDNFMEEFIAILH RQAFATESK"
misc-feature	148706..148774	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
misc-feature	148880..149296	/gene="tolQ"
		/note="Pfam match to entry PF01618 MotA-ExbB, MotA/TolQ/ExbB proton channel family, score 220.60, E-value 2.4e-62"
misc-feature	149060..149128	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
misc-feature	149171..149239	/gene="tolQ"
		/note="one of 3 probable transmembrane helices predicted for YPO1121 by TMHMM2.0"
gene	149363..149791	/gene="tolR"
		/note="synonym: YPO1122"
CDS	149363..149791	/gene="tolR"
		/note="Similar to Escherichia coli TolR protein SW:TOLR-ECOLI (P05829) (142 aa) fasta scores: E(): 0, 83.1% id in 142 aa, and to Vibrio cholerae TolR membrane protein vc1838 TR:Q9KR09 (EMBL:AE004259) (146 aa) fasta scores: E(): 5.5e-15, 39.4% id in 137 aa"
		/codon-start=1
		/transl-table=11
		/product="TolR colicin import

misc-feature 149387..149788

misc-feature 149411..149479

gene 149903..151069

CDS 149903..151069

misc-feature 149939..150007

gene 151189..152481

CDS 151189..152481

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/db-xref="SPTREMBL:Q8ZGZ3"
/translation="MARVRGRKRRELKSEINIVP
LLDVLLVLLLIIFMATAPIITQSVE
VNLPDATDSKTVSSDDNPPVIVEVSGVGQYTVVV
DHQRMELLPSQVVAEAQARLKTN
PKTVFLIGGAKEVPYDEIIKALNMLHQAGVTSVG
LMTQPI"
/gene="tolR"
/note="Pfam match to entry PF02472
ExbD, , score 67.50, E-value
2.8e-16"
/gene="tolR"
/note="1 probable transmembrane
helix predicted for YPO1122 by
TMHMM2.0"
/gene="tolA"
/note="synonym: YPO1123"
/gene="tolA"
/note="Similar to Escherichia coli
TolA protein SW:TOLA-ECOLI
(P19934) (421 aa) fasta scores:
E(): 5.1e-27, 57.9% id in 423 aa,
and to Pseudomonas aeruginosa TolA
protein SW:TOLA-PSEAE (P50600)
(347 aa) fasta scores: E():
6.6e-09, 33.2% id in 319 aa"
/codon-start=1
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/product="TolA colicin import
membrane protein"
/protein-id="CAC89966.1"
/db-xref="GI:15979190"
/db-xref="SPTREMBL:Q8ZGZ2"
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KQAETAAAQAKAEADKIVKAQAEQKKAEAEAKK
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KAAADAAEKKAAADAEEKKAAAANKVAAAAEAKKK
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PKSGSGAGAAAAGKGGGKSGASGADISGYLGQI
TGAIQSKFYDADLYKGRTCDLRIK
LAPDGLLIDVKAEGGDPALCQAAIAAAKQAKIPK
PPSTDVYEQFKNAPLVFKPQ"
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/note="1 probable transmembrane
helix predicted for YPO1123 by
TMHMM2.0"
/gene="tolB"
/note="synonym: YPO1124"
/gene="tolB"
/note="Similar to Escherichia coli
TolB protein precursor
SW:TOLB-ECOLI (P19935) (430 aa)
fasta scores: E(): 0, 84.9% id in
430 aa"
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/transl-table=11
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protein"
/protein-id="CAC89967.1"
/db-xref="GI:15979191"
/db-xref="SPTREMBL:Q8ZGZ1"
/translation="MKQAFRVALGFLVLWASVLH
AEVRIEITQGVDSARPIGVVPFKW
MGPGTPPEEIGAIVGADLRNSGKFNPIDAARMPQ
QPSTAAEVTAAWTALGIDAVVVG
QVQPSADGSYVVSQYQLVDTSGSAGSILAQNQYKV
TKQWLRYSHTVSDEVFEKLTGIK
GAFRTRIAYVVKTNNGKFPHELRSYDYGYNQFV
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		FESGKSALVIQTLANGAIRQVASFPRHNGAPAFS PDGTKLAFALSKSGSLNLYVMDLA SGQISQVTDGRSNNTEPSWFPDSQNLAYTSDQGG RPQVYKVNINGGVPQRITWEGSQN QNADVSPDGKFLVLVSSNGGAQHIAKQDLETGAV QVLTDTLLDETSPSIAPNGTMVIYS STQGLGSVLQLVSTDGRFKARLPATDGQVKFPAW SPYL"
gene	152532..153038	/gene="pal"
CDS	152532..153038	/note="synonyms: excC, YPO1125" /gene="pal" /note="Similar to Escherichia coli peptidoglycan-associated lipoprotein precursor Pal or ExcC SW:PAL-ECOLI (P07176) (173 aa) fasta scores: E(): 0, 84.4% id in 173 aa, and to Vibrio cholerae peptidoglycan-associated lipoprotein vc1835 TR:Q9KR12 (EMBL:AE004259) (172 aa) fasta scores: E(): 0, 59.9% id in 172 aa" /codon-start=1 /transl-table=11 /product="peptidoglycan-associated lipoprotein Pal" /protein-id="CAC89968.1" /db-xref="GI:15979192" /db-xref="SPTREMBL:Q8ZGZ0" /translation="MQLNKVLKGLMLALPVLAVA ACSSNKSANNDQSGMGAGTGTENG SNLSSEEQARLQMQLQKNNIVYFGFDKYDIGSD FAQMLDAHAAFLRSNPSDKVVVEG HADERGTPEYNIALGERRASAVKMYLQGKGVSA QISIVSYGKEKPAVLGHDEAAFAK NRRAVLVY"
misc-feature	152565..152597	/gene="pal" /note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site."
misc-feature	152730..153017	/gene="pal" /note="Pfam match to entry PF00691 OmpA, OmpA family, score 171.40, E-value 1.5e-47"
misc-feature	152829..152963	/gene="pal" /note="PS01068 OmpA-like domain."
gene	153048..153857	/gene="YPO1126"
CDS	153048..153857	/gene="YPO1126" /note="Similar to Escherichia coli hypothetical 28.2 kDa protein in pal-lyst intergenic region precursor YbgF SW:YBGF-ECOLI (P45955) (263 aa) fasta scores: E(): 0, 70.0% id in 270 aa, and to Pseudomonas aeruginosa periplasmic protein TR:Q9RNV2 (EMBL:AF177774) (274 aa) fasta scores: E(): 6.6e-17, 34.2% id in 225 aa" /codon-start=1 /transl-table=11 /product="putative exported protein" /protein-id="CAC89969.1" /db-xref="GI:15979193" /db-xref="SPTREMBL:Q8ZGY9" /translation="MNSNFRRLVGLSLLVGVAV PWAATAQAPISNVGSGSVEDRVTO LERISNAHSQLLTQLQQQLSDSQRDVDSLGRGQIQ ESQYQLNQVVERQKQIYQQMESLS GGQGAQNSASAASGATADNTAAGSSGNADAGAAA STAAPAASTGDENSDYNVAVSLAL EKKQYDQAITVFQSFVKQYQPKSTYQPNANYWLGO LYYNKGKKDDAAYYYAVVVKNYPK SPKSSEAMFKVGVIMQDKGQSDKAKAVYQQVIKQ YPNTDAKQAQKRLSAL"
misc-feature	153603..153704	/gene="YPO1126"

misc-feature	153714..153815	TPR, TPR Domain, score 8.70, E-value 5.6" /gene="YPO1126" /note="Pfam match to entry PF00515 TPR, TPR Domain, score 11.80, E-value 2.6"
tRNA	154048..154123	/product="tRNA-Lys" /note="tRNA Lys anticodon TTT, Cove score 95.27"
tRNA	154151..154226	/product="tRNA-Lys" /note="tRNA Lys anticodon TTT, Cove score 95.27"
tRNA	154255..154324	/note="tRNA Pseudo anticodon TTT, Cove score 40.49"
gene	154693..155754	/gene="nadaA"
CDS	154693..155754	/note="synonyms: nicA, YPO1127" /gene="nadaA" /note="Similar to Escherichia coli quinolinate synthetase A NadA or Nica SW:NADA-ECOLI (P11458) (347 aa) fasta scores: E(): 0, 82.1% id in 346 aa" /codon-start=1 /transl-table=11 /product="quinolinate synthetase A" /protein-id="CAC89970.1" /db-xref="GI:15979194" /db-xref="SWISS-PROT:Q8ZGY8" /translation="MSEIFDVNAAIYPFPARPVP LDTNEKAFYREKIKTLLKQORDAVL VAHYITDPEIQALAEETGGCVADSLEMARFGNNH PASTLLVAGVRFMGETAKILNPEK KVLMPITLNAECSLDLGCVPDEFATFCDSHPDRTV VVYANTSAAVKAKADWVVTSSIAV ELIEHLDSLGEKIIWAPDRHLGSYVQKKSGADVL CWQGACIVHDEFKTQALARMKALY PDAAVLVHPESPQAVVDMADAVGSTSQLIQAAKT LPQKTLIVATDRGIFYKMQQACPD KELFEAPTAGEGATCRSCAHCPPWMAMNGLRAIAE GLEQGGVMHEIHVDEELRQQALIP LNRMLDFANQLKLQVKGNA"
misc-feature	154777..155715	/gene="nadaA" /note="Pfam match to entry PF02445 NadA, , score 609.80, E-value 1.6e-179"
gene	155876..156601	/gene="pnuC"
CDS	155876..156601	/note="synonym: YPO1128" /gene="pnuC" /note="Similar to Escherichia coli PnuC protein SW:PNUC-ECOLI (P31215) (239 aa) fasta scores: E(): 0, 76.1% id in 238 aa" /codon-start=1 /transl-table=11 /product="integral membrane NMN transport protein PnuC" /protein-id="CAC89971.1" /db-xref="GI:15979195" /db-xref="SPTREMBL:Q8ZGY7" /translation="MDFLSTGNILVHIPLGAGGY DLWIEAIGTLFGLLCIWFASKEK IINYLFGLINVTLFAVIFQIQLYASLLLQLFFF GANIYGWYAWSKQTPDNQAEKIR WLSLPKALAWAAVCIAGIVLMTLHIDTVFAWLTR VAVTVMQSLGANVQMPPELQDAFP FWDSTMMVLSIAAMILMTRKYVENWLIWVVIDVI SVAIFAYQGVYAMALEYAFITLIA LNGSWLWIKSAARNHSRPLSTQG"
misc-feature	155933..155992	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156011..156079	/gene="pnuC" /note="one of 7 probable

misc-feature	156089..156142	for YPO1128 by TMHMM2.0" /gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156203..156271	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156347..156406	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156425..156484	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
misc-feature	156494..156553	/gene="pnuC" /note="one of 7 probable transmembrane helices predicted for YPO1128 by TMHMM2.0"
gene	complement(156716..1576 54)	/gene="YPO1129"
CDS	complement(156716..1576 54)	/gene="YPO1129"  /note="Similar to Escherichia coli hypothetical 34.7 kDa protein in pnuC-aroG intergenic region YbGR SW:YBGR-ECOLI (P75757) (313 aa) fasta scores: E(): 0, 66.1% id in 307 aa, and to Bacillus subtilis cation transport protein TR:O07084 (EMBL:U93876) (311 aa) fasta scores: E(): 0, 41.4% id in 309 aa" /codon-start=1 /transl-table=11 /product="putative cation transport protein" /protein-id="CAC89972.1" /db-xref="GI:15979196" /db-xref="SWISS-PROT:Q8ZGY6" /translation="MAVSTIFSQDSNSKRLLI AF AITTLFMVTEAIGGWLSGSLALLA DAGHMLTDSAALFIALMAVHFSQRKPDPRHTFGY LRLTTLA AFVNAAALLLIVILIVW EAVHRRFFSPHEVMGTPMLIIAIAIGLLANIFCFWI LHKGEEKKNINVRAAALHVLSDLL GSVGAMIAAIVILTTGWTPIIDPILSVLVSVLILR SAWRLKESFHELLEGAPQEIDIN KLRKDLCTNIYEVARNIHVHLWQVGEQRLMTLHA QVIPPLDHDALLQRIQDYLLHHYR ISHATVQMEYQHCGTPDCGINQAAPADGHRHHH HE"
misc-feature	complement(156791..1574 50)	/gene="YPO1129"  /note="Pfam match to entry PF01545 Cation-efflux, Cation efflux family, score 250.50, E-value 2.3e-71"
misc-feature	complement(157139..1572 04)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"
misc-feature	complement(157244..1573 09)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"
misc-feature	complement(157355..1574 20)	/gene="YPO1129"  /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0"

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10)~
misc-feature complement(157541..157606) /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0" /gene="YPO1129"
gene join(158103..159062, 161022..161114) /note="one of 5 probable transmembrane helices predicted for YPO1129 by TMHMM2.0" /gene="aroG"
CDS join(158103..159062, 161022..161114) /note="synonym: YPO1130" /pseudo /gene="aroG"
/EC-number="4.1.2.15"
/note="Similar to Escherichia coli phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive AroG SW:AROG-ECOLI (P00886) (350 aa) fasta scores: E(): 0, 86.6% id in 320 aa. The IS insertion occurred near the C-terminal end (following codon 320). This CDS is disrupted by the insertion of IS100. The insertion occurred near the C-terminus. It is not clear whether this insertion affects the function of the protein." /pseudo /codon-start=1 /transl-table=11 /product="phospho-2-dehydro-3-deoxyheptonate aldolase, phe-sensitive, AroG (pseudogene)" /db-xref="PSEUDO:CAC89973.1" /db-xref="REMTREMBL:CAC89973" /gene="aroG"
misc-feature 158112..159092 /note="Pfam match to entry PF00793 DAHP-synth-1, DAHP synthetase family, score 755.60, E-value 2e-223" /pseudo
misc-feature complement(159063..161016) /note="insertion sequence, IS100"
misc-feature 159063..159090 /gene="aroG" /note="IS100 inverted repeat" /pseudo
gene complement(159129..159911) /gene="YPO1131"
CDS complement(159129..159911) /note="synonym: ypmt1.57c" /gene="YPO1131"
/note="Similar to Escherichia coli insertion sequence IS21 putative ATP-binding protein, IstB SW:ISTB-ECOLI (P15026) (265 aa) fasta scores: E(): 0, 47.4% id in 249 aa. Also almost identical to Yersinia pestis and Escherichia coli putative IS100 transposase ypmt1.57c TR:Q9R3L5 (EMBL:AL117211) (260 aa) fasta scores: E(): 0, 99.6% id in 260 aa." /codon-start=1 /transl-table=11 /product="insertion sequence IS100, ATP-binding protein" /protein-id="CAC89974.1" /db-xref="GI:15979197" /db-xref="SPTREMBL:Q9R3L5" /translation="MMELQHQRMLMALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLEEKLARHQKQAMYTRMAAFPAVKTFEY"

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NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF  
 TTAADLLLQLSTAQRQGRYKTTLO  
 RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR  
 YEKSAMILTSNLPFGQWDQTFAGD  
 AALTSAMLDRIHHSHVQIKGESYRLRQKRKAG  
 VIAEANPE"

misc-feature	complement (159204..159743)	/gene="YPO1131"  /note="Pfam match to entry PF01695 IstB, IstB-like ATP binding protein, score 367.20, E-value 1.7e-106"
misc-feature	complement (159561..159584)	/gene="YPO1131"  /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	complement (159908..160930)	/gene="YPO1132"  /note="synonyms: y1093, ypmt1"
CDS	complement (159908..160930)	/gene="YPO1132"  /note="Similar to Escherichia coli transposase for insertion sequence element IS21 IstA SW:ISTA-ECOLI (P15025) (390 aa) fasta scores: E(): 3e-27, 33.1% id in 329 aa. Identical to the previously sequenced Yersinia pestis, Yersinia pseudotuberculosis, and Escherichia coli pesticin plasmid insertion sequence transposase Y1055 TR:P74993 (EMBL:U59875) (340 aa) fasta scores: E(): 0, 100.0% id in 340 aa" /codon-start=1 /transl-table=11 /product="transposase for insertion sequence IS100" /protein-id="CAC89975.1" /db-xref="GI:15979198" /db-xref="SPTREMBL:P74993" /translation="MVTTFETVMEIKILHKQGMSSRAIARELGISRNTVKRYLQAKSEP PKYTPRPAVASLLDEYRDYIRQRIADAHYPKIPA TVIAREIRDQGYRGGMTILRAFIR SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS PLHVFVAVLGYSRMLYIEFTDNMR YDTLETCHRNAFRFFGGVPREVLVDNMKTVVLQR DAYQTGQHRFHPSLWQFGKEMGFS PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL RPMGITVDVETANRHGLRWLHDVA NQRKHETIQARPCDRWLEEQQSMALPPEKKEYD VHLDENLVNFDKHPLHPLSIYDS FCRGVA"
misc-feature	complement (160052..160585)	/gene="YPO1132"  /note="Pfam match to entry PF00665 rve, Integrase core domain, score 81.90, E-value 1.6e-22"
misc-feature	complement (160814..160879)	/gene="YPO1132"  /note="Predicted helix-turn-helix motif with score 2147 (+6.50 SD) at aa 18-39, sequence MSSRAIARELGISRNTVKRYLQ"
misc-feature	complement (160823..160906)	/gene="YPO1132"  /note="Pfam match to entry PF00239 recombinase, Site-specific recombinases, score 25.70, E-value 4.7e-06"
misc-feature	complement (160989..161016)	/note="IS100 inverted repeat"
gene	complement (161296..162048)	/gene="gpmA"  /note="synonyms: gpm, YPO1133"

48) -

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/EC-number="5.4.2.1"
/note="Similar to Escherichia coli
phosphoglycerate mutase 1
SW:PMG1-ECOLI (P31217) (249 aa)
fasta scores: E(): 0, 88.0% id in
249 aa"
/codon-start=1
/transl-table=11
/product="phosphoglycerate mutase
1"
/protein-id="CAC89976.1"
/db-xref="GI:15979199"
/db-xref="SWISS-PROT:Q8ZGY5"
/translation="MAVTKLVLRHGESQWNNEN
RFTGWYDVDLSEKGRSEAKAAGKL
LKDEGFTFDFAITSVLKRAIHTLWNILDELDQAW
LPTEKTKWKLNERHYGALQGLNKSE
TAEKYGDEQVKQWRRGFATPPALEKSDEFPGH
DPYAKLTDAELPTTESLALTIER
VIPYWNVDVIKPRIASGERVIAAHGNSLRALVKY
LDDLGEDEILELNIPTGVPLVYEF
DENFKPIKHYYLGNADIEIAAKAAVANQGKAK"
misc-feature complement(161386..1620 /gene="gpmA"
30)
/note="Pfam match to entry PF00300
PGAM, Phosphoglycerate mutase
family, score 447.60, E-value
1.1e-130"
misc-feature complement(161998..1620 /gene="gpmA"
27)
/note="PS00175 Phosphoglycerate
mutase family phosphohistidine
signature."
gene complement(162395..1627 /gene="psiF"
30)
/note="synonym: YPO1134"
CDS complement(162395..1627 /gene="psiF"
30)
/note="Similar to Escherichia coli
phosphate starvation-inducible
protein PsiF precursor psiF
SW:PSIF-ECOLI (P27295) (106 aa)
fasta scores: E(): 1.2e-15, 54.5%
id in 112 aa"
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/transl-table=11
/product="putative
starvation-inducible protein"
/protein-id="CAC89977.1"
/db-xref="GI:15979200"
/db-xref="SPTREMBL:Q8ZGY4"
/translation="MRLFPLWLLSAGLLLSANVM
AADPPKTPSPAQAQQQQMTDCNQ
QASTQSLKGDERKNFMSQCLKAQTAPDGKALTPQ
QQKMKSCNAEAAQKMLKGDERKTF
MSTCLKKAA"
gene complement(163023..1640 /gene="galM"
92)
/note="synonym: YPO1135"
/pseudo
CDS complement(163023..1640 /gene="galM"
92)
/EC-number="5.1.3.3"
/note="Similar to Escherichia coli
aldose 1-epimerase galM
SW:GALM-ECOLI (P40681) (346 aa)
fasta scores: E(): 0, 60.2% id in
344 aa. There is a frameshift
following codon 39. The frameshift
occurs within a homopolymeric
tract of 6G. The sequence has been
checked and is believed to be
correct"
/pseudo

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misc-feature complement(163038..1639 19) /transl-table=11  
/product="aldose 1-epimerase (pseudogene)"  
/gene="galM"  
  
/note="Pfam match to entry PF01263 Aldose-epim, Aldose 1-epimerase, score 377.60, E-value 1.3e-109"  
/pseudo

misc-feature complement(163533..1635 62) /gene="galM"  
  
/note="PS00545 Aldose 1-epimerase putative active site."  
/pseudo

gene complement(164086..1652 37) /gene="galK"

CDS complement(164086..1652 37) /note="synonyms: galA, YPO1137"  
/gene="galK"  
  
/EC-number="2.7.1.6"  
/note="Similar to Escherichia coli galactokinase SW:GAL1-ECOLI (P06976) (381 aa) fasta scores: E(): 0, 72.5% id in 382 aa"  
/codon-start=1  
/transl-table=11  
/product="galactokinase"  
/protein-id="CAC89979.1"  
/db-xref="GI:15979201"  
/db-xref="SWISS-PROT:Q8ZGY3"  
/translation="MSLKQHTQTIFRQQFDRES  
ITIKAPGRVNLIGEHTDYNDGFVL  
PCAINYETVISCGKRDDRQIRVIAADYENQQDIF  
SLDAPIVPHPEYRWADYVRGVVKH  
LQMRNADFGGADLVICGNVPOGAGLSSSASLEVA  
VGQALQSLYQLPLSGVELALNGQE  
AENQFVGCNCGIMDQLISALGKKDHALLIDCRTL  
ETRAVPMPEENMAVVIINSNIQRGL  
VDSEYNTRRQQCEAAARFFGVKALRDVEPSLFFS  
IQDELDPVVAKRARHVISENARTL  
AAADALAAGNLKLMGQLMQESHISMRRDDFEITVP  
PIDRLVEIVKSVIGDQGGVRMTGG  
GFGGCIIALMPLELVEQVRTTVAQEYPAHSGGKK  
ETFYVCQASQGAGLC"  
/gene="galK"

misc-feature complement(164737..1649 64) /note="Pfam match to entry PF00288 GHMP-kinases, GHMP kinases putative ATP-binding proteins, score 83.90, E-value 2.5e-22"

misc-feature complement(164842..1648 77) /gene="galK"

misc-feature complement(165124..1651 59) /note="PS00627 GHMP kinases putative ATP-binding domain."  
/gene="galK"

gene complement(165234..1662 86) /note="PS00106 Galactokinase signature."  
/gene="galT"

CDS complement(165234..1662 86) /note="synonyms: galB, YPO1138"  
/gene="galT"  
  
/EC-number="2.7.7.10"  
/note="Similar to Escherichia coli galactose-1-phosphate uridylyltransferase GalT or GalB SW:GAL7-ECOLI (P09148) (348 aa) fasta scores: E(): 0, 82.4% id in 347 aa"  
/codon-start=1  
/transl-table=11  
/product="galactose-1-phosphate uridylyltransferase"  
/protein-id="CAC89980.1"

		/db-xref="SPTREMBL:Q8ZGY2" /translation="MTHFNPVDHPHRRYNPLKDQ WVLVSPHRAKRPWQGQQEAPATEN LPAHDPDCFLCPGNTRVTGDVNPDYSSSTVFTND FAALMPDTPDAPPSHDLPLMRSQSA RGTSRVICFSPDHSKTLPLQLTLPALQVQVQVQWQQ QSAELGKIYPWVQVFENKGAAMGC SNPHPHGQIWANSFLPNEAEQEDRLQQQYFQQHQ SPMLLDYVERERRDQRTVVETE WLAVVPYWAAWPFETLLLPKAAVLRLEDLSAEQR SDLAIALKKLTSRYDNLFSCSFPY SMGWHGAPYNANDNTHWQLHAHFYPPLLRASVR KFMVGYELLAETQORDLTAEQAAAL LRAVSDVHYKEAGAKS" /gene="galT"
misc-feature	complement(165252..166283)	/note="Pfam match to entry PF01087 GalP-UDP-transf, Galactose-1-phosphate uridyl transferase, score 702.60, E-value 1.8e-207" /gene="galT"
misc-feature	complement(165783..165836)	/note="PS00117 Galactose-1-phosphate uridyl transferase family 1 active site signature." /gene="galE"
gene	complement(166296..167312)	/gene="galE"
CDS	complement(166296..167312)	/note="synonyms: galD, YPO1139" /gene="galE" /EC-number="5.1.3.2" /note="Similar to Escherichia coli UDP-glucose 4-epimerase Gale or GalD SW:GALE-ECOLI (P09147) (338 aa) fasta scores: E(): 0, 76.0% id in 338 aa. Previously sequenced in Yersinia pestis as TR:AAG22000 (EMBL:AF282311) (338 aa) fasta scores: E(): 0, 100.0% id in 338 aa" /codon-start=1 /transl-table=11 /product="UDP-glucose 4-epimerase" /protein-id="CAC89981.1" /db-xref="GI:15979203" /db-xref="SWISS-PROT:Q9F7D4" /translation="MYVLVTGGSGYIGSHTCVQL IEAGYKPVILDNLCSKSSVLARI HSLTGYTPELYAGDIRDRTLDSIFAAHPIHAVI HFAGLKAVGESVNRPLEYNNNVF GTLVLLLEAMRAAQVKNLIFSSSATVYGDQPQIPY VESFPTGSPSSPYGRSKLMVEQIL QDVQLADPQWNMTILRYFNPVGAHPSGLMGEDPQ GIPNNLMPFIAQVAVGRRESLAIF GNGYPTPDGTGVRDYIHVVLDLADGHVAAMKTLHG KPGVHIFNLGAGVGHSVLOVVAAF SKACGKPLAYHFAPRREGDLPAYWADATKAAEQ L GWRVSRSLDEMAADTWHWQSKNPQ GYPD"
misc-feature	complement(166314..167306)	/gene="gale" /note="Pfam match to entry PF01370 Epimerase, NAD dependent epimerase/dehydratase family, score 559.10, E-value 2.9e-164"
gene	complement(167672..168490)	/gene="YPO1140"
CDS	complement(167672..168490)	/gene="YPO1140" /note="Similar to Vibrio cholerae hypothetical protein VC1074 TR:Q9KT31 (EMBL:AE004189) (276 aa) fasta scores: E(): 0, 45.5% id in 275 aa"



		/transl-table=11 /product="putative membrane protein" /protein-id="CAC89982.1" /db-xref="GI:15979204" /db-xref="SPTREMBL:Q8ZGY1" /translation="MWGVLTSLFLPLSQVLSL LFLVSSLAMACYSGVLTFFPATAFL LAIILVLLLLQKYRQRNGVAAGLELLLVLGVI FLHLVPGFHNKLVLDKVRTGPLSA PFTMYYNLDKALVPFILLACLPTLFKVKKHPSVG RMGWVVLILSVPALLLLAVALGGL KIELHTPVWIGSFIIANLFFVCLAEEALFRGYLQ QRLGQWLGSYPALVITALLFGSAH FAGGPLLMLFAALAGVIYGLAWLWSGRLWVAVAF HFALNLMHLLFFTYPLYLPH"
misc-feature	complement(167681..167746)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(167768..167833)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(167849..167899)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(167939..167995)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(168011..168076)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(168113..168178)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(168239..168304)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(168326..168391)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
misc-feature	complement(168404..168469)	/gene="YPO1140"  /note="one of 9 probable transmembrane helices predicted for YPO1140 by TMHMM2.0"
gene	complement(168707..170197)	/gene="modF"  /note="synonyms: phrA, YPO1142"
CDS	complement(168707..170197)	/gene="modF"  /note="Similar to Escherichia coli putative molybdenum transport ATP-binding protein ModF or PhrA SW:MODF-ECOLI (P31060) (490 aa) fasta scores: E(): 0, 75.0% id in 484 aa" /codon-start=1 /transl-table=11 /product="putative molybdenum

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modF"-
/protein-id="CAC89983.1"
/db-xref="GI:15979205"
/db-xref="SPTREMBL:Q8ZGY0"
/translation="MSELQISQGCFLSQTQTLI
LPALHIQAGDCWAFVGGANGSGKSA
LAKALSGELALLEGSRSQSHFRHGVRLSFEQLQQL
VNEEWQRNNTDLLSAEDDDTGRTT
AEIIQEAARDPQRCQQLAALFGISHLLSRRFKYL
STGETRKTLLCQALMPQPDLLILD
EPFDGLDVAARAQLAEMLSLTLAQGVTLVLVLNR
FDDIPDFVQYVGVVLADCHLTHMGP
RQQILSEALIAQLAHSENLDGLSLPETEDPQHHL
RIPKNEPLIILNDGVVEYNDRPIL
HNLSWQVNPGEHWQIIGQNGAGKSTLLSLITGDH
PQGYSDNLTFLGRRRGSGETIWDI
KRHIGYVSGSLHLDYRVSTRVTVILSGFFDSIG
LYQAASDRQQQLADQWLSLLGFST
SVANQPFHSLSWGQQRLVLIARALVKHPALLILD
EPLQGLDPLNRLLVRRFIDVMIGE
GETQLLFVSHHAEDAPQCITHRLTFVPFGDIYHY
QQEKSPSQPVK"

```

misc-feature complement(168761..1693 42) /gene="modF"

```

/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
155.20, E-value 1.1e-42"

```

misc-feature complement(169298..1693 21) /gene="modF"

```

/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."

```

misc-feature complement(169565..1701 13) /gene="modF"

```

/note="Pfam match to entry PF00005
ABC-tran, ABC transporter, score
87.10, E-value 3.7e-22"

```

misc-feature complement(170069..1700 92) /gene="modF"

```

/note="PS00017 ATP/GTP-binding
site motif A (P-loop)."

```

gene complement(170307..1710 98) /gene="modE"

```

/note="synonyms: modR, YPO1143"

```

CDS complement(170307..1710 98) /gene="modE"

```

/note="Similar to Escherichia coli
molybdenum transport protein
SW:MODE-ECOLI (P46930) (262 aa)
fasta scores: E(): 0, 70.5% id in
264 aa"

```

```

/codon-start=1
/transl-table=11
/product="molybdenum transport
protein ModE"

```

```

/protein-id="CAC89984.1"
/db-xref="GI:15979206"
/db-xref="SWISS-PROT:P58497"
/translation="MQAEILLTLKLQQLFADPR
RIALLKQIQHTGSISQGAKLAGIS
YKSAWDAINDMNTLSEEILVERATGGKGGGAHL
TRYGERLIQLYDLLATIQQKAFDT
LKDDSLPLDSLAAISRFSLQTSARNQFFGTIE
RDHQVQVQHVNILLSGKTRLTAA
ITQQSADRLQLSAGKEVLALIKAPWVKLVTDPAL
AGAADNALPGTVASIEPGNDHSEV
IVTLTGGANLCSTQNNSELHALNLRVGSAVIAQF
NADRVIIATLC"

```

gene 171415..171567 /gene="YPO1144"

CDS 171415..171567 /gene="YPO1144"

```

/note="Similar to Escherichia coli
hypothetical 5.3 kDa protein in
modE-modA intergenic region
precursor YbhT SW:YBHT-ECOLI
(P75759) (49 aa) fasta scores:
E(): 8.4e-11, 82.5% id in 40 aa.

```

many eukaryotic ATPase subunits  
 eg. Mesembryanthemum crystallinum  
 vacuolar H<sup>+</sup> ATPase subunit C  
 TR:Q9S953 (EMBL:UNKNOWN ACCESSION)  
 (76 aa) fasta scores: E(): 3.9,  
 54.5% id in 33 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="putative membrane  
 protein"  
 /protein-id="CAC89985.1"  
 /db-xref="GI:15979207"  
 /db-xref="SPTREMBL:Q8ZGX9"  
 /translation="MFELLKSLVFVAVVMVPVMA  
 VILGLIYGLGEVFNVISKTGHPKE RNTLRS"  
 /gene="YPO1144"  
 /note="1 probable transmembrane  
 helix predicted for YPO1144 by  
 TMHMM2.0"

misc-feature 171433..171501

gene 171802..172581

CDS 171802..172581

/gene="modA"  
 /note="synonym: YPO1145"  
 /gene="modA"  
 /note="Similar to Escherichia coli  
 molybdate-binding periplasmic  
 protein precursor ModA  
 SW:MODA-ECOLI (P37329) (257 aa)  
 fasta scores: E(): 0, 71.1% id in  
 246 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="molybdate-binding  
 periplasmic protein precursor"  
 /protein-id="CAC89986.1"  
 /db-xref="GI:15979208"  
 /db-xref="SPTREMBL:Q8ZGX8"  
 /translation="MKNQYGKVSYWVAGAVLLTA  
 FSGPAFAADKITVFAAASLTNALQ  
 DIAVQYKQEKQVDVVASYSSTLARQIEQGAPA  
 DLFISADQQWMDYAIKQQIVANT  
 RYTLLGNELVLIAPQDSQIDKVEIDKKTDWKKLL  
 EGGRLAVGDPDHVPAGIYAKESLE  
 NLGAWSTLAPEMARANNVRSAMALVERAEAPLGI  
 VYGSDAVASKKVKVVGIFPEASHK  
 PVEYPMATVKGHDNPTVTAFYDYLKSPAAAVIFK  
 NYGFTPR"

misc-feature 171826..171885

gene 172581..173276

CDS 172581..173276

/gene="modA"  
 /note="1 probable transmembrane  
 helix predicted for YPO1145 by  
 TMHMM2.0"  
 /gene="modB"  
 /note="synonyms: chlJ, YPO1146"  
 /gene="modB"  
 /note="Similar to Escherichia coli  
 molybdenum transport system  
 permease protein Modb or ChlJ  
 SW:MODB-ECOLI (P09834) (229 aa)  
 fasta scores: E(): 0, 76.3% id in  
 228 aa"  
 /codon-start=1  
 /transl-table=11  
 /product="molybdenum transport  
 system permease protein ModB"  
 /protein-id="CAC89987.1"  
 /db-xref="GI:15979209"  
 /db-xref="SPTREMBL:Q8ZGX7"  
 /translation="MILSEYEWQAIIISLKVSGV  
 AVACSLPLGILMAWVLVRCRFPKG  
 SLLDSVIHLPLVLPVVIYLLLLISMGRRGFIGE  
 WLYSWFGINFSSFSWRGAALASAVV  
 AFPLMVRAIRLALEAVDTRLELAARTLGATPWRV  
 FFTITLPLSLPGVIAGTVLSFARS  
 LGEFGATITFVSNIPGETRTIPLAMYTLETPGA  
 EAAAARLCVIAIILSLVSLLLSEW  
 LANWGGKKRMGAPC"  
 /gene="modB"

misc-feature 172623..172691

misc-feature	172725..172793	transmembrane helices predicted for YPO1146 by TMHMM2.0" /gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	172851..172919	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	172920..173150	/gene="modB" /note="Pfam match to entry PF00528 BPD-transp, Binding-protein-dependent transport systems inner membrane component, score 78.90, E-value 1e-19"
misc-feature	172980..173048	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
misc-feature	173169..173237	/gene="modB" /note="one of 5 probable transmembrane helices predicted for YPO1146 by TMHMM2.0"
gene	173270..174349	/gene="modC" /note="synonyms: chlD, narD, YPO1147"
CDS	173270..174349	/gene="modC" /note="Similar to Escherichia coli molybdenum transport ATP-binding protein ModC or ChlD or NarD SW:MODC-ECOLI (P09833) (352 aa) fasta scores: E(): 0, 69.1% id in 349 aa" /codon-start=1 /transl-table=11 /product="molybdenum transport ATP-binding protein ModC" /protein-id="CAC89988.1" /db-xref="GI:15979210" /db-xref="SPTREMBL:Q8ZGX6" /translation="MLELNFSQQLGDLHLQVATD LPAQGITAIFGLSGAGKTSLINVI GGLTRPQQGRVILNGRVLVDAEKNIYLPPEKRRV GYVFQDARLFPHYRVRGNLQYGMA ASMRGQFDIAIVGLLGIEPLLNRFPTLSGGGEKQR VAIGRALLTAPELLLMDEPLASLD LPRKRELLPYLERLAQDVNTPILYVSHSMDEILR LADQVVVMDAGKVRAVGGLLEEVWA SSALRPWLQREEPSSILRVSVIGHH DRYAMTALA LGDQRLWVGKLDAAEGNSMRIRIN AADVSLALQPPHSSSIRNIPVKVAECLDVDGQV DVKLAIGEQLWARITPWARDELG LKPGQWVYAQIKSVSFNRQNGPVPD"
misc-feature	173339..173884	/gene="modC" /note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 203.30, E-value 3.7e-57"
misc-feature	173360..173383	/gene="modC" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	173654..173698	/gene="modC" /note="PS00211 ABC transporters family signature."
gene	complement(174405..175226)	/gene="YPO1148"
CDS	complement(174405..175226)	/gene="YPO1148"  /note="Similar to Escherichia coli hypothetical protein YbhA SW:YBHA-ECOLI (P21829) (272 aa) fasta scores: E(): 0, 64.0% id in 272 aa, and to Vibrio cholerae hypothetical protein VCA0243"

		fasta scores: E(): 0, 39.2% id in 273 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89989.1" /db-xref="GI:15979211" /db-xref="SPTREMBL:Q8ZGX5" /translation="MTYRIIALDLDTLLDHKKR ILPESLSALAQARAEGVKVIVVTG RHHVAIHPFYQALQLDTPAICCNGTYIYDYQNKK VLDSNPLTPQQAVQVLQLEKTQI HGLMYVDDAMLYQQITGHVTRTLSPAESLPPAQR PTFLQVNSLLDAAHSATAIWKFAT SHPDTAQLKAFAARVEAEMGLACEWSWHDQVDIA QAGNSKGKRLQQWVESQGLSMQEV IAFGDNFNLDLSMLEAAGLGVMGNSDDAIKQRAD LVITDNEQPGIAAVIRQHVLA" /gene="YPO1148"
misc-feature	complement(174447..1752 14)	/note="Pfam match to entry PF00592 DUF3, Cof family DUF3, score 280.90, E-value 1.6e-80" /gene="YPO1148"
misc-feature	complement(174498..1745 66)	/note="PS01229 Hypothetical cof family signature 2." /gene="YPO1149" /gene="YPO1149" /note="Similar to Escherichia coli hypothetical protein YbhE SW:YBHE-ECOLI (P52697) (331 aa) fasta scores: E(): 0, 56.8% id in 329 aa, and to Buchnera aphidicola (subsp. Acyrthosiphon pisum) hypothetical protein BU293 SW:Y293-BCUAI (P57380) (334 aa) fasta scores: E(): 0, 35.8% id in 330 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89990.1" /db-xref="GI:15979212" /db-xref="SPTREMBL:Q8ZGX4" /translation="MKQAVYVASPDSQQIHVWQL DSAGELTLLQTVDPVPGVQVPMAS PNQRHLYVGVVPDFGIVSYHIADDGTLTAAGMAP LPGSPTHIDTDROGRFLFSASYSF NCVSISPIDTHGVVQAPIQQLDDLPAHPSANIDP TNQILLVPCLKEDKVRLFDLSAEG QLTPHAQADITVAAGAGPRHMAFHPNHQVAYCVN ELNSSVDVYQISNNGQEYHLVQSL DAMPADFTGTRWAADIHITPNGRYLYISDRTANL LGIFTVSEDGRVISLVGHHLTEAQ PRGFNIDHSGNFLIASGQKSDHIEVYRIDQNTGE LTTTLKRYPPVGKGPWVSIRGAQNS " /gene="bioA"
gene	175517..176521 175517..176521	
CDS		
gene	complement(176706..1779 74)	/note="synonym: YPO1150" /gene="bioA"
CDS	complement(176706..1779 74)	/EC-number="2.6.1.62" /note="Similar to many eg. Escherichia coli adenosylmethionine-8-amino-7-oxono nanoate aminotransferase BioA SW:BIOA-ECOLI (P12995) (429 aa) fasta scores: E(): 0, 74.6% id in 417 aa" /codon-start=1 /transl-table=11 /product="adenosylmethionine-8-ami

		<pre> aminotransferase" /protein-id="CAC89991.1" /db-xref="GI:15979213" /db-xref="SPTREMBL:Q8ZGX3" /translation="MTPSDLVFDQQHIWHPYTSMT TEPLPCYPVVGAEGLVQLADGRR LIDGMSSWWAAIHGYNHPVLNFAAHQQLDKMSHV MFGGITHPPAVKLCRQLVAMTPPP LECVFLADSGSVSVEVALKMALQYWQAKGERRQR ILTLRHGYHGDTFGAMSVCDPQNS MHSLYQGYLAENLFANAPQCGFDDPWDPQDIANF VALITQHANEIAAVILEPVPVQAG GMRIYHPSYLREVRALCDKHQILLIADEIATGFG RTGKLFACEHAQIVPDILCLGKAL TGGYLTLSATLTTRAVAETISKGDAGCFMHGPTF MANPLACAVASANLSLLAENSWQQ QVSKIEDQLKRELLPLAQEDTVADVRVLGAIGVV EMKKPVNVARLQRSFVEQGVWIRP FGKLIYLMPPYIISQHALTRLTAAVDRGS" /gene="bioA" </pre>
misc-feature	complement(176766..177875)	<pre> /note="Pfam match to entry PF00202 aminotran-3, Aminotransferases class-III pyridoxal-phosphate, score 527.10, E-value 8.3e-183" /gene="bioA" </pre>
misc-feature	complement(177138..177251)	<pre> /note="PS00600 Aminotransferases class-III pyridoxal-phosphate attachment site." /gene="bioB" </pre>
gene	178073..179110	<pre> /note="synonym: YPO1151" /gene="bioB" </pre>
CDS	178073..179110	<pre> /EC-number="2.8.1.6" /note="Similar to many eg. Escherichia coli biotin synthase BioB SW:BIOB-ECOLI (P12996) (346 aa) fasta scores: E(): 0, 84.6% id in 344 aa" /codon-start=1 /transl-table=11 /product="biotin synthase" /protein-id="CAC89992.1" /db-xref="GI:15979214" /db-xref="SPTREMBL:Q8ZGX2" /translation="MATYHHWTVGQALALFDKPL LELLFEAQQVHRQHFDPRQVQVST LLSIKTGACPEDCKYCPQSSRYKTGLESERLMQV EQVLESAKKAKAAGSTRFCMGAAW KNPHERDMPYLAKMVEGVKALGMETCMTLGSLSK QQAHLADAGLDYYNHNLDTSPEF YGSIIITRSYQERLDTLNEVRDAGIKVCSGGIVG LGETVRDRAGLLVQLANLKPPEPES VPINMLVKVKGTPLENNAEVDAFEFIRTIAVARI MMPSSYVRLSAGREQMNEQTQAMC FMAGANSIFYGCKLLTTPNPDEDKDLQLFRKLGL NPQQTATSHGDREQQQALTEQLLH GDTAQFYNAAV" /gene="bioB" </pre>
misc-feature	178085..179005	<pre> /note="Pfam match to entry PF01792 Biotin-synth, Biotin synthase, score 689.90, E-value 1.2e-203" /gene="bioF" </pre>
gene	179110..180261	<pre> /note="synonym: YPO1152" /gene="bioF" </pre>
CDS	179110..180261	<pre> /EC-number="2.3.1.47" /note="Similar to many eg. Escherichia coli 8-amino-7-oxononanoate synthase BioF SW:BIOF-ECOLI (P12998) (384 aa) fasta scores: E(): 0, 65.8% id in 383 aa" /codon-start=1 /transl-table=11 /product="8-amino-7-oxononanoate </pre>

		/protein-id="CAC89993.1"
		/db-xref="GI:15979215"
		/db-xref="SPTREMBL:Q8ZGX1"
		/translation="MSWQDKIAQGLQRRRDAAAY RTRQVNEGANGRWLQSGERQYLNF SSNDYLGLSQNDEVIAAWQQGARRYGVGSGGSGH VTGYSQPHARLEQQALADWLGYPRA LLFISGYAANQAVLTALTADDDRILADKLSHASL LEAAAHSPAQLRRFQHNQPEALQN LLIKPCQGGQTLVVTEGVFSMDGDSAPLAALQQQT SAAGGWLLVDDAHGIGVHGEGRG SCWLQGVQPELLVVTFGKAFGLSGAAVLCQEPVA EYLLQYARHLIYSTAMPPAQACAL QAALRQVQQGDALRQQQLQQRIRQFRTAAHLPLQ LGASKTAIQPLLVDNQSLIWAE QLRAAGLWVTAIRPPTVPPGSARLRITLSAAHQ EDIDRLLEVLYGLCH"
misc-feature	179350..180186	/gene="bioF" /note="Pfam match to entry PF00222 aminotran-2, Aminotransferases class-II, score 337.40, E-value 1.6e-97"
misc-feature	179806..179835	/gene="bioF" /note="PS00599 Aminotransferases class-II pyridoxal-phosphate attachment site."
gene	180245..181048	/gene="bioC"
CDS	180245..181048	/note="synonym: YPO1153" /gene="bioC" /note="Similar to many eg. Escherichia coli biotin synthesis protein BioC SW:BIOC-ECOLI (P12999) (251 aa) fasta scores: E(): 0, 49.6% id in 250 aa" /codon-start=1 /transl-table=11 /product="biotin synthesis protein BioC"
		/protein-id="CAC89994.1"
		/db-xref="GI:15979216"
		/db-xref="SPTREMBL:Q8ZGX0"
		/translation="MASVTEHAQWGVGCLPPLNV DKQAIAAAFSRAAESYDSAANLQR ETGHRVLVQLGQQHTGFVVLDAGCGTGHFSQHWRL LGKRVIALDLAAGMLDYARQQQVA DDYLLGDIEHIPLPDQSDICFSNLAVQWCSDLG AALSEFYRVTRPGGIIILFSTLAEG SLDELGQAWQQVDGQRHVNDLPLQHIQTACQYY RHHLTTALYQPRFPNVIALMRSLO GIGATHLHHGRQAGLQGRQLAALQRAYVMQSGG YPLSYHVMVYGVYRD"
gene	181041..181763	/gene="bioD"
CDS	181041..181763	/note="synonym: YPO1154" /gene="bioD" /EC-number="6.3.3.3" /note="Similar to many eg. Escherichia coli dethiobiotin synthetase BioD SW:BIOD-ECOLI (P13000) (224 aa) fasta scores: E(): 0, 71.2% id in 229 aa" /codon-start=1 /transl-table=11 /product="dethiobiotin synthetase" /protein-id="CAC89995.1"
		/db-xref="GI:15979217"
		/db-xref="SWISS-PROT:Q8ZGW9"
		/translation="MTKRWFITGTDTDVGKTVAS CALLQAATAQGYRTAGYKPVASGS QMTADGLRNSDALALQANSSQRLGYSQVNPFTFL EATSPHIASESEGRAIPLTALSQ LRQLEPSADWILIEGAGGWFTPLSPQATFADWVQ QEQLPVIMVVGKLGKINHALTA QAIQHAGLTLAGWVANEVTPAGRRQAQAYQATLTR MITAPLLGIIPYLSIDIEENPVTR RDLGHYLDLTVLRAAEREAVNM"

-	25)	-	
CDS	complement(181915..1826	/gene="YPO1155"	
	25)		/note="Similar to Synechocystis sp high-affinity branched-chain amino acid transport ATP-binding protein TR:Q55753 (EMBL:D64002) (249 aa) fasta scores: E(): 5.8e-31, 43.3% id in 238 aa, and to Escherichia coli high-affinity branched-chain amino acid transport ATP-binding protein LivF SW:LIVF-ECOLI (P22731) (237 aa) fasta scores: E(): 5.1e-22, 36.3% id in 237 aa" /codon-start=1 /transl-table=11 /product="putative amino acid transporter" /protein-id="CAC89996.1" /db-xref="GI:15979218" /db-xref="SPTREMBL:Q8ZGW8" /translation="MLSLTAVNQYYGNHILWDI NLELPRGQCTCLIGRNGVGKTTLI NCIMGHLPIKSGTMIWQPHHEPPQNQQPVERR NALGIGYVPQGGQIFSQLSVEDNL LVAVLAGRHKSHPIPGWVFELFPLLHDKRSQRG ELTRNQQQQLAIARALVAEPELLI LDEPGSGTSPALSEDISTVLHQLSRNLGMTLLLV EHRLPFIQHIADRFCLMAGGRNVA QGTLDDLNEGLISEHLAR"
misc-feature	complement(181984..1825	/gene="YPO1155"	
	47)		/note="Pfam match to entry PF00005 ABC-tran, ABC transporter, score 135.40, E-value 1.1e-36"
misc-feature	complement(182503..1825	/gene="YPO1155"	
	26)		/note="PS00017 ATP/GTP-binding site motif A (P-loop)."
gene	183715..185730	/gene="uvrB"	
		/note="synonym: YPO1156"	
CDS	183715..185730	/gene="uvrB"	
		/note="Similar to many eg. Escherichia coli excinuclease ABC subunit B UvrB SW:UVRB-ECOLI (P07025) (673 aa) fasta scores: E(): 0, 85.9% id in 673 aa" /codon-start=1 /transl-table=11 /product="excinuclease ABC subunit B" /protein-id="CAC89997.1" /db-xref="GI:15979219" /db-xref="SWISS-PROT:Q8ZGW7" /translation="MSKSFKLHSVFKPAGDQPEA IRKLEEGLENGLAHQTLGVTGSG KTFTVANVIADLNRPTMILAPNKTLLAAQLYGEMK EFPDNAVVEYFVSYYDYYQPEAYV PSSDTFIEKDASVNEHIEQMRLSATKALLERRDV VVVASVSATYGLGDPDLYLKMMHL LTRGMIIDQRSILRRLSELQYSRNDQVFQRGTR VRGEVIDIFPAESDEWALRVELFD EEVERLSIFDPLTGQLQHEVPRFTVYPKTHYVTP RERILQAMEEIKVELAERRQVLLA NNKLLLEEQRLSQRTQFDLEMMNELGYCSGIENYS RYLSGRGPGEAPPTLFDYLPADGL LIVDESHVTIPQIGGMYKGDRSRKETLVEYGFRL PSALDNRPMPRFEEFEALAPQTIYV SATPGKYELEKSGGDIIEQVVRPTGLLDPLIEVR PVATQVDDLLSEIRIRAAINERVL VTTLTKRMAEDLTDYLSEHGAKVRYLHSDIDTVE RVEIIRDLRLGFEFDVLVGINLLRE GLDMPEVSLVAILDADKEGFLRSERSLIQTIGRA ARNLNGKAILYGDRITASMEKAIG ETERRRAKQQAYNEERRIIPQGLNKKIGDILQLG	



		LSPKALDQKIRELEAKMYTYAQNLEFEQAAELRD QVHQLRQQFIAIS"
misc-feature	183829..183852	/gene="uvrB" /note="PS00017 ATP/GTP-binding site motif A (P-loop)."
misc-feature	185092..185352	/gene="uvrB" /note="Pfam match to entry PF00271 helicase-C, Helicases conserved C-terminal domain, score 78.20, E-value 1.7e-19"
misc-feature	185605..185712	/gene="uvrB" /note="Pfam match to entry PF02151 UVR, UvrB/uvrC motif, score 58.00, E-value 2e-13"
gene	186022..186267	/gene="YPO1157"
CDS	186022..186267	/gene="YPO1157" /note="Similar to Vibrio cholerae hypothetical protein VC1816 TR:Q9KR31 (EMBL:AE004257) (71 aa) fasta scores: E(): 6.9e-17, 64.7% id in 68 aa, and to Vibrio marinus genes, complete cds, similar to eicosapentaenoic acid synthesis gene cluster TR:Q9RA23 (EMBL:AB025342) (72 aa) fasta scores: E(): 1.2e-16, 68.3% id in 63 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89998.1" /db-xref="GI:15979220" /db-xref="SPTREMBL:Q8ZGW6" /translation="MSEHLSKDPLHGITLEQLLT KLVENYGWDGLADRIQINCFISDP SIKSSLKFLRRTTPWARQKVEALYIEMSDKAEWLK GQS"
gene	complement(186398..1873 21)	/gene="YPO1158"
CDS	complement(186398..1873 21)	/gene="YPO1158"  /note="Similar to Escherichia coli hypothetical protein YbhK SW:YBHK-ECOLI (P75767) (302 aa) fasta scores: E(): 0, 77.7% id in 301 aa, and to Vibrio cholerae hypothetical protein VC1023 TR:Q9KT82 (EMBL:AE004184) (296 aa) fasta scores: E(): 0, 53.9% id in 297 aa" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC89999.1" /db-xref="GI:15979221" /db-xref="SWISS-PROT:P58589" /translation="MRNRTLADLERVVALGGGHG LGRVMSSLSSLSRLTGIVTTTNDN GGSTGRIRRSEGGIAWGDTRNCLNQLITEPSVAS AMFEYRFTGNAGELAGHNLGNLMLK ALDHLISIRPIEAINLVRSLKVDALLIPMSEQPV DLMAIDHEGHPIYGEVNIDQLAQM PQEMLLSPPVHATREAVEAINQADVILIGPGSFL TSLMPLLLLDLTDALRRSSASMI YIGNLGRELSPAAAALSLQDKLTIMESKIGRKII DAVIVSPTIDISGVKDRIIVQQPL EAKDIPHRHDRELLRQALENTLQQNLGADSV"
misc-feature	complement(186416..1872 88)	/gene="YPO1158"  /note="Pfam match to entry PF01933 UPF0052, Uncharacterised protein family UPF0052, score 345.20, E-value 7.4e-100"

CDS	187853..188833	/note="synonyms: bisA, chlA, chlA1, narA, YPO1159" /gene="moaA" /note="Similar to Escherichia coli molybdenum cofactor biosynthesis protein A MoaA SW:MOAA-ECOLI (P30745) (329 aa) fasta scores: E(): 0, 78.2% id in 326 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein A VC1024 TR:Q9KT81 (EMBL:AE004184) (334 aa) fasta scores: E(): 0, 65.0% id in 329 aa" /codon-start=1 /transl-table=11 /product="molybdenum cofactor biosynthesis protein A" /protein-id="CAC90000.1" /db-xref="GI:15979222" /db-xref="SWISS-PROT:Q8ZGW5" /translation="MVQLTDAFARKFYYLRLSITDVCNFRCTYCLPEGYRPDGVKSFLSLDEINRVSRFAALLGTEKIRLTGGEPSMRRDFTDIIATIRQNPAIRTLAVTTNGYRLVRDVAQWRDAGLTAINVSVDSLDPRQFHAITGQDKFYQVMQGIDAAFDAGFDKVKVNAVLMRDVNDRQLSAFLDWIKPRPIQLRFIELMETGEGGNLFRKHHVSGGVIRQQLLLEQG WQQQDRARSDGPAQVFHHSYQGEIGLIMPYEKDFCASCNRLRVSA LGNLHLCLFGEQGITLRDLLGSDDQQDELIARIQSALQTKKQTHFLHQN SGITQNL SFIGG" /gene="moaA" /note="PS01305 moaA / nifB / pqqE family signature."
misc-feature	187907..187942	/gene="moaA"
misc-feature	188012..188656	/note="Pfam match to entry PF01444 MoaA-NifB-PqqE, moaA / nifB / pqqE family, score 258.80, E-value 7.5e-74" /gene="moaA"
gene	188934..189413	/gene="moaC"
CDS	188934..189413	/note="synonyms: chlA3, YPO1160" /gene="moaC" /note="Similar to Escherichia coli molybdenum cofactor biosynthesis protein C MoaC SW:MOAC-ECOLI (P30747) (160 aa) fasta scores: E(): 0, 87.9% id in 157 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein C VC1026 TR:Q9KT79 (EMBL:AE004184) (160 aa) fasta scores: E(): 0, 78.5% id in 158 aa" /codon-start=1 /transl-table=11 /product="molybdenum cofactor biosynthesis protein C" /protein-id="CAC90001.1" /db-xref="GI:15979223" /db-xref="SWISS-PROT:Q8ZGW4" /translation="MTQLTHINTAGEAHMVDVSAKNETVREARAEAFVDMQAATLAMIIDGSHHKGDVFATARIAGIQAAKKTWELIPLCHPLLTKVEVKLEAQPEHNRVRIETCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMIIGPVRLLTKSGGKSGDFKVDI" /gene="moaC" /note="Pfam match to entry PF01967 MoaC, MoaC family, score 306.40, E-value 3.3e-88"
misc-feature	188976..189383	/gene="moaD"
gene	189410..189655	/note="synonyms: chlA4, chlM, YPO1161" /gene="moaD"
CDS	189410..189655	/note="Similar to Escherichia coli

		factor, subunit 1 MoaD SW:MOAD-ECOLI (P30748) (81 aa) fasta scores: E(): 2.9e-23, 71.6% id in 81 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein D vc1027 TR:Q9KT78 (EMBL:AE004184) (81 aa) fasta scores: E(): 2.4e-17, 63.0% id in 81 aa" /codon-start=1 /transl-table=11 /product="molybdopterin [mpt] converting factor, subunit 1" /protein-id="CAC90002.1" /db-xref="GI:15979224" /db-xref="SPTREMBL:Q8ZGW3" /translation="MIQILFFAQVRELVGVDKLO LAAEFPTVEALRQSLCQRGERWQL ALEEGKLLTAVNQSLVSAQHPLAAGDEVAFFPPV TGG"
gene	189655..190110	/gene="moaE"
CDS	189655..190110	/note="synonyms: chlA5, YPO1162" /gene="moaE" /note="Similar to Escherichia coli molybdopterin [mpt] converting factor, subunit 2 MoaE SW:MOAE-ECOLI (P30749) (149 aa) fasta scores: E(): 0, 81.7% id in 120 aa, and to Vibrio cholerae molybdenum cofactor biosynthesis protein E VC1028 TR:Q9KT77 (EMBL:AE004184) (150 aa) fasta scores: E(): 0, 68.3% id in 120 aa" /codon-start=1 /transl-table=11 /product="molybdopterin [mpt] converting factor, subunit 2" /protein-id="CAC90003.1" /db-xref="GI:15979225" /db-xref="SWISS-PROT:Q8ZGW2" /translation="MMENTRIRVGAEAFSVGDEY TWLSQCDEDGAVVTFTGKVRNHNL GASVSALTLEHYPGMTEKALTEIIADARSRWSLQ RVSVIHRVGPLFPGDEIVFVGVT AHRSMFAEAAEFIMDYLLKTRAPFWKREATVEGER WVESRSDSHIAAKRW"
misc-feature	189748..190023	/gene="moaE" /note="Pfam match to entry PF02391 MoeA, , score 123.70, E-value 3.4e-33"
gene	190253..190963	/gene="YPO1163"
CDS	190253..190963	/gene="YPO1163" /note="Similar to Escherichia coli hypothetical 25.9 kDa protein in moaE-rhlE intergenic region SW:YBHL-ECOLI (P75768) (234 aa) fasta scores: E(): 0, 73.3% id in 236 aa, and to Borrelia burgdorferi conserved hypothetical integral membrane protein BB0539 TR:O51489 (EMBL:AE001155) (232 aa) fasta scores: E(): 0, 49.3% id in 215 aa" /codon-start=1 /transl-table=11 /product="putative membrane protein" /protein-id="CAC90004.1" /db-xref="GI:15979226" /db-xref="SPTREMBL:Q8ZGW1" /translation="MDRYPRSNNGSIVERAGSGIQ AYMAQVYGWMTCLLLTAVVAWYA ANTPSIIIFALQSNQILFFGLIIAQLGLVFVISGM VNRLSGTAATSLFMYLSALTGLTL

		RDLSGMSGMLFMGLIGIILASLVN IWLKSPALMWVVITYIGVLVFLVGLTAYDTQKLKLN GAQLDVNDKDSFRKYSIVGALTLY LDFINLFLMLLRIFGNRR"
misc-feature	190313..190381	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190373..190960	/gene="YPO1163" /note="Pfam match to entry PF01027 UPF0005, Uncharacterized protein family UPF0005, score 190.90, E-value 2e-53"
misc-feature	190424..190492	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190511..190579	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190592..190651	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190670..190738	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190751..190810	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	190883..190951	/gene="YPO1163" /note="one of 7 probable transmembrane helices predicted for YPO1163 by TMHMM2.0"
misc-feature	191053..191764	/note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	191198..191656	/gene="tnp"
CDS	191198..191656	/note="synonym: YPO1164" /gene="tnp" /note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Identical to the Yersinia pseudotuberculosis IS1541 element transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa" /codon-start=1 /transl-table=11 /product="transposase for the IS1541 insertion element" /protein-id="CAC90005.1" /db-xref="GI:15979227" /db-xref="SPTREMBL:Q9X9F5" /translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRAIGSILRKL CEWKNVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKGKSSMLLYEQFGDLKFKYRN REFWCRGYYVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	191252..191563	/gene="tnp" /note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	complement (191885..193588)	/gene="betaA" /note="synonym: YPO1165"

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/EC-number="1.1.99.1"
/note="Similar to many eg.
Escherichia coli choline
dehydrogenase BetA SW:BETA-ECOLI
(P17444) (556 aa) fasta scores:
E(): 0, 79.4% id in 553 aa, and to
Homo sapiens choline dehydrogenase
ChdH TR:Q9NY17 (EMBL:AJ272267)
(482 aa) fasta scores: E(): 0,
50.1% id in 467 aa"
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CGRGKGLGGSSLINGMCYIRGNAM
DFDHWASLSGLEDWSYLDCLPYFRKAETRDIGPN
DFHGGE GPVSVTTPKIGNNPLFHA
MVAAGVQAGYPRTDDLNGYQQEGFGPMDRTVTPK
GRRASTARGYLDQARPRNNLTIIT
HALTDRI LFEGKRATGVRYLKGDAGTGQTAYARR
EVLLCGGAIASPOILQ RSGIGPAE
LLQRLDIPLVQALPGVGENLQDHLEMYLQYSCKQ
PVS LYPALLWFNQPKIGIEWLFNG
TGVGASNQFEAGGFIRSRDAFTWPNIQYHFLPVA
INYNGSNAVKEHGFQAHVGS MRSP
SRGRIQVKS KDP RQHPSILFNYSSEQDWHEFRD
AIRITREIIAQPALDPYRGREISP
GANVQNDELDAFIREHAETAYHPSCSCKMGDDK
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AYFIAGDTPARTSPVRHSLPVT SY P"
/misc-feature complement(192008..1935 /gene="betA"
82)
/note="Pfam match to entry PF00732
GMC-oxred, GMC oxidoreductases,
score 963.20, E-value 6.6e-286"
/misc-feature complement(192770..1928 /gene="betA"
14)
/note="PS00624 GMC oxidoreductases
signature 2."
/misc-feature complement(193274..1933 /gene="betA"
45)
/note="PS00623 GMC oxidoreductases
signature 1."
/gene complement(193611..1950 /gene="betB"
83)
/note="synonym: YPO1166"
CDS complement(193611..1950 /gene="betB"
83)
/EC-number="1.2.1.8"
/note="Similar to Escherichia coli
betaine aldehyde dehydrogenase
BetB SW:DHAB-ECOLI (P17445) (489
aa) fasta scores: E(): 0, 76.7% id
in 489 aa, and to Homo sapiens
aldehyde dehydrogenase, E3 isozyme
AldH9 or AldH7 or AldH9A1
SW:DHAG-HUMAN (P49189) (493 aa)
fasta scores: E(): 0, 51.3% id in
483 aa"
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dehydrogenase"
/protein-id="CAC90007.1"
/db-xref="GI:15979229"
/db-xref="SPTREMBL:Q8ZGV9"
/translation="MSRYGLQKLYINGAYTDSTS
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 YTRREPLGVVAGIGAWNYPLQIAL  
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 AGLPAGVFVNLTGSGDQVGQMLTE  
 HPGIAKVSFTGGIASGKKVMANAAGSTLKDVTME  
 LGGKSPLIIFADADLDKAADIAMM  
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 KRIHIGDPSDERTNFGPLVSFQHR  
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 VAPTTFTHCRDDMQIVREEIFGPV  
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 SFNSVF"

misc-feature	complement (193635..195044)	/gene="betB"  /note="Pfam match to entry PF00171 aldedh, Aldehyde dehydrogenase family, score 804.40, E-value 4.1e-238"
misc-feature	complement (194214..194249)	/gene="betB"  /note="PS00070 Aldehyde dehydrogenases cysteine active site."
misc-feature	complement (194310..194333)	/gene="betB"  /note="PS00687 Aldehyde dehydrogenases glutamic acid active site."
gene	complement (195141..195737)	/gene="betI"  /note="synonym: YPO1167"
CDS	complement (195141..195737)	/gene="betI"  /note="Similar to Escherichia coli regulatory protein of the osmoregulatory choline-glycine betaine pathway BetI SW:BETI-ECOLI (P17446) (195 aa) fasta scores: E(): 0, 64.1% id in 192 aa" /codon-start=1 /transl-table=11 /product="TetR-family regulatory protein" /protein-id="CAC90008.1" /db-xref="GI:15979230" /db-xref="SPTREMBL:Q8ZGV8" /translation="MPKVGMQPIRRQQLIEATMA AVNEVGMHEASIAQIAKRAGVSNG IISHYFRDKNGLLEATMRYLIRHLGEAVKQHLAA LSVNDPRARLRAIAEGNFDDSQIN SAAMKTWLAFWASSMHSPQLYRLQQVNNRRLYSN LCAEFKRCLPREQAQLAAKGMAGL IDGLWLRSAISGEHFNQRQEALLIIHNYIEQQLNI KYKC"
misc-feature	complement (195537..195584)	/gene="betI"  /note="PS00038 Myc-type, 'helix-loop-helix' dimerization domain signature."
misc-feature	complement (195558..195698)	/gene="betI"  /note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 53.90, E-value 2.3e-12"
misc-feature	complement (195570..195662)	/gene="betI"  /note="PS01081 Bacterial regulatory proteins, tetR family signature."
misc-feature	complement (195585..195650)	/gene="betI"

		motif with score 1758 (+5.17 SD) at aa 30-51, sequence ASIAQIAKRAGVSNGLIISHYFR"
gene	196102..198123	/gene="betT"
		/note="synonym: YPO1168"
CDS	196102..198123	/gene="betT"
		/note="Similar to Escherichia coli high-affinity choline transport protein BetT SW:BETT-ECOLI (P17447) (677 aa) fasta scores: E(): 0, 77.6% id in 678 aa, and to Erwinia amylovora high-affinity choline transport protein BetT TR:AAG31040 (EMBL:AF264948) (676 aa) fasta scores: E(): 0, 80.0% id in 681 aa"
		/codon-start=1
		/transl-table=11
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		/db-xref="GI:15979231"
		/db-xref="SPTREMBL:Q8ZGV7"
		/translation="MVTSDIDTKPQKDTLNPVVF FTSAGLILAFCLMTIFYTDLSNRW IGITLNNWSATFGWYYLLAATLYIVFVIYIATSR YGSIKLGPEQSKPEFSLVSWAAML FAAGIGIDLMFFSVAEPVTQYMPPEQGQQTLEA ARQAMVWTLFHYGLTGWSMYALMG IALGYFSYRYNPLPLTIRSAFYPIFGKRIDGPIGH SVDIAAVIGTIFGIATTLGIGVVQ LNYGLNVLFHIPESLAVQAGLILLSVMAAVSVT SGVNGGIRILSEVNVLLALGLILF LLNALVLNVGDYINRFLGMTLNSFAFDRPTQWMN SWTLFFWAWVWVWSPFVGLFLARI SRGRTIRQFVVGTLIIPFVFTLLWLSIFGNSALY QILHGNIAFANEVMEFPERGFYSL LAQYPGFTLSASVATITGLLFYVTSADSGSLVLG NETSRLADINNDSPNWLRTFWSIT IGLLTLGMLMTDGVAALQONATVIMGLPFSFVIFV VMVGLYKSLKIEDYRKASSQQTPT PTLISGNEVLNWKQRLSRVMNYPGTTYTAKILDT ICRPAMEEVAQELAVRGVKVEFNE LPPKEDEQLNRLNHLELLVHLGDEQNFVYQIWPQ RYSVPAFTYRARSQKSHYYRLEY LLEGTQGNLMDYSKEQIINNILDQYERHNMFLH IQSEAPGNIMTFPDQ"
misc-feature	196144..196212	/gene="betT"
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misc-feature	196156..197589	/gene="betT"
		/note="Pfam match to entry PF02028 BCCT, BCCT family transporter, score 909.00, E-value 1.3e-269"
misc-feature	196255..196323	/gene="betT"
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misc-feature	196384..196452	/gene="betT"
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misc-feature	196534..196602	/gene="betT"
		/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
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misc-feature	197026..197094	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
		/gene="betT"
misc-feature	197032..197061	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
		/gene="betT"
misc-feature	197128..197187	/note="PS01303 BCCT family of transporters signature."
		/gene="betT"
misc-feature	197278..197346	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
		/gene="betT"
misc-feature	197434..197502	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
		/gene="betT"
misc-feature	197512..197571	/note="one of 12 probable transmembrane helices predicted for YPO1168 by TMHMM2.0"
		/gene="betT"
gene	198355..199248	/gene="YPO1169"
CDS	198355..199248	/gene="YPO1169"
		/note="Similar to many eg. Escherichia coli xanthosine operon regulatory protein WapR SW:XAPR-ECOLI (P23841) (294 aa) fasta scores: E(): 0, 38.3% id in 287 aa"
		/codon-start=1
		/transl-table=11
		/product="putative LysR-family regulatory protein"
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		/db-xref="GI:15979232"
		/db-xref="SPTREMBL:Q8ZGV6"
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misc-feature	198388..198816	/gene="YPO1169"
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misc-feature	198427..198492	/gene="YPO1169"
		/note="Predicted helix-turn-helix motif with score 1460 (+4.16 SD) at aa 25-46, sequence LHFHGKAAERLHISQPPLSLQIK"
misc-feature	198430..198522	/gene="YPO1169"
		/note="PS00044 Bacterial regulatory proteins, lysR family signature."
gene	complement(199286..200167)	/gene="YPO1170"
CDS	complement(199286..200167)	/gene="YPO1170"
		/note="Weakly similar to Bacillus subtilis hypothetical 35.8 kDa protein in lplD-pel intergenic region SW:YETK-BACSU (O31540) (330



22.5% id in 298 aa, and to Erwinia  
chrysanthemi PecM protein pecM  
SW:PECM-ERWCH (P42194) (297 aa)  
fasta scores: E(): 0.00048, 20.9%  
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FGCLGMALNPVVKKLHRGEHALVLTGWSLICAT  
LLTVIIAYQLPEIEWRNISVITW  
SGVLYLATFATALSFFLFQKACIVLSPTKVSGYV  
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misc-feature	complement(199292..1993 42)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199298..1996 78)	/gene="YPO1170"  /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 41.70, E-value 1.6e-08"
misc-feature	complement(199358..1994 23)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
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misc-feature	complement(199559..1996 24)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199652..1997 17)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(199748..2001 19)	/gene="YPO1170"  /note="Pfam match to entry PF00892 DUF6, Integral membrane protein DUF6, score 54.80, E-value 1.9e-12"
misc-feature	complement(199748..1998 04)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
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misc-feature	complement(199883..1999 48)	/gene="YPO1170"  /note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"

	53)		/note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
misc-feature	complement(200066..200131)		/gene="YPO1170"
gene	200480..201343		/note="one of 10 probable transmembrane helices predicted for YPO1170 by TMHMM2.0"
CDS	200480..201343		/gene="xapA" /note="synonyms: pndA, YPO1171" /gene="xapA" /EC-number="2.4.2.-" /note="Similar to Escherichia coli xanthosine phosphorylase XapA or PndA SW:XAPA-ECOLI (P45563) (277 aa) fasta scores: E(): 0, 70.2% id in 272 aa, and to Mus musculus purine nucleoside phosphorylase SW:PNPH-MOUSE (P23492) (289 aa) fasta scores: E(): 0, 42.6% id in 265 aa" /codon-start=1 /transl-table=11 /product="xanthosine phosphorylase" /protein-id="CAC90012.1" /db-xref="GI:15979234" /db-xref="SPTREMBL:Q8ZGV4" /translation="MTTVNSNINVDAFNFELPFQ AVKYIQKIKPGFKPQIAFILGSGL GDLVDQITNDTTISYADIPGFVSSVHGHAGELV LGDLCGVPVMCMKGRGHFYEGKGM SIMTNPVVRTFKLMGCEFLFCTNAAGSLRPEVLPG SVVMLKDHINTMPGTPLVGPNDNR FGPRFFSLANAYDKDLRADMAKIAQQLDIPLTEG VFVSYLGPCFETPAEIRMMQIIGG DVVGMSVVPEVLSAAHCGLKVIALTAITNLAEG SDVVLSEQTLKFAKVASVNFTKL IEAFLKSKALR" /gene="xapA"
misc-feature	200585..201220		/note="Pfam match to entry PF00896 Mtap-PNP, phosphorylases family 2, score 362.50, E-value 4.6e-105"
gene	201482..202126		/gene="xapB'"
CDS	201482..202126		/note="synonym: YPO1172" /pseudo /gene="xapB'" /note="Gene interrupted by IS1541. Similar to Escherichia coli xanthosine permease XapB SW:XAPB-ECOLI (P45562) (418 aa) fasta scores: E(): 0, 62.5% id in 216 aa, and to Escherichia coli nucleoside permease NupG nupG SW:NUPG-ECOLI (P09452) (418 aa) fasta scores: E(): 0, 49.6% id in 248 aa" /pseudo /codon-start=1 /transl-table=11 /product="xanthosine permease (pseudogene)"
misc-feature	201500..201568		/gene="xapB'"
misc-feature	201596..201664		/note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0" /pseudo /gene="xapB'"
misc-feature	201683..201742		/note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0" /pseudo /gene="xapB'"

		for YPO1172 by TMHMM2.0"
misc-feature	201770..201838	/pseudo
		/gene="xapB"
		/note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201875..201931	/pseudo
		/gene="xapB"
		/note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	201959..202027	/pseudo
		/gene="xapB"
		/note="one of 6 probable transmembrane helices predicted for YPO1172 by TMHMM2.0"
misc-feature	202127..202838	/pseudo
		/note="IS200-like insertion sequence: IS1541. Contains a 'G' at nucleotide position 315"
gene	202272..202730	/gene="tnp"
		/note="synonym: YPO1173"
CDS	202272..202730	/gene="tnp"
		/note="Similar to Salmonella typhimurium, and Salmonella typhi transposase for insertion sequence IS200 TnpA SW:T200-SALTY (Q57334) (152 aa) fasta scores: E(): 0, 94.1% id in 152 aa. Also identical to the Yersinia pseudotuberculosis IS1541-like elements transposase Tnp TR:Q9X9F5 (EMBL:AJ238014) (152 aa) fasta scores: E(): 0, 100.0% id in 152 aa"
		/codon-start=1
		/transl-table=11
		/product="transposase for the IS1541 insertion element"
		/protein-id="CAC90014.1"
		/db-xref="GI:15979235"
		/db-xref="SPTREMBL:Q9X9F5"
		/translation="MRDEKSLAHTRWNCKYHIVF APKYRRQVFYREKRRRAIGSILRKL CEWKVNILEAECCVDHIHMLLEIPPKMSVSGFM GYLKGKSSLMLYEQFGDLKFKYRN REFWCRCGYVVDTVGKNTARIQEYIKHQLEEDKMG EQLSIPYPGSPFTGRK"
misc-feature	202326..202637	/gene="tnp"
		/note="Pfam match to entry PF01797 Transposase-17, Transposase IS200 like, score 236.10, E-value 5.1e-67"
gene	203145..204074	/gene="YPO1174"
CDS	203145..204074	/gene="YPO1174"
		/note="no significant database hits"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="CAC90015.1"
		/db-xref="GI:15979236"
		/db-xref="SPTREMBL:Q8ZGV3"
		/translation="MPQVNNISTNNIHSAGFNNS NSIQKYTGAVSSISDDLRLINNEKC KSDIGTISGDIKINRHSAYGVNVSVDITVKN SIVDKDITTVSGDVNAVNSTIGKN IKTVSGSIEVEQSTVSGNLETTSGGIDIDTTKIN GNVHTTSGSISMNDSTIDGSVTCK AGSVTIVNSTIKESLNVLTSEKIIVGTASCIGKIN ISPPESVNFNIMNFGNDSIVMGMR NFCISGEVNFTITNGKVFVNEQRVGHTASQSTSK KVEEVTINIAKNASVNDIVFYTKK CHIILEGNAKYNGEKKDGMQFTHVNAPKSHAYA"
gene	204368..205312	/gene="YPO1175"
CDS	204368..205312	/gene="YPO1175"

		Escherichia coli hypothetical protein YohI SW:YOH1-ECOLI (P33371) (315 aa) fasta scores: E(): 0, 83.3% id in 311 aa, and to Vibrio cholerae hypothetical protein VC1105 TR:Q9KT00 (EMBL:AE004191) (323 aa) fasta scores: E(): 0, 58.9% id in 309 aa"
		/codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="CAC90016.1" /db-xref="GI:15979237" /db-xref="SPTREMBL:Q8ZGV2" /translation="MSMRVILAPMEGVLDLSLVRE LLSEVNDYDLCITEFLRVVDQLLP AKSFYRLCPPELHNQSRQSGTLVRIQLLGQYPEW LAENAAARAVALGSYGVDLNCGCPS KLVNGSGGGATLLKDPPELIYQGAKAMRAAVPAHL PVTVKIRLGWDSGDRQFEIADAVQ QAGATELAVHGRTKEDGYQAERINWQAIGEIRQR LTIPVIANGEIWDYQSAQECMKVT GCDVAMLGRGALNVPNLSRVVKYNEPRMPWLEVV KLLQKYVQLEKQGDGTGLYHVARIK QWLGYLRLKEYTEATDLFGEIRALKNSKDIALAIQ RINR"
misc-feature	204383..205297	/gene="YPO1175" /note="Pfam match to entry PF01207 UPF0034, Uncharacterized protein family UPF0034, score 428.70, E-value 5.2e-125"
misc-feature	204647..204703	/gene="YPO1175" /note="PS01136 Uncharacterized protein family UPF0034 signature."
gene	205904..206839	/gene="pbpG" /note="synonym: YPO1176"
CDS	205904..206839	/gene="pbpG" /EC-number="3.4.99.-" /note="Similar to Escherichia coli penicillin-binding protein 7 precursor PBP7 SW:PBP7-ECOLI (P33364) (313 aa) fasta scores: E(): 0, 73.5% id in 309 aa, and to Vibrio cholerae D-alanyl-D-alanine endopeptidase vca0870 TR:Q9KL77 (EMBL:AE004414) (316 aa) fasta scores: E(): 0, 61.1% id in 314 aa" /codon-start=1 /transl-table=11 /product="penicillin-binding protein 7 precursor" /protein-id="CAC90017.1" /db-xref="GI:15979238" /db-xref="SPTREMBL:Q8ZGV1" /translation="MYVKIRFALLSFLLLSTGIS VAPLAIARGSAVEVKGTAPLELAS GSAMVVDLQTNKVIYANNADKVVP IASITKLMTA MVVLD AKLPLDEILSVDIDQTKEL KGVFSRVVNSEISRKDM LLLTLMSS ENRAAASL AHHYPGGYNAFIKAMNAKAKSLGM NSTHYVEPTGLSINN VSTARDLAKLLMATKQYPL IGQLSTTTTEKMATFREPNYTL PFR NTNHLVYNDKWN IQLTKTGFTNQAGHCLVMRTVI GKRPVALVVLDAFGKYTHFADANR LRSWIETGKAAPIPGA AKSYRQQKDSQGRLAQVS E"
misc-feature	205994..206764	/gene="pbpG" /note="Pfam match to entry PF00768 Peptidase-S11, D-alanyl-D-alanine carboxypeptidase, score 380.50, E-value 1.7e-110"
gene	complement(206960..2086	/gene="dld"

CDS	complement(206960..208675)	/note="synonym: YPO1177" /gene="dld" /EC-number="1.1.1.28" /note="Similar to Escherichia coli D-lactate dehydrogenase Dld SW:DLD-ECOLI (P06149) (570 aa) fasta scores: E(): 0, 66.1% id in 558 aa, and to Neisseria meningitidis D-lactate dehydrogenase NMB0997 TR:Q9JZL7 (EMBL:AE002450) (563 aa) fasta scores: E(): 0, 60.9% id in 558 aa" /codon-start=1 /transl-table=11 /product="D-lactate dehydrogenase" /protein-id="CAC90018.1" /db-xref="GI:15979239" /db-xref="SPTREMBL:Q8ZGV0" /translation="MMSQFNNEKIQLLLTQLQHI VGTRYLLTGERQTERYRTGFRSGK GVALAVVFPSTLLQQWQLLQACVAADTIIIMQAA NTGLTEGSTPSGDDYDRPIVILNT LRLNNIQLLDDGKQVIGFPGSTLNQLEKRLKPYG REPHSVIGSSCIGASVVGICNNS GGSLVQRGPAYTEMALYAQIDAQGELQLINHLGI SLGNTPEEILQRLQEQGYGAEDIE QTGQQASDSEYATRVRDIDATTPSRFNADPRRLF EASGCAGKLAIFAVRLDTFPSEKQ QQVFYIGTNQTQVLTELRIILRDFKHLPIAGEY LHRDIFDIAETYGKDTFVMINSMG TNNMPRFFFTLKGKIDARLNKIPHLVDHLTDRVMQ GFSQILPNHLPKRLKTYRNQYEH LLLKMSGDGITEAQOHLRAFFATAEGNFIACTAD EGKKAFLHRFAAAGAAVRYHAVHA DQVEDILALDIALRRNEKQWFETLPPEIEKCLIA KLYYGHFLCHVFHQDYIVKKGVDV KALKEKMLSLLNDKGAEYPAEHNVGHLYLAKPAL KDFYQQIDPTNSFNPGIGKTSKRK RWQQD"
misc-feature	complement(208031..208633)	/note="Pfam match to entry PF01565 FAD-binding-4, FAD binding domain, score 104.80, E-value 1.7e-27"
gene	208882..209421	/gene="cyaB"
CDS	208882..209421	/note="synonym: YPO1178" /gene="cyaB" /EC-number="4.6.1.1" /note="Belongs to a family of thermophilic adenylate cyclases. Similar to Aeromonas hydrophila adenylate cyclase 2 CyaB TR:O69199 (EMBL:AJ223730) (190 aa) fasta scores: E(): 8.9e-33, 50.9% id in 175 aa" /codon-start=1 /transl-table=11 /product="adenylate cyclase 2" /protein-id="CAC90019.1" /db-xref="GI:15979240" /db-xref="SPTREMBL:Q8ZGU9" /translation="MSEHFVGKYEVELKFRVMDL TTLHEQLVAQKATAFTLNNHEKDI YLDANGQDLADQQISMVIREMNPISGIRLWIVKGP GAERCEASNIEDVSKVQSMLATLG YHPAFTTIEKQRSIYFVGKFHITVDHLTGLGDFAE IAIMTDDATELDKLKAECRDFANT FGLQVDQQEPRSYRQLLGF"
misc-feature	208912..209418	/gene="cyaB" /note="Pfam match to entry PF01928 Adenylate-cyc-2, Adenylate cyclase, score 136.60, E-value 4.6e-37"
gene	complement(209447..2097	/gene="YPO1179"

/note="Similar to Escherichia coli  
hypothetical protein YajD  
SW:YAJD-ECOLI (P19678) (109 aa)  
fasta scores: E(): 0, 84.7% id in  
98 aa"  
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protein"  
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5461	agtgtgacca	ccgtcggcgc	cactgaccgc	accctgcacg	ggctggattt	aaatggcggt
5521	acgctgatct	ttgacggttc	accgcccga	tctcaggcca	atggggctcg	cacggttact
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5761	ggcacagcca	ttacctctgg	tacgcaaggg	gtggagtctg	ccatccagca	gggcggtagc
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17941	attcgcgaga	tattgctctt	cattgacgga	tttatcagct	gattttccat	tattcattgg
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18421	agggcagtg	ctttattcag	gtgatgttga	aaaaaatgct	caacgtcact	ccacagcgta
18481	ttttaacgcc	agcggctcgtc	tttatcgggtg	tggttagcca	tgctgcctct	gattcagctt
18541	atgtgatcct	gatgcctgtc	gccgcgatga	tggtctatgc	cagtgggctg	caccatttag
18601	ccggtattgc	cgccgctttc	gctgggttag	cagggggatt	ctctgcccagc	tatacgccat
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18721	gttataacgt	caatgtgctg	tggaactact	tccctcagtt	cggtagcacc	tttggcgta
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18961	ccgcagcact	ctatccggaa	aactcccttat	tgcgttcacc	agatggcagc	ctgaccgcc
19021	ctgatgcacc	gattatgcaa	gcgatgtgct	cactgctgtt	ctttatgttt	gcgattctctg
19081	gcctgatcta	tgggtttcagt	tctggcacct	ttaaagacac	caaagatgtt	accgccagca
19141	tggāaaacat	tacccgctca	ttggtctcgt	ttttggtctt	tagcttcttc	tgcgcccgat
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19861	ggcgcatag	ttagctgaag	aactgcgtca	gttgggggtg	gaagatatcc	tgattgatga
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20041	acgctttacc	ggtagcgatc	tttgccāaa	cgcagagcag	ggcatctatc	tacgtaccgc
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20821	cgatggtgcg	gcgttatcaa	ccāaaagggt	gctgacccca	aattatttta	ccggggcgca
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21361	attaatgatg	gtattttatc	ggaagttttt	tactgtāacg	gttttāattt	cattaccctg
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26161	acagtgcagc	gċgċgtgtcġ	tġgggggċgt	gaatttactc	ctatcggcac	aaatagaaca
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26341	gġċċġtgata	ġatgġċġatc	ċtġċtċtāġc	ġatcattġag	gġċagġtċġ	tġġġcagġa
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26461	ġċttttacag	cġagċatċat	tġġtċċċġa	tġatātċtċġ	tċattġġaaa	ċċcatġġaac
26521	gġġtacttċġ	tġagggġatc	ċġġttġagċt	aagċġċċatt	ġatċġtġtċt	atġġtċaacġ
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26641	ggggggattt	ġcattāġċcā	ggġċtġtċġc	ġcagatācāā	caacagaaġġ	ċċtttġġtċā
26701	ċċċċċġċtā	aatāġċtātā	acċċactġat	agcagāāāāā	tċatcāġġtt	attatttċġā
26761	tāaġatāġċt	tġċċttġġġ	tāatċāāāġ	tġtġċċatc	aatġċtttāā	ġċtttaccġġ
26821	aacġatġġċt	ġġġċċġtġt	tġagāāāġċċ	tāċġġcagġtt	ġċtāġatċāā	tāāāġtċāāt
26881	tacatċāātā	aagġcagċcā	ċatċāātāāā	atċāġttācā	tċāātāāātġ	tāacġaacġġ
26941	tġcāātāġtġ	atċċācāċċċ	aacġċċtġāā	atċāġatċcā	ggġġġtāātċ	tġġtċtċċtġ
27001	attcāġġāġā	ġtttātġġtċ	acttttġāġā	ċāġttātġġā	aattāāāātċ	ċtġcācāāġc
27061	aggġāātġāġ	tāġċġġġġġc	attġċċāġāġ	aactġġġġāt	ċtċċċġcāāt	acċġttāāāċ
27121	ġttātġtġġcā	ġġcāāāātċt	ġāġċġċcāā	aātātāċġċċ	ġġāċċġtġċt	ġttġċttċāċ
27181	tċċtġġātġā	atāċċġġġāt	tātattċġtċ	aacġċatċġc	ċġātġċtċat	ċċttācāāāā
27241	tċċċġġcāāċ	ġġtāātċġċt	ċġġāġātċā	ġāġāċċāġġġ	ātātċġtġġċ	ġġāātġāċcā
27301	tċtċtċāġġġc	attċattċġt	tċtċtċtċġġ	tċċċtċāġġā	ġcāġġāġċċt	ġċċġttċġġt
27361	tċġāāāċtġā	acċċġġāġġā	ċāġātġġāġġ	tġāġtġġġġġ	ċactātġġġt	aatġġtċġġt
27421	ċāċġġċttċā	ċġtġttċġtt	ġċtġttċtċġ	ġātācāġċġġ	aatġġtġtāċ	atċġāattċā
27481	ċtġācāātāt	ġġġttātġāċ	acġtġġġāġā	ċċtġċċatċġ	tāātġġttċ	ċġċttċtttġ
27541	ġtġġtġtġċċ	ġġġġāāġtġ	tġtātġāġā	ātātġāāāāċ	tġtġġttċtġ	ċāacġtġāċġ
27601	ċātātċāġāċ	ċġġtċāġċāċ	ċġġttċċatċ	ċttċġġtġtġ	ġcāġttċġġċ	aāġġāġātġġ
27661	ġċttċtċtċċ	ċġāġtġtġt	ċġċċċttċā	ġġġċāġāġāċ	tāāāġġtāāġ	ġtġġāāċġġā
27721	tġġtġcāġtā	ċāċċġtāāċ	āġtttttācā	tċċċactāāt	ġactċġċċtġ	ċġċċġātġġ
27781	ġġātċactġt	ċġātġttġāā	acāġċcāāċċ	ġċċāġġtċt	ġġġtġġġtġ	ċcāġātġtġġ
27841	ċtāāċcāāġ	āāāġātġāā	acāātċāġġ	ċċġtċċċtġ	ġġātċġtġġġ	ċtġāāġāġċ
27901	āġcāġtċċāt	ġġtġġcāċtġ	ċċtċċġġāġā	āāāāāġāġtā	tġāġtġġċāt	ċttġātġāāā
27961	ātċtġġtġāā	ċttċġācāāā	ċāċċċċtġċ	ātċātċċact	ċtċċātċtāċ	ġactċattċt
28021	ġcāġāġġāġt	ġġġtġātġā	tġġāāċtġcā	acātċāāġġā	ċtġātġġġġċ	tġġċġġġġcā
28081	ġttġcāāċtġ	ġāāāġċċttā	tāāġġġāġġ	ġċċtġġġtġ	tċācāācāġġ	ċāġtāġāċcā
28141	ġġāātġġāġt	tātātġġāġt	tċċtġġāġā	tċtġġttċāt	ġāāġāāāāāċ	ġġġcāġtċā
28201	tċāāġtāāā	ċāġġġātġt	ātāċċġāāt	ġġġāġċċtċ	ċġġġġġtġā	āāāġttċġā
28261	āġāġtātġāċ	tċcācāttċġ	ċcāċġġāġġ	acġġcāāāġ	ċāactċċāġt	ċġttāġġtċ
28321	actcāġċttċ	ātāġāāġtā	ātġāāāātāt	ċġtātātactġ	ġġġċċātċāġ	ġtġtġġġġāā
28381	āāċċċātċtġ	ġcāātāġġcā	tġġġġtātġā	āġcāġtċġt	ġcāġġtātċā	āāġttċġċtt
28441	ċācāācāġcā	ġcāġātċtġt	tāċttċāġtt	ātċtāċġġcā	ċāacġtċāġġ	ġċċġttātāā
28501	āāġcāġġtt	ċāġġtġġāġ	tāātġġċċċ	ċġġċtġġtċ	ātċātġātġ	āāātāġġċtā
28561	tċtġġġttċ	āġtċāāāāġ	āāġcāāāġt	ġttċttċċāġ	ġtċātċġtā	āacġttāġcā
28621	āāāġāġġcā	ātġātċċtġā	ċātċcāātċt	ġċġttċġġġ	ċāġtġġġātċ	āāacġttċġċ
28681	ċġġtġātġcā	ġcactġāċċt	ċāġġātġġt	ġġāċġtātċ	tċācāċċact	ċācātġtġġt
28741	tċāāātċāāā	ġġāāāāġġt	ātġāġtċāġ	acāāāāāġcā	āāġġċġġġġ	tċātāġcāġā
28801	āġċtāātċċt	ġāġtāāāāġ	ġtġġātċāāt	ātġġġċġġt	tġġtġġāġāt	ātāāġtġġāt
28861	ċacttttċāt	ċġġtċġttā	ċāāātāāġċ	tċċġġtācā	āāāāāāāāġ	ġġtttttāċġ
28921	ġtġttġāāā	tācāġċċcāā	ġġġġtāācā	tċātactċāġ	tāġċċċġcā	ġāġġtātċ
28981	ġtċtġġttāt	ċtċāāġċġt	ġġġġtātāā	ġġttātġtāġ	tġāācāācāā	tċċātġġcāġ
29041	ġcātċċātċt	ātġċċtttāġ	tġġtċāātġt	ċttġtċtāċċ	ċcactċāāġ	ċġcāġċcāāċ
29101	acġāāċġġġ	ġġttttāċċt	tġċċtġāāt	ġātġġtġġġ	ċtāāġtttċġ	ġtāġċċtġāt
29161	āġġġtġāġċ	acāġcācāġġ	tċttāċċcāā	ātātāāġċcāġ	ċāāātttċġġ	tġttġcāācā
29221	ġcātātċġċ	ċttġāātġāġ	tāātġāātċā	ġġċātġġġġ	ġċātġġāġā	āāāātġġġ
29281	ċāġāġġġġċ	tċttġċċāġ	ġġāātġtċā	ġġġġāġġċċ	ātāāċġātāġ	āacātātċt
29341	ċġġtġāāāġ	ġċtċactċtt	ġċċtġātġt	tġċttātġāt	ċttāātġtġcā	ātġġġāġātġ
29401	ġġāāġġġġġ	āāācātċāāġ	āġtċāāātā	tċttġġġtāt	ċġġtāġġcā	ātāāāġġġtt
29461	āġāġātċāġ	ċġtġġġāāċ	tġāāctġċcā	tġġċġtġġt	tġġġāāāāāċ	tġtttġātċċ
29521	acġāātġtt	actġtġāċtċ	acttttċġt	āāċċċċtċtġ	tċtġġġcāāċ	tċttċāāāt
29581	ġġġġtġtġ	ġġġcātāāāā	ċġġġtāātċċ	āġċtātċċāċ	ċātċāġtġā	ċttāċċttāt
29641	ċġtġġāāt	āāġġātġāċ	ġcāġtātċtt	ċāāġāġġcā	ġcāġtāċċċt	ġġġġġġġtt
29701	ātġāċċttt	tċttċtttġġġ	ātātātċttġġ	ċtātċāġġcā	tācātċġġcā	ātātāġācāt
29761	ātċċāġcāāā	tċāċġġāġā	ġġāācāāġġċ	tātċttāċġġġ	ċttācāātċā	ġġġtāātċā
29821	tċactċāāċt	ġġġġtġtċāġ	ċcāġġġtġġ	ġġġtċāġāā	tāċċttġġġġ	ġġtāġġttċā
29881	ġcātġġċāt	ġcātġġcācā	tċāġġāġtċ	ġġċttāāāāġ	ċttġġġtāā	ġġġtċātċā
29941	ċtġġġġġtt	tċtttātċtċt	ċāāāġāġāā	āġtċttċġġċ	tġġġtġġġt	ċċċċġġtġ
30001	ātġġtttāċċ	āāġtġttāā	actāāāġġcā	ġttācāġġāā	ġttċġġġġāā	tċātċāġttġ
30061	ātġācāġġċ	ċtċātġġttġ	ġttġġātċtt	tġċċċtġātā	āġġātġcācā	ġttttġġċtċ
30121	ġātātāātāāċ	ċāāācāġġċt	tātġġācāāā	ċtātċttċāġt	ġġāġācāġġċ	ġġtttċāāċċ
30181	tāġtċāċċt	ġġtġġātċċ	āġċttāċtġġ	āāġttttġāt	tġċġġcātāā	tċtttċtċāā
30241	tċtċactāċt	ġġġġtāċtġ	ċāātāċċātċ	āġġċactttt	acāġġġċttt	ġċċċċċāt
30301	ġġcāācāāġ	ġcāāġċġtġġ	tċġtġġttāċ	ātċāātātāt	ġġāġātċāġ	āġġġtācāġ
30361	āċċċġāāġā	acġġtġġġġc	ċċtġāāġtġā	āāāāġġġtġ	ġcactātċġċ	ċāātċttātċġ
30421	ātġġcātġā	ġġġġātġġċ	ċġġāātċttā	ġġtāāāġtt	ġātāāċċġġċ	ċāāġactċġċ
30481	ċāġtāġāāt	āāġġġātġġ	tċtttġttċāā	ċtġāġātġāt	tġāġġtātġ	tātċāċġāt
30541	āċċtġttġġġ	ċāġāċtċāt	ātċāāġttāġ	āġtātċāāċ	ġtċāġāāċt	ātċċātċāġċ

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30781	catggcccaa	tggttacaaa	tgcaactggc	tcaacagttc	agtattgctg	ccaatatagt
30841	gtttcctcta	cccgctactt	ttatctggga	tatgtttacc	cgcgttctgc	ctgatattcc
30901	taaagaaagt	gcattcagca	aagaggctat	gacatggaaa	cttatgtggc	tactgccaga
30961	tttatgggag	aatccactat	ttctcccat	gaagcgctat	ttaagtgatg	atggggatcg
31021	gcgtaaaatt	caccaactcg	cggcacgggt	agccgatctt	tttgaccaat	atctgggtga
31081	tcgtccggaa	tggctggaaa	gttgggaacg	tgggcaattg	attgaggggc	ttgatgatgc
31141	acagcaatgg	caagcattac	tgtgggttga	actgacccgc	tatactcgcc	aattggaaca
31201	accggaatgg	caccgggcaa	acctctatca	gcgttttatc	caccaactac	tcaagtcgga
31261	cgtttgcccg	caagggttac	cgaacgggt	atttatatgt	ggtatatcgg	cgttgccacc
31321	tatctattta	caggccctac	aagcattagg	tttaacacatt	gatatccatt	tgatgtttac
31381	taaccctctgc	cgttacttct	ggggagatat	tcaggattac	actttcctcg	ctaaattaca
31441	aagccgtaaa	cgtcggcatt	accgtgaatc	gattgaacta	agtctgtttc	gccaccgcga
31501	gcaggcagag	caactattta	ataccgatgg	tgagcagaac	ctcagtaacc	cactcttggc
31561	ctcatggggg	cgattagggg	gggatcacat	gtatttgctc	tctcaaattg	atgaaattca
31621	agaggttcat	gcttttgcgc	atatcgagcc	agataactct	ttgcatggca	ttcaacacga
31681	tatgctggag	ttggaagatc	acgcggttat	tggcaaaccc	ccagaaacct	tagcgctag
31741	tgatcaaaaa	cgcgatttag	atctggatga	tcgttcactt	agtttccatg	tctgccacag
31801	cccacaacga	gaagttgagg	tgctgcaaga	tcatttactt	gggctattag	ccgcagaccc
31861	tgaattgacc	ccgcgcgaca	tcatttgtgat	ggtgggtgat	atcgacagtt	atacaccgta
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32161	catccgttgg	ggattggatg	atgataatgt	gcgggagcta	tccttacctg	ctacgggtca
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32281	aggggatttg	caaggtatct	tgccctacga	tgaatccagc	gggctggcag	cggaaactcg
32341	cgggcagttg	gccgatatgc	tgatgcacct	gagtcaatgg	cggcaacaat	taggtcagcc
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32521	ctacgggtatt	gcagcccaat	atccagacgt	tgtgccactt	aatctgctac	gagacgaatt
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32641	ctgtacctta	atgccaatgc	gctccatccc	atttaaagtg	gtttgtctat	tgggcatgaa
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32881	gcgttatcct	tcctgtctgg	taagcgagtt	aattgaatat	gtcgcacaaa	gctatcattt
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33961	acatttggac	ataattttac	atgaaactga	acgttatatt	ttaccgatag	ctcgccataa
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35041	tacctatatt	agctacttga	tcagtaatcg	cagtaaaaac	accttatctg	actggctaca
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35221	cg̃t̃c̃g̃c̃g̃gca	attttt̃gat̃f̃	acatcaatat	g̃c̃t̃gcãt̃āā	gãg̃g̃g̃gatta	āāāāāg̃c̃t̃a
35281	tt̃tc̃gat̃gaa	att̃gcacat̃g	tatt̃gaat̃c̃t	cgatt̃t̃cc̃g̃t	t̃at̃cc̃c̃t̃c̃t̃a	t̃cacc̃c̃g̃t̃ga
35341	tat̃ggact̃at	at̃cgaat̃g̃c̃	t̃c̃g̃t̃ggat̃at	gat̃gt̃t̃ac̃ga	gt̃t̃c̃c̃t̃gt̃t̃g	cacat̃ac̃g̃c̃t
35401	t̃gat̃g̃c̃g̃c̃c̃t	tat̃c̃t̃g̃g̃c̃t̃g	at̃cag̃tat̃ga	t̃cc̃c̃c̃aag̃ca	att̃gc̃at̃c̃c̃c̃	gatt̃g̃g̃c̃c̃ga
35461	gat̃gac̃g̃c̃c̃t	gaaat̃at̃g̃c̃c̃c̃	g̃cat̃c̃t̃g̃g̃t̃t̃	t̃gt̃cag̃c̃c̃c̃t̃	gaagaacc̃g̃c̃	ataac̃aaag̃t̃
35521	ag̃c̃t̃t̃at̃t̃t̃t̃	gt̃c̃gat̃g̃c̃ac̃	c̃t̃t̃at̃cag̃gt̃	cgataāāāa	gg̃c̃gt̃ac̃ag̃c̃	gg̃at̃gaãga
35581	at̃gg̃cag̃caa	ct̃gg̃gg̃cāāā	agatt̃g̃c̃g̃c̃t̃	aag̃t̃t̃t̃g̃c̃c̃a	gc̃act̃gaacc̃	c̃gt̃acatt̃c̃c̃
35641	t̃gataat̃t̃t̃c̃	act̃c̃t̃gat̃ca	aag̃cag̃acāā	gaacatt̃acc̃	cg̃cc̃c̃ac̃aga	ac̃gt̃gg̃c̃aga
35701	cc̃ag̃cc̃ag̃ga	t̃t̃g̃c̃gg̃gt̃g̃t̃	t̃t̃t̃ac̃at̃g̃c̃c̃	aag̃t̃cag̃tat̃	t̃t̃t̃g̃c̃t̃g̃ac̃g̃	aacc̃c̃c̃aag̃c̃
35761	cg̃acatt̃ac̃g̃	gt̃t̃g̃c̃t̃t̃t̃c̃c̃	g̃c̃aacc̃c̃c̃t̃c̃a	t̃gc̃att̃gaac̃	t̃cag̃c̃t̃cg̃c̃c̃	at̃cag̃gt̃g̃c̃t̃
35821	t̃t̃t̃t̃g̃c̃c̃c̃t̃g̃	ac̃gg̃att̃acc̃	t̃t̃g̃c̃gg̃gt̃c̃t̃	c̃t̃c̃act̃t̃gat̃	caact̃gag̃t̃t̃	at̃cag̃g̃c̃c̃t̃c̃
35881	tatt̃t̃gg̃t̃gg̃g̃	at̃cag̃t̃t̃t̃c̃t̃	ct̃acc̃cg̃c̃acc̃	gaac̃aat̃gg̃c̃	t̃t̃gt̃at̃gt̃t̃a	at̃gt̃c̃gg̃t̃gg̃
35941	t̃t̃t̃t̃ac̃ac̃ag̃	c̃gt̃at̃g̃c̃c̃g̃c̃	ag̃t̃t̃act̃g̃ac̃	at̃c̃t̃t̃t̃g̃g̃t̃t̃	t̃cag̃g̃c̃t̃at̃g̃	cc̃ag̃t̃t̃t̃t̃ac̃
36001	t̃cc̃g̃ac̃ag̃aa	gag̃caatt̃gg̃	t̃ac̃agg̃c̃t̃aa	at̃c̃t̃t̃g̃g̃t̃at̃	c̃gt̃gag̃caat̃	tag̃ac̃gt̃gg̃c̃
36061	ag̃ag̃aaag̃gc̃	aaag̃c̃t̃t̃at̃g̃	ag̃t̃t̃gg̃c̃t̃at̃	t̃cag̃cc̃c̃g̃c̃t̃	aag̃c̃t̃g̃c̃t̃at̃	c̃gaat̃gt̃g̃c̃c̃
36121	t̃t̃at̃t̃c̃g̃g̃ag̃	c̃gaag̃t̃g̃ag̃c̃	gac̃g̃t̃aaact̃	act̃t̃gat̃ag̃c̃	at̃cag̃t̃gt̃g̃c̃	agg̃at̃gt̃g̃c̃t̃
36181	gac̃c̃tat̃aga	gat̃gat̃t̃t̃ac̃	t̃gaaac̃ag̃t̃c̃	t̃gc̃gat̃ag̃aa	gt̃t̃t̃t̃g̃g̃c̃g̃	t̃gg̃g̃c̃aat̃at̃
36241	gac̃ag̃cc̃g̃aa	caag̃t̃c̃act̃g̃	aact̃c̃act̃ga	at̃c̃g̃t̃g̃aaa	aaac̃ag̃c̃t̃ga	act̃taat̃c̃g̃g̃
36301	aacc̃ac̃gt̃gg̃	t̃gg̃gt̃c̃g̃gt̃g̃	aag̃at̃gt̃c̃at̃	tatt̃gag̃aaa	ac̃ac̃ag̃t̃t̃gg̃	ccaat̃at̃gg̃a
36361	ac̃gg̃gt̃c̃g̃g̃c̃	ag̃tag̃t̃t̃c̃t̃g̃	ac̃g̃c̃g̃g̃c̃t̃t̃t̃	gg̃c̃ag̃c̃ag̃t̃t̃	t̃at̃gt̃cc̃c̃t̃a	c̃t̃gg̃c̃t̃at̃ac̃
36421	ag̃aaatt̃g̃c̃t̃	gg̃tat̃gg̃c̃ac̃	g̃tag̃t̃g̃c̃c̃t̃t̃	gt̃tag̃gg̃c̃ag̃	at̃catt̃c̃aac̃	cat̃gt̃t̃c̃t̃a
36481	t̃gat̃caatt̃a	c̃gg̃ac̃ag̃aãg̃	aac̃ag̃c̃t̃t̃gg̃	t̃t̃at̃gt̃c̃t̃g̃t̃a	t̃t̃t̃t̃c̃t̃t̃t̃c̃c̃	caat̃gt̃c̃g̃gt̃
36541	t̃gg̃t̃cat̃caa	t̃gg̃gg̃c̃at̃c̃g̃	g̃c̃t̃t̃c̃t̃t̃act̃	g̃c̃aaag̃taat̃	ag̃taag̃gaac̃	ctaatt̃at̃c̃t̃
36601	t̃tacc̃ag̃c̃ga	tac̃c̃t̃cg̃cat̃	t̃t̃t̃at̃c̃cg̃ca	ag̃t̃g̃taāāāā	cg̃c̃c̃t̃g̃c̃g̃c̃g̃	aaat̃gaag̃c̃c̃
36661	cg̃at̃gat̃t̃t̃t̃	gaac̃aat̃ata	ag̃c̃ag̃gg̃gt̃c̃t̃	gg̃t̃caat̃caa	ct̃att̃g̃c̃aaa	gg̃cc̃ac̃ag̃ac̃
36721	att̃ag̃at̃g̃aa	gag̃gc̃ag̃ag̃c̃	g̃c̃t̃acc̃g̃t̃aa	ag̃act̃t̃caat̃	ct̃caataat̃t̃	t̃t̃gc̃att̃t̃ga
36781	tag̃cc̃gt̃g̃ag̃	aag̃at̃gat̃t̃g̃	ct̃caag̃t̃g̃aa	ac̃ag̃c̃t̃t̃ac̃g̃	g̃c̃taat̃gaac̃	t̃gg̃c̃g̃g̃att̃t̃
36841	c̃t̃t̃cc̃ag̃caa	g̃c̃g̃gt̃c̃at̃ta	aacc̃acaag̃g̃	t̃c̃t̃gg̃c̃act̃g̃	c̃t̃t̃t̃c̃t̃caag̃	t̃taaag̃gt̃ca
36901	gg̃gg̃c̃ag̃g̃c̃c̃	gg̃agg̃att̃c̃g̃	cag̃t̃aac̃c̃g̃ga	gg̃gat̃gg̃ac̃g̃	act̃tat̃cc̃aa	cc̃act̃t̃c̃cg̃c̃
36961	t̃t̃t̃ac̃ag̃gt̃	ac̃g̃c̃t̃g̃c̃g̃c̃	agaag̃gt̃at̃t̃	gg̃c̃acc̃at̃ga	cac̃cc̃ac̃g̃ac̃	t̃cc̃cc̃ag̃c̃g̃g̃
37021	c̃t̃t̃gag̃c̃g̃c̃	t̃gg̃c̃g̃c̃t̃t̃c̃c̃	c̃c̃t̃c̃t̃at̃gg̃c̃	gag̃ag̃gt̃ga	tag̃aag̃c̃c̃t̃c̃	t̃g̃c̃c̃g̃gt̃act̃
37081	gg̃taag̃ac̃at̃	t̃tacc̃at̃c̃g̃g̃	gg̃t̃c̃c̃t̃t̃at̃	c̃t̃tag̃att̃gt̃	t̃g̃c̃t̃t̃gg̃gt̃t̃	agg̃gg̃g̃c̃gat̃
37141	g̃c̃t̃g̃c̃att̃c̃c̃	gt̃c̃g̃c̃c̃c̃t̃t̃t̃	gat̃gg̃t̃g̃g̃ag̃	gaaat̃c̃c̃tag̃	t̃gg̃t̃g̃ac̃c̃t̃t̃	tact̃gaag̃c̃c̃
37201	g̃c̃g̃acc̃gaag̃	ag̃c̃t̃cag̃gg̃g̃	g̃c̃gaatt̃c̃g̃c̃	gataat̃att̃c̃	at̃gg̃gt̃t̃g̃c̃g̃	t̃at̃c̃g̃c̃t̃t̃g̃c̃
37261	gt̃t̃c̃gg̃gg̃ag̃	t̃cag̃t̃gat̃ga	cc̃caat̃gt̃ac̃	cag̃g̃c̃t̃c̃t̃at̃	tag̃cc̃g̃aaat̃	cac̃cg̃att̃gg̃
37321	g̃c̃c̃gt̃ag̃c̃g̃	c̃c̃g̃c̃g̃caat̃t̃	att̃gg̃c̃g̃gt̃c̃t̃	gag̃c̃gt̃c̃aga	t̃gg̃at̃gaag̃c̃	c̃g̃c̃g̃att̃t̃ac̃
37381	act̃att̃cat̃g̃	gt̃t̃t̃c̃t̃g̃c̃c̃a	aagaat̃g̃c̃t̃g̃	g̃c̃aaataac̃g̃	c̃t̃t̃t̃t̃gaat̃c̃	c̃gg̃c̃att̃t̃t̃a
37441	t̃t̃c̃gaac̃aaa	c̃gt̃tag̃t̃t̃ca	gg̃at̃gaact̃c̃	c̃c̃gt̃tat̃gg̃c̃	gg̃c̃ag̃g̃c̃c̃t̃g̃	t̃g̃c̃t̃g̃act̃t̃c̃
37501	t̃gg̃c̃g̃g̃c̃gt̃c̃	att̃gt̃t̃at̃c̃c̃	g̃c̃t̃t̃c̃c̃c̃t̃t̃a	gt̃cat̃c̃g̃c̃ac̃	gg̃g̃c̃g̃gt̃c̃ag̃	t̃cag̃g̃ag̃t̃gg̃
37561	ag̃c̃g̃gg̃c̃c̃g̃g̃	agg̃c̃att̃act̃	cag̃t̃gat̃c̃t̃g̃	ag̃t̃g̃c̃t̃t̃at̃t̃	t̃acaag̃gt̃ga	aac̃g̃cc̃aaag̃
37621	t̃t̃t̃c̃gg̃caag̃	c̃g̃c̃c̃c̃g̃gt̃ga	cg̃at̃g̃aaac̃g̃	at̃c̃c̃t̃tag̃c̃c̃	g̃cc̃at̃c̃ag̃ca	c̃gt̃t̃gt̃g̃aca
37681	cag̃att̃gat̃g̃	cact̃t̃aaag̃c̃	ag̃ag̃t̃gg̃c̃g̃c̃	t̃tag̃c̃c̃g̃c̃c̃c̃	ct̃gaatt̃tag̃a	ag̃c̃att̃aat̃t̃
37741	ag̃t̃c̃gt̃t̃c̃t̃g̃	g̃c̃g̃t̃t̃g̃ataa	ac̃g̃c̃ag̃t̃t̃at̃	ag̃c̃ag̃caag̃c̃	act̃t̃acc̃c̃c̃aa	c̃t̃gg̃c̃t̃gg̃aa
37801	aaag̃tag̃gat̃	t̃at̃gg̃g̃c̃g̃ga	g̃c̃ag̃g̃aaac̃g̃	gaag̃att̃at̃c̃	aatt̃acc̃c̃c̃aa	agaact̃gg̃aa
37861	aaatt̃t̃c̃g̃c̃c̃	ag̃t̃c̃g̃gt̃gt̃t̃	att̃gg̃aaaag̃	accaagaag̃g̃	gag̃c̃c̃g̃c̃c̃c̃c̃	acaac̃atact̃
37921	t̃t̃at̃t̃tag̃t̃g̃	c̃gat̃ag̃act̃c̃	gat̃at̃t̃t̃g̃aa	cag̃c̃c̃c̃c̃t̃aa	c̃gt̃t̃gag̃gg̃a	t̃c̃t̃t̃at̃t̃t̃t̃a
37981	g̃c̃c̃c̃g̃ag̃c̃c̃a	t̃cag̃c̃g̃aaat̃	ac̃g̃gt̃t̃t̃t̃c̃t̃	gt̃ac̃ag̃c̃ag̃g̃	āāāāāc̃g̃g̃ca	g̃c̃g̃t̃g̃c̃ag̃ag̃
38041	c̃t̃g̃g̃gt̃t̃t̃g̃	at̃gat̃t̃t̃act̃	cag̃t̃aãgt̃t̃a	gat̃g̃c̃c̃g̃cat̃	t̃acaac̃aat̃c̃	gg̃gg̃gg̃t̃g̃ag̃
38101	t̃t̃g̃c̃t̃c̃g̃c̃c̃c̃	aat̃c̃t̃at̃t̃c̃g̃	t̃acc̃c̃g̃t̃t̃at̃	c̃c̃c̃gt̃t̃g̃caa	t̃gatt̃gat̃ga	att̃t̃cag̃gat̃
38161	acc̃g̃acc̃c̃g̃c̃	aac̃aat̃acc̃g̃	catt̃t̃t̃c̃c̃ac̃	acc̃gt̃t̃t̃at̃g̃	g̃c̃g̃gg̃c̃aaga	ag̃c̃gt̃g̃c̃g̃c̃t̃
38221	t̃t̃act̃gt̃t̃ga	t̃c̃g̃gt̃gat̃c̃c̃	t̃aaac̃ag̃g̃c̃t̃	att̃t̃at̃g̃c̃t̃t̃	t̃t̃c̃gt̃gg̃c̃g̃c̃	ag̃at̃at̃att̃t̃
38281	ac̃c̃tat̃at̃t̃c̃	g̃c̃g̃c̃c̃c̃gt̃t̃c̃	agaag̃taag̃c̃	g̃c̃c̃c̃act̃aca	catt̃gg̃aaac̃	caact̃gg̃c̃g̃c̃
38341	t̃c̃t̃t̃c̃t̃t̃t̃t̃c̃	cc̃at̃gg̃t̃g̃ca	at̃cag̃t̃gaac̃	agg̃c̃t̃at̃t̃t̃a	gt̃c̃t̃gg̃t̃t̃aa	t̃ac̃g̃c̃c̃t̃t̃t̃c̃
38401	t̃t̃at̃t̃t̃gag̃c̃	aaat̃c̃c̃c̃c̃t̃t̃	tatt̃aat̃gt̃c̃	g̃c̃c̃g̃c̃c̃g̃c̃c̃a	aaaagaat̃ca	t̃gatt̃t̃at̃c̃c̃
38461	t̃t̃t̃g̃aaatt̃a	aag̃gag̃aaaa	g̃c̃aac̃c̃t̃g̃c̃g̃	ct̃ac̃att̃t̃t̃t̃t̃	gg̃c̃t̃g̃c̃aacc̃	c̃g̃gt̃g̃ac̃g̃gt̃
38521	gt̃t̃gg̃t̃gt̃aa	gt̃gag̃t̃acca	acaag̃taat̃g̃	g̃c̃tag̃acaat̃	gt̃g̃c̃ag̃c̃g̃ca	aatt̃c̃gt̃gat̃
38581	t̃gg̃t̃t̃g̃act̃g̃	c̃c̃gg̃cc̃ag̃ca	gg̃gg̃c̃aag̃ca	gaact̃act̃ga	cc̃ac̃g̃aaag̃g̃	acc̃aaaacc̃g̃
38641	gt̃t̃cag̃g̃cat̃	cag̃at̃ataac̃	c̃at̃act̃gg̃t̃g̃	c̃gt̃ag̃c̃c̃gg̃g̃	cag̃ag̃g̃c̃c̃g̃c̃	att̃gat̃ac̃gt̃
38701	gat̃gc̃act̃t̃a	gt̃g̃c̃g̃c̃t̃gg̃c̃	gat̃c̃c̃c̃at̃c̃g̃	gt̃c̃t̃at̃t̃t̃at̃	ctaact̃c̃gt̃ga	cag̃t̃gt̃c̃t̃t̃t̃
38761	gag̃act̃ac̃ag̃	aag̃cc̃aaag̃a	t̃c̃t̃c̃t̃gt̃t̃g̃g̃	t̃t̃act̃g̃caag̃	c̃c̃gt̃gt̃t̃ag̃c̃	acc̃ag̃ag̃c̃ag̃
38821	gag̃c̃g̃c̃g̃c̃ac̃	t̃ac̃gt̃ag̃t̃g̃c̃	t̃at̃gg̃c̃t̃ac̃g̃	gg̃gat̃c̃t̃t̃gg̃	gg̃t̃t̃gg̃at̃g̃c̃	cag̃aat̃gt̃t̃g̃
38881	gat̃g̃c̃gt̃taa	at̃cac̃gat̃ga	g̃c̃g̃ag̃c̃t̃t̃gg̃	gat̃g̃c̃g̃c̃t̃gg̃	t̃c̃gat̃gag̃t̃t̃	t̃gat̃c̃act̃at̃
38941	c̃g̃cc̃ag̃c̃att̃	gg̃c̃ag̃c̃g̃c̃c̃g̃	t̃gg̃gg̃t̃at̃t̃a	c̃c̃cat̃g̃c̃t̃g̃c̃	gg̃g̃ag̃at̃gat̃	gg̃c̃c̃c̃g̃c̃c̃g̃c̃
39001	catt̃t̃tag̃c̃t̃g̃	aaaact̃t̃gt̃t̃	gg̃c̃aac̃acc̃c̃c̃	gg̃t̃g̃gg̃gg̃ag̃c̃	gt̃c̃g̃g̃c̃t̃g̃ac̃	ag̃att̃t̃act̃a
39061	cat̃c̃t̃t̃t̃gg̃g̃g̃	aatt̃act̃g̃ca	ag̃ag̃g̃c̃c̃g̃c̃c̃	t̃c̃g̃caact̃gg̃	at̃ag̃t̃gag̃ca	c̃gc̃act̃aat̃t̃
39121	c̃g̃c̃t̃gt̃t̃t̃gg̃	c̃c̃c̃ag̃caaat̃	t̃gt̃c̃caacc̃c̃	at̃c̃c̃c̃c̃c̃ag̃t̃	cag̃at̃ag̃c̃c̃a	ac̃aatt̃ac̃g̃c̃
39181	t̃t̃gg̃aaag̃t̃g̃	at̃c̃g̃c̃c̃att̃t̃t̃	gg̃t̃t̃c̃g̃ag̃t̃g̃	gt̃t̃act̃at̃c̃c̃	ataaat̃c̃g̃aa	agg̃gt̃t̃gg̃aa
39241	t̃at̃cc̃att̃tag̃	t̃t̃t̃gg̃c̃t̃g̃c̃c̃	t̃t̃t̃t̃at̃c̃g̃gt̃	aatt̃t̃t̃t̃c̃g̃g̃c̃	aac̃aac̃ag̃aa	t̃gt̃g̃c̃t̃t̃t̃ac̃
39301	cat̃g̃acc̃g̃ac̃	at̃ag̃c̃t̃t̃t̃ga	gg̃c̃t̃t̃t̃act̃c̃	gat̃c̃t̃t̃aat̃g̃	ct̃gat̃gaaga	aag̃cc̃ag̃g̃c̃t̃
39361	t̃tag̃c̃t̃gaag̃	aagaac̃gt̃c̃t̃	gg̃c̃t̃g̃ag̃gat̃	t̃t̃ac̃gg̃c̃t̃at̃	t̃gt̃at̃gt̃c̃g̃c̃	gt̃t̃g̃ac̃g̃c̃gt̃
39421	t̃c̃g̃gt̃t̃t̃at̃c̃	at̃t̃g̃c̃ag̃c̃gt̃	gg̃g̃c̃att̃g̃ca	c̃c̃g̃c̃t̃g̃at̃t̃a	aag̃gg̃gg̃gg̃ag̃	g̃aaaag̃c̃caa
39481	gg̃c̃g̃ag̃ag̃t̃g̃	at̃at̃g̃cat̃c̃g̃	cag̃t̃g̃c̃gt̃t̃a	gg̃t̃t̃at̃t̃t̃gg̃	t̃t̃cag̃c̃at̃gg̃	t̃c̃aac̃c̃c̃g̃gt̃
39541	gat̃g̃c̃t̃cat̃g̃	t̃t̃c̃taag̃c̃ga	aaag̃t̃t̃aact̃	gag̃t̃tag̃c̃g̃c̃	g̃c̃t̃cat̃c̃g̃aa	t̃gg̃t̃gat̃at̃t̃
39601	t̃g̃c̃gt̃t̃t̃c̃g̃c̃	c̃c̃gt̃t̃g̃ag̃c̃c̃	t̃c̃c̃t̃gat̃gat̃	aaac̃c̃t̃t̃gg̃c̃	aacc̃ac̃ag̃c̃c̃	c̃gaag̃c̃c̃t̃t̃g̃
39661	c̃c̃t̃gaact̃t̃a	c̃c̃g̃c̃c̃c̃g̃c̃c̃a	t̃t̃t̃t̃act̃c̃ga	aaaat̃g̃caag̃	att̃att̃gg̃c̃g̃	c̃gt̃aacc̃ag̃c̃

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90421	ġcġcagġġġcġ	ċtġġagġċċa	ġcatġtġtaat	aaaacċtċaa	ċtġcġattċa	tttġcġċttt
90481	ġacattāagġ	ċċtċaagċċt	ġċċagagġtat	tataaagaaa	ġġttattġtt	ġċtaaatagċ
90541	ċatttġġtġa	ċagġtġaagġ	tġttġtċatċ	ataaaagċac	agġaataccġ	ċagċċaagat
90601	atġaaċġġtġ	agġtġġcatt	ġġcġcġċtġġ	ġtagċactċa	tġcġċagġc	aatġġtġġta
90661	ġaaaagġġċċċ	ġtċġagċġac	aaaacċaacc	aaagġttċaa	aaatċagġġcġ	agttġagġġt
90721	aaagġċċġċa	aagġġġcġac	aaaagcġctġ	cġtġġtaaaa	tacatċaagā	ġtġaagġċġa
90781	tatttatatġ	aacġttġata	ċattġcġġtt	ġatātġactt	ċattċċatat	atatċġġaca
90841	ċagtatġġġa	ġaatċactġt	ġagġaaatta	acġataacġc	tacttttġġc	agtagġtġcġ
90901	ċtġtċattat	tagġctġtaā	tāatċġctċt	ċaacċtġctġ	aacagġtttt	ġċaacċaatġ
90961	ċagċagagċt	atċagġġcġt	attacċttġt	ġcġġattġċa	ġtġġċttāġa	ċacttċtttġ
91021	tġċċtċġata	ġtġatġġġac	ttttatċttġ	aaġaagttt	atċtċġġċac	tāaagatġġc
91081	ġacċaaactt	tġġcagāata	tġġtaaatġġ	ġċacġtactġ	ċtġataagtt	agġtġtaacc
91141	aacġġtċagġ	ġaġaaaaacġ	tġacttċċac	ċċtġtċġata	aaagċttġġt	ġatġctċġat
91201	ċagċaagġtt	tacċċattāa	atċġacactġ	aattatċagġ	tġġaaccċag	ċġaccagċċġ
91261	tġatċċaaaa	ċġċċaatġċċ	actāagġġt	atġtataaat	actttġġtġa	tġċċġċċata
91321	tġtactġatt	ġtġtaacġġġ	taagġcġttċ	ċċġġtagāġa	ataatātċġa	actġġaaċċ
91381	ġġġtatġttāa	acġtċġcag	aaacċċtġġa	ġaacċtġtġt	ttttġacċċt	ċaatġġġtat
91441	tttġattċaa	ġġċċatċaat	ġġaagāagġġ	cġaacġaata	aaacġctġat	tċċġġagġġġ
91501	ġatattċagġ	tġaatġċċaa	tāaaagttġt	ġaġaaaaaat	agċċċttġtċ	ċatagċtāaa
91561	ataagāagċċ	ġċacġġtagġ	tċaagttċtċ	cġġcġġċttċ	atċagġāaaa	tacċċċġċtt
91621	atġġġġactċ	tttattttatġ	ġcġġġtatċt	ttattttatġa	cġġġtatata	ġċċattacġ
91681	ġttttattttġ	ġctċagċaag	aactċāacaa	ttċġctġġt	ċttāatċatt	tġtttċtċac
91741	ġġacġcġtċġ	ġttttttġtat	tċċacttċtċt	cġġtatċġag	attacġġtċa	ċċaatġacġa
91801	tattġtġtġġ	ċacġċċaatċ	aattċċatat	cġġċaaacat	ċacacċtġġġ	cġctċtttāc
91861	ġġtċġtċġag	aataacġtċa	atacċġtġag	aacġcagġġt	ġġtġtagāġc	tċttċtġċċa
91921	ġttċtttċac	tċġġaagat	ttġtġċatat	tċatagġtag	aatagċāacċ	tġġaatġġġcġ
91981	ċaatagċatċ	tġġċċagatġ	atacċġcġġt	ċatċatġġtt	ċtġċtċaata	ġċċċċċċa
92041	ċċacacġġġa	tacċċċtatġ	cġġtagċāac	ċċatġġtċat	ċacċtġattā	cġċċċċċtċt
92101	ġċċċtġāac	ġġtġġċtttċ	atġacttċag	aatatttġġt	ċċċtaactġġ	aaaatatġġc
92161	ċċacttċaat	accġcġtttġ	atċtġtagāġ	tġċċtttġċċ	atċagġġċtġ	atatċġċċtt
92221	ċtactacġtt	acġċaaatċa	ġċaacġagċġ	ġċagċġċċaa	atċacġċtċċ	ċagttāatāc
92281	ċaaagġaatġ	ċttċċċatċa	atattċġċac	ċċġacċċġaa	atċġtċatċ	accġċċacac
92341	tġtġġtċagċ	aataacagġc	aatġataaat	taacġġġċċ	taatġaacċt	ġġċċċagċċ
92401	cġatagġtġc	acġaatġttċ	tċttċġċtag	ċaaagġtċag	tġġċttġġċa	acttġġġċa
92461	ġċttċtċtġc	tttġatċtċa	tttāaatċat	ġatċġċċġcġ	ċaccagġāġc	ġċaacċaact
92521	tatġaccact	ċtċttċġtġa	ġcatġaacċa	ataagġtttt	ċacġġttttċ	tċaatġġġta
92581	ġtttġaattġ	ċtċtācċaac	tċġġcġatġġ	tttttġcġtt	cġġġġtġtċa	acġattċġċa
92641	ġċtċttċtġt	agċċġġtġcġ	cġtġġttċag	ttġġcġċtaā	tġċttċagċġ	aattċaatat
92701	tġġtġcġtā	atċagāġċċa	ġtġġagāaaa	cġatātċatċ	ttċġċċactt	tċtġċċacġa
92761	ċttġġāattċ	ġtġġġatġċa	ċtġċċġcġġa	tāġagċċġġt	atċċġċcagġ	accġċacġġa
92821	agttċaaatċ	ċatċċġġctġ	aaaatċttāc	tġtācġcġġt	atācātċġcġ	tċġtaagttt
92881	ċċtġtaāāġa	ċtċttġcġtā	ġtatġġaagġ	aatacġċatċ	tttċatċāaa	aactċacġġġ
92941	cġcġċatġac	acċaaagċġc	ġġġcġċactt	ċatċacġāaa	ċttġġtċtġa	atttġġaāġa
93001	aattċagċġġ	ċagttġtttġ	tāagagttāa	tċtċġċċġcġ	ġatċagatċa	ġtaatċactt
93061	ċttċatġġġt	tġġġċċāāġa	acāaaagġġc	ġċtċġċċġcġ	ġtċāacāaaa	ġċāacāact
93121	ċagġġcġġa	ċtġtċċċag	cġġċċactċt	ċttġċċataā	ġtċċġċġġġt	tġtāccactġ
93181	ġċattġatāc	ttċġatāġċa	ċċtġcġttat	tċatttċttċ	ġċġċġġatġ	ttttċaactt
93241	ttttċaacac	ċċġaacċċġcġ	ġtċġġtagċċ	agġtġtaāag	acċtġagġċċ	agtttġcġġa
93301	tċatċċċġġc	acġġagċatġ	agttġatġġc	tġataacttċ	agċatċġġċa	ġġtġtċtċt
93361	tċtġagġtġġa	ġagċagatāt	tġġċtagġac	ġċatġatġtt	tttġttċċat	tāġċattġċa
93421	attāġġġġġa	ġċċāaaagġt	āaaagġtġġc	ċtagtttācċ	agġtāġcāċ	ġġttġtċāaa
93481	agāġagċāġa	ġtġāaatġttā	ġcġtġġġtċġ	agġtātaācā	ċttċtġtttġ	ċtġġċċāata
93541	acċġċċāġc	ġċacattāaa	ttċċagġtaat	āaaacġġċat	attċacġġċt	ttċattatċġ
93601	tċtttācġġt	aagġtġġġcġ	tġġatċttġt	ġċtaāaaactt	ġġċtġatāaa	acġġcġāāġa
93661	tġtġġatāac	ġċtġġtġġtġ	ġtġagġtaac	tġttġġtċġġ	cġġcġġġāġa	āaagċāaaact
93721	tġċatċtċtġ	tātċtġġtġc	agattġcġċa	āaaċcāġcġc	ġċġċċtġagġ	ttġġċtċtċa
93781	ġċġāaagġċa	ġataagġttt	aatatċāata	acagġcġtġc	ċatċāactāa	atċcagġctġ
93841	ċċċaatġċċa	ġaatċacċtċ	acċġttttġġ	ċāacġāacġc	ċtttċāactċ	aatċagċġac
93901	atġċċtatċġ	ġġtttġġacġ	āaaagttġāa	cġġġtċġāaa	atācġċċċat	tċġtġatġtt
93961	ċċċċċāġac	ġġġġagġġġcġ	aacagttġġa	cġċċagċċac	ċċtċċatċġt	ċtġatġġāaa
94021	acġaatatċa	ċċċataaatġ	ġċtġāagġċa	ġataagċċġc	ġtācġċtttċ	tġġttġġttġ
94081	tāagġtġċċa	ġċaactġtaā	ttċġċċacċa	ċċatċċtċāa	ċċāaaċċġġġ	ttġċċġtġġt
94141	acċġċāaaact	tttċttttāta	cġġtġāacġġ	atċacġċċġa	tċtġattāaa	agāġaatġta
94201	ċċċattttāġa	tġāaacġttċ	agġtġġāac	ċċtġacācāc	cġċttġttġa	tagāġcġcāġ
94261	ġġacāccact	ttġtatġttċa	ċattċatġċa	ġtaagācġġc	atttġċtttċ	atataagatġ
94321	ċāġaatġttġ	ċattċtċtċta	cġagċġġttġ	āaaactġġġ	tġġāaatċċ	tġāacġġttġ
94381	attġġāāāġa	ttċaccāġac	acttċacċta	ġatċġcġāaa	agġċttācċa	acāagttċtċt

94501	tāāccggagg	tggttgctta	atcggāttat	ctgtggtgga	tggcttīgā	ggāāgcaggg
94561	tacatccagt	tagcgataga	gctaacagac	acagaggtaa	cgcacgcata	aaaattcctc
94621	agccttatct	atttaagttg	tgctattgaa	gcaatctatt	attcaaataa	caagacgggc
94681	tatagcccgt	cttgctcgata	tattcaataa	aagaggtaat	taaagattac	cagcctttta
94741	ctgcgccacc	gttgaatgct	ttattcgctg	catcataaac	ttcgtcagac	tggtaagcct
94801	gaacaaatct	tttcacatct	tccgcatctt	tattgtcttc	gcgggcaaca	atcagattca
94861	atacaggtga	ttctttatct	tccacaacaa	gacctatctt	agctggtgtc	aggccaatct
94921	ggctagcgta	agtgggtattg	ataatcgcca	gagcgatttg	ttggctatcc	aaagaacgtg
94981	gtaattgagg	tgcttccaac	tcaaccagtt	tcagattttt	agggttctca	accacatcta
95041	atacgggttg	cagcaggcca	acaccgtctt	tcagcttaat	cagaccaacg	ctttgtagca
95101	ataacagaga	acggcccaaa	ttagttaggt	catttggtag	ggcgacctga	gatccagggt
95161	gtagttcatc	cagtgacttg	attttcttgg	aatagccggc	aatggggtaa	acgaacgagt
95221	tgccaacaga	aaccagtttg	tagccacggt	ctttgatttg	ctgatccaga	taagggttat
95281	gctggaaagc	gttaagggtcg	atatccccct	tgctcagtgc	ttcgtttggt	aacacatagt
95341	cattgaatgt	caccagttca	acgtccagac	cgtacttttc	tttagccact	ttctgagcca
95401	cttcggcaac	ttgttgctct	gcaccgacaa	taacgccaac	tttaatatgg	tttggcgctt
95461	tttcctgctg	gccgcaaccc	accaaagtca	aggtaccaat	cagcgcata	attgtctgca
95521	tagatttgaa	ttttaaagac	atatcccttc	ctctatagac	attcgttaag	atgcgcgct
95581	gtgtgaggca	gtcgctgatt	aatcactatt	tgctcgtaac	ggctttgact	atccgatcac
95641	cacttaactg	aattaggtag	accagaatta	ctagtaatac	taatacagta	ttcatcaccg
95701	tagcgttata	cccaatataa	ccatactgat	aaccgatttg	acctaagcca	ccggcaccta
95761	ctgctcctcc	catagcggaa	tagcctacca	gagtaattaa	tgtaatcggt	gccgcattca
95821	ctaagccggg	cagggtcttc	ggtaataata	cctttttgat	gatctgcac	ggtgttgctg
95881	ccatgcacg	tgccgcttca	accaaacttg	accgaatctc	tagcagagcg	ttttccacca
95941	tacgggcaat	gaaaggcgcg	gctcctaccg	ttaacggcac	gatagcgggc	tgcaatccaa
96001	tcgatgtgcc	gacgatcatg	cgtgtaaatg	gaatcatcca	taccaataag	ataataaaag
96061	gaatggagcg	gaaaatatct	accacaccag	acagcgcttc	ataaatttta	ttgttagcga
96121	taatttgccc	aggacgggtg	acatataaca	gcacccctac	aggtaacccc	agaacaaagc
96181	caaagaaacc	ggaaacaaaa	gtcatcataa	gagtttccca	gacgcctcga	gccattaacc
96241	acatcattgc	ctcagacata	acccagaacc	tctactttca	catgatgatc	ttgtaaaaac
96301	ttgatggcag	ccaggccatc	ctgaacgtcg	ccatgtagct	ctgccaacat	gacaccgaat
96361	ttcacccac	cggcataatc	catctgcgag	cttaggatac	cgatatcaat	attgaagcgg
96421	cgcacggctt	gtgagattaa	cggagcatca	actgacttac	cggtgaaactc	cagcttcaga
96481	agcgggacgt	gatctaccgt	tggtccggg	ctcatacgtt	tggcgtaatc	ttccggaata
96541	tccaaatgca	gggtggattg	aataaattgt	tggtctaattg	gtgtcttggtg	atgagagaac
96601	acctcactga	cactgtcttt	ttcaatcagt	ttgccttcac	ttattactgc	aacttgatca
96661	cagatgcgtt	tcacgacatc	catctcatga	gtgataagca	aaatcgttaa	cccaaaccgg
96721	cggttaatat	cttttagcag	ctccaatatt	gagcgggtgg	tggtcggttc	taatgcgctg
96781	gtggcttcat	cacacagcaa	aacttttagga	ttactggcca	gcgcgcgagc	gatcgcgacc
96841	cgctgttttt	gcccaccgga	cagattagcg	gggtaagcat	cttgcttatc	ggtcaaccct
96901	actaaatcca	gtaattcatt	cactctcttc	tttatactg	cacgcgatgt	attgtccaac
96961	tcaagaggca	atgcaatatt	gccgtataca	gtgctgtatg	agagtaaaat	aaatgctgta
97021	aaaatcatgc	caatctgacg	acgcgcgcgt	gttaattggc	cttcagacaa	ggtggtcaga
97081	tcttggtcat	caaccagaac	ttgaccgctg	gttgcccggt	ctaacatatt	agcgcaccga
97141	atcagggtac	ttttacctgc	gccagaagcg	ccgataacgc	cataaatttg	cccggcaggg
97201	acgtgaagac	tcacgtctga	tagcgcggta	atagtgcgcg	aaccctgctg	gaacactttg
97261	ctgatgtggg	tgagttaaat	catattatct	ttattttatc	gttattttccg	tggtctagata
97321	aaaagtggac	tttagtagaa	ccaaagtgtg	gatcggatgt	taaggcgtct	agacggctaa
97381	gtcaactgac	aacgtggatt	ctcttcggtt	ctcaataggt	aataaaacat	gcgatactat
97441	cgggggtttac	agccctcagg	agtatataag	tgactcagtc	cgttcccgcga	atatttttag
97501	atcgtgatgg	tacagttaat	gtcgatcatg	gttatgtcca	cgaatttgac	aactttcaat
97561	ttatcgatgg	tgttattgat	gcattgccgtg	aattgaaaga	aatgggtttt	gcgttggtgt
97621	tggttaacaa	tcaatcgggt	atcgcccgcg	ggtatgtttac	cgaagaacag	tttttaagtc
97681	taaccgaatg	gatggactgg	tcattggctg	atcgcggtgt	tgattttagat	ggcatctatt
97741	tctgccacaa	tcactcctgat	ggcagtgctg	ctgaattcag	tgaacatgt	gaatgccgca
97801	aaccattacc	cggaatgtta	ttgcaagcgc	agaatgaact	taatattgat	atggctgctt
97861	cttatatggt	tggcgacaaa	attgaagata	tgaggcggcg	attagcggcg	aatattggca
97921	ctaaagtatt	ggttcgaacg	ggtaagccag	tcactgccga	gggtgaagca	gcggccgatt
97981	gggtgtctaa	tagtctggca	gacctacca	aagcaataaa	agcgcgttat	aaatagcctg
98041	tacgttcaaa	taatacaaaa	acgaaaaaaa	tgtgaagata	aacccttgcc	attctgaagc
98101	agctccctat	aatgcgcac	catcgacacg	gcgctgtgag	caacttcaca	gagtggccgg
98161	ggagagcaga	gaaaattaac	tgattaaagt	gttgactctg	tagcgggaaa	gcgtattatc
98221	tgccctccgc	gttaccgtaa	gattcgccgc	aaggcaaacg	ggtaacgaac	gctctttaac
98281	aatttatcag	acaatctgtg	tgggcactcg	caagacgata	tcgacgcctg	tttcggcagg
98341	cagaaataat	atcaagtctt	gaagagtgc	caaagcagta	aacattttga	ctccggtcag
98401	aatgcctatt	tcagaaaagt	aatctttgag	caccgctgct	tttacgcaag	taaaagtcag
98461	caaatcaaac	aaatcttaaa	ttgaagagtt	tgatcatggc	tcagattgaa	cgctggcggc
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122041	ċacttttttt	ġttċċttġga	tagtatġtca	ċtttġagatt	tttttġċtġt	tttttċttċt
122101	gatttttttaa	tttċaatġġt	tatatttttt	ttactattta	tttċġtġtġc	ġċġtttttca
122161	aacttatċat	tġġtġaatġa	tattaaċġaa	ttġġagtcac	tttċaatġac	attattataa
122221	ċttċġttċġc	tċttattġċt	ttġċtċtġta	atċtċċtċat	ċttttataac	tagċaaattt
122281	attattċġġt	tġacttċtġa	ċtċtaagġat	tċġagttġġt	tttttġċaag	ttċcatatca
122341	atċaaaatġc	tagtġġġatġ	tġċtatagaa	ttttċatġta	ttġttċċaca	tġttġġġċac
122401	tċtatġtċac	ċatċttċċat	ġttttċġacġ	ġaaaaaatat	aatċttttatċ	tagċtċacta
122461	ataatċċċtt	tġġċtaattt	gattttġġġc	tċaagtcġta	ttttttċaac	ttċtaagttta
122521	ġttċttttċt	ċaagaaġġtt	ttttttġġtt	ċtttċtġatt	ċttġtataac	actaaaaata
122581	aactċġġtġc	aagġaaġtac	attġtċtġta	tċġataagġt	tttġċċtġag	tattataact
122641	ġċattattċa	ġttċagtaac	ġċttttċtċa	acttċttċta	actċtċtttt	tattacataa
122701	atatċttttt	ċaacttċaaa	ġtġtġċtttt	ataaataatċ	ċtġagtgġġta	ġġagatġact
122761	ġġtttttġċċ	agċtactata	ttġċtġaaga	ttċtċġaaac	tatċċċaagġ	tttagċċċat
122821	ġttċtttttt	ġġtċaatata	aaagġġtatġ	aagtaaatatġ	ċagġtgġagġ	ġġtttċtagt
122881	ġttaattġac	ċtttċttagġ	ġagtaaatċa	ttāaaattaa	ċaagttċtġa	aaaataċttt
122941	ġaataatċac	ċġġttatttt	ġġġaaatċġ	tġtagttttac	ċattġċtatġ	ċċtaattttta
123001	attttċatttt	tatatċtatġ	aataatġtaa	ġġtġċattat	ttatċtċaaa	ċtċtataaatt
123061	ġatġtacagt	ċtaatġttċt	ċċaaċċtċġ	ġaaaaaatġġ	ġċtċacagċċ	aaaagttċċaa
123121	aaaatċattt	ttġċaaġċġt	agattttċċċt	acġċtattat	ċatċatċtġc	tġttatċagt
123181	ġttagatġċt	ċtċġaaċtċ	ġaattġċċtċ	ġġġatttttċ	ċtġaatċtġa	ġagtatċatġ
123241	atċttċtttta	ġtattġaattt	tttċataaac	ċttċatċċċt	aagċttċġaa	ċċaatagċtt
123301	ġtagtttttt	tċċatttttag	ttġtttġċċt	ċtaccattttċ	ġtaaatġatċ	ġċagatġata
123361	tagaaatatt	atċċtċaaac	aaacċaatag	tatċtttttġa	taagttċtatġ	attagċċttt
123421	ċġagċaatċc	ataagacatt	tċaatttċaa	tttttttġaga	ġttċtttttta	agtaactċtt
123481	ġtatttċttt	ttġġġċtttġ	ataattġċaa	ġġtċġġtġa	ġagtagġġtt	agttaatatġ
123541	aattttatttt	ttġtattatt	tttġċċttaa	tċġtġċċtt	taaatttġaga	tċatċtāata
123601	tġtatttttat	tġċttċaaaa	tttaaattċġġ	aattacċttt	tġagactatt	ttġġttacta
123661	ċġġtatġġat	atċttttatag	ġtċagttġċt	ttttagtaag	agċatċattċ	ċaattttċat
123721	agttāaaaac	ġttċttċċċt	ċtġatġċġta	atġagttċċat	taatattċta	taaatatċtt
123781	tċġtacġaag	tagatġttġt	ġġatāċactt	ċttċġacġċt	atċagttġatċ	ċttġatattġ
123841	tatġċtċata	atagċtttċt	agagġaatġt	ċagagġtagt	ġaagttġtatt	atttċttġġcġ
123901	ġaaacttttċ	ġaagtttagċġ	agċtċatċac	ttagġċattt	tataatttċa	ċtāċċċċat
123961	ċactacttaa	ġtġagacġt	ttatatġaag	ċċaagtttaa	ċttġttġttt	ttagttagġt
124021	tġaatċċact	tġtagttata	aaatċtaatt	tttċaacċtt	ttċaaagtat	tttttġtċġc
124081	taactġaact	āċaaagċttċ	ċċtaaaagag	atġġtttttġt	accattċtċt	ċġċttġġtta
124141	ataċtttttġc	agttataagtt	ttċttttġċat	tġġċtttāat	ttġattġaaa	ġtaaatttta
124201	ċttttattttt	atċtatagaa	ttċġċatġga	ċaacatċttċ	atġatattċċ	atġaagattġ
124261	ċaaagtċatt	ġċttttċttġ	tatġaactġa	atġċtttāca	aagagċċċaa	ġataattġġt
124321	attċaaatċġ	atċtatagċac	tġġġċċċtġ	ċġġactċtċt	ttġġġttċġ	ġāċaagġġat
124381	tġtċagatġt	ġtċttċacta	tċċatttttag	tġġċċtġtċċ	atttttatġag	tġataċtaaa
124441	agataataċġ	tġċtaagġġa	aacġtċtatġ	actttċactt	acġttāaaata	ċttċtttttag
124501	tġtatatċtċ	taatċċċċac	ċaattċattā	actċttġġġcġ	ttġtatġaga	tagġtagaac
124561	ġattataagċ	tttċċtġact	tċattċttat	ċactatġċġc	tagċġġagċc	tċaatċacat
124621	ċagċattāaa	ċċċagċċtċa	ttċatġġtġ	tactġġġġat	agaacġġtaā	ċċġtġagċaa
124681	ċġagċttċċ	tċċataacċa	atāċġtttċa	agġċtġċatt	tġċtġtttġġ	ċtattċatġt
124741	ġattacġtġġ	ġtċattġġġa	ċttġġġaata	ċġtġċtġacġ	attāċċactā	attġġacġċa
124801	ttattttċċag	ċaactċtaag	ġċttġttċċġ	āċāāċġġġac	tatatġġtċġ	ċġċtttġċtt
124861	tċattċġttċ	tġċċġġtata	ċāċċactġċt	tattċtċtāa	atċġatċtċt	atċċaagċtġ
124921	ttġċtġatġc	ttċāġċġġġ	ċġtatċagag	ttagtaattġ	ċcattċaagtt	aagċāġċġġġ
124981	ttġġċagttġa	ġagattġċtċ	atġġċaatġġ	tāċġatġag	tttagġtagt	tċtċāġġtċ
125041	tġatġġtġġġ	ċatattġtġc	ttċttġġġġc	ġttċāaaagċ	attāċċġata	ċċtġaagċtġ
125101	ġġttāġċatċ	aatċāaaċċt	āċattġāċġ	ċatagatċat	tatċtċġttt	atāċġttġta
125161	ċċaatċġċċt	ġāċġtċtċt	aatġtċċāċ	ġtġċtttġat	tġġtċċaat	acttġaatċa
125221	ġagttċġtġc	tttaagttċt	tġġatġġġaa	tatttttċġat	ġtġġġtāag	atġtċttttt
125281	ċaatāġaāċġ	ċċāaatatċt	ttċġċatġġġ	ċtġċġċtāāc	atġġċtttċt	ttċaactċġa
125341	accatttġġcġ	ġġġāċattċ	āċāāāaatġc	ttċċtċċġc	tatċtġġagċ	ttttċāġċċt
125401	ċttċāċċāċġ	ċċtċġtttġa	ġġġtċtġtċċ	ċtċtġactāa	ċatċġtāġt	ttttċtġċġc
125461	ġtatċtċtċt	ġġċatċtġġcġ	āġġatāġtġ	ċtġġġtāagċ	āċġāġġċtġ	atċatāġtġc
125521	ġċttġċtact	ġttġġġaagċ	tġatāġċġġa	āāċġċāaat	tttċttġġċġ	ġtagtttttġa
125581	ċtagċāāāāā	taaāċċatċā	ċċatċatġġa	ġġġttāġġtċ	tttġtċġġtġ	ġċtttttġċtt
125641	tttġtacttċ	ġġtġtġġġtġ	āġġġġġċġtġ	ttġtċċttġc	ċatġtatġġt	tċttċċċtta
125701	attġġtatāc	ġtċċattġat	āċċtatċttā	ġġtatāċāc	atttġtatāc	ċāatāġāċāc
125761	tġġattċāġc	ġġatċċtċt	tġġactactā	ċāġāċāāāā	taaātātċċt	ċġġċatāġc
125821	ċġāġġtttt	tċatatġġġc	ċtataāġġċt	ċtġttāċċāġ	ċġġġċċċtā	āċāġġġċat
125881	ċġġatċtġa	ċatttġċatċ	tatġġattāc	ttāċġġċċġ	taaāċġġġċt	āċġġġāatāc
125941	ġġġatċġāġa	ġttġġtċāċċ	ċatttttatċċ	tċttċċāatt	ġġtġċtttat	ġtattċttġt
126001	atċċtġġċġġ	tġttttttċċċ	tāċġtatċā	āċġtaātāċċ	ċtġāċāċāċā	āāactċċċtġ
126061	ttāċġġtat	tġāacttċāā	atġċċāāāc	tġċtċtāāāā	ġċatċāġat	ġċtċtttċċċ
126121	ttċāġġtāċċ	ċċataāātċċ	ċġāċāactċ	atċttġġġġcġ	ġġatċtċċāġ	āāġċatātġġ
126181	atġtġatċċā	ċāċāġtatċtċ	tġġtċċāġġ	atattċāġġt	ttttċċattċ	ġċāċāġtttt
126241	ċttāāāatāc	tġċċaatċġc	tċtġġġtttt	tċċċtġtāġa	āċāċċtġċċt	tċġġtacttċ
126301	ġġġċāāāāā	ċtātātġatā	tttāċāġttċ	ċatċġġġtġt	ġġġtāāġċt	ċttttċatċċ

126421	ttttaacāāā	tcaaaagggg	tttttatāac	tgacccaaāg	cTgaāagcTt	taCtgaaccC
126481	ccagcctagc	tgggggtttt	ctgggcacaa	aaaagcccg	aaacctagaa	gggatgcggg
126541	ctttccgtac	ttcaccggac	ttatctggta	ataaccgggt	taacattttg	tggagctggg
126601	gggatttgaa	ccccgcTcg	aaattactac	accgtcggca	ctacatgctt	agtccaatca
126661	ttacatttcg	cggccagctg	cggatggaca	cgctactgac	aaactatcct	gattagtttt
126721	aatgcttcca	ccccaggcaa	ggtttccaca	cgagctcttt	taggtttgac	ctctcttgat
126781	ccccgtccta	agagcggagg	ctagggagag	agggtcttaa	gcaggttatt	aagctgctag
126841	tgcgtagttt	tcgtcgtttg	caactatttt	ttttgcgggt	ttttacgagg	ccaccgcacc
126901	tcggcatgca	ccttggggtt	cgcgaatccc	gtcgaatcca	gaatcagccc	caaagaactc
126961	agctagtata	acagaactat	gtcctgcgat	gccagttact	taacgatttg	cgtgcttcat
127021	gatgcgcgct	ttgtctaact	tccactcacg	atctctaata	tcatcgcgct	tgtcgttatc
127081	ttttttacct	tttgctacgc	cgatttttaac	tttcacccag	gcattttttcc	aatacattgga
127141	gagagcgaca	accgtgtagc	cttctcgggt	cactcggcca	aacaaggaat	ccagttcgcg
127201	tttgttcaac	agcagtttac	gggtacgcat	aggctcgcaa	acaacatgag	tcgacgcaac
127261	gttcaacggc	gtaattgtgg	ccccaaacag	gaatgcctca	ccgttttttaa	acattacgta
127321	gctgtcactg	atattttgctt	tgcctgcacg	cagtgtattt	acttcccaac	cttgacgtgc
127381	aagcccagct	tcgaactcct	cttcaatgaa	gtattctgta	cgggctcgtt	tattttgcgc
127441	aatgggtgcg	gaaccgggtt	tgtatgcttt	tttctttgtc	atagtatcgg	tctattatact
127501	gtatgcggag	gcgaatgaaa	tcctttcccg	taagatgctt	atgtattttg	tctcattttgt
127561	tgcgaggaat	gcctggcaga	ttttttgtct	ggcggtagat	aaatgggtatt	atcagtgcgt
127621	tttatgtctc	acaggaaatg	ttatgccaca	gattagccga	tctgcactgg	ttccgttcag
127681	tgtaaaacag	atgtatcaac	tcgttaatga	tgttcgttct	taccagagat	ttttacccgg
127741	ttgtaccggg	agccgggtac	ttgatgccac	tgaataatgaa	atgatagccg	ccgtggatgt
127801	cgccaaggcc	gggataagta	aaacatttac	tacacgcaat	acgctaacag	ataaccagag
127861	tatcaatatg	cagttggtgg	atggggccgtt	tcgtaaatta	atgggcggat	ggcatttttac
127921	accactaagt	gcagatgctt	gcaaagttga	attgcatctt	gattttgaa	ttacaaataa
127981	gctaattgaa	ttggcattcg	gtaaaatatt	caaggagtgt	gctgggaata	tgggtgcaggc
128041	tttctactcaa	cgggctaaag	aggctctacag	tgcctgatat	tcgcgttgag	gttgtatatg
128101	ccttatctga	acgccaatac	ttgcgcactg	tatcttttgt	ggttggcagt	actgttgagg
128161	atgcgatcaa	ggcatcagge	ttactggagt	tacggccaga	cattgacctg	gaaaaaata
128221	aagtgggtat	ctatagtcgc	ccggtaaaac	tcggtgacaa	actcaatgat	gggtatcggg
128281	ttgaaatata	tcgcccatta	atagccgacc	ccaaagagct	tcgcccggcag	cgagctgagc
128341	aggcaaaaaa	gtaaggcaca	atcagcgcct	tattttttgt	tgtcactctg	ggcagccatt
128401	gaaagagaaa	cgccggactat	cttgtggctg	agttaacatc	aataggttta	gaacctaaca
128461	ccataaccgg	catttcccaat	ctgttctgca	attctcaaat	aacttagctt	ccggttaacg
128521	cgggctcatt	tttgatatca	gtcagtaaac	cactgctatc	aaagggtcaac	ggttaacgtt
128581	gttgcgttat	tttttcgtga	ccaggttgtt	ggcggaaaac	gtagaaccag	gtttgagtg
128641	caaacggatc	ttgtagcatc	ggcgtgccta	aggatatacg	cacttggttg	tgtgtcatac
128701	ctttatgaat	tttgagggca	tcaatagggt	ataaatagtt	accctgatta	atatcaggcc
128761	ggtagaccac	cttctccaac	gttgaacaac	ccgcagtaag	cattgcaagc	atcacagcgg
128821	cggcagtcag	catttttacag	cgcataagtaa	tcacattcct	ttagggcata	ggatgacgat
128881	gataatagac	cttgcggcag	ttggaaaacct	ttacagggca	cctgtatgac	cacaaaaaag
128941	gaaaaaagtt	aatcttttct	atgcagcaag	caattctttt	gcgttttgcca	agggtgtttt
129001	tgtcacctca	ctaccgcca	gaagacgcgc	caactcttgt	aagcgggctt	ttttatctaa
129061	ccgatgcata	tgagttttcag	tctcagtacc	atcgggttgt	ttactcacia	agaaatgttg
129121	atgaccacag	ccggcaactt	gcggaaagtg	ggttacgcac	atgacttgag	ttgattcgcc
129181	aagttgacgt	agcaggcgge	caactatgcc	cgcctgtggg	ccgctgatac	ctacatctac
129241	ctcatcaaag	attaatgctg	gggtgtccat	tttactgtct	gtaattacct	gaatagccaa
129301	ggcgatgcga	gacagctcac	caccagatgc	aactttgacc	agtgccttga	ggggttggcc
129361	tggattgggtg	gtgacacaga	actcaattcg	ggttgccctt	tcgcactaa	gatgttctgg
129421	ctcaaatatt	gtttcaatgg	cgaacttgcc	atgtggcatc	gatagctcat	gcattgctttc
129481	agtaatcagt	gcagccagtt	cattggcata	atattgacgc	tcttggtgta	gccgttttgc
129541	tattgccagt	gcttgctgat	agttagtatt	tactgcatta	ctaagttggt	cgtgacatt
129601	ttcttgttgt	gagagcagtt	cttgttcatc	cagtaattgc	tgatgaaatt	gtggcaattc
129661	ttccggtgct	acatggtgtt	tcgcgcgag	atttaattgc	cgagataacc	gtttttctag
129721	ctcatataga	cgatttggtat	ccatatctaa	ttgttccgca	tagtgacgta	actcatcact
129781	ggcttcactg	atttggattg	aggcttcttc	taacatatct	agtagattat	taaattgttc
129841	gtccatactg	gccagctcgg	tcaactgatg	tttggcagcg	taaagctggc	tgaggatatt
129901	gtttttgttca	tcactctgaca	gtaattgtaa	agtcctgctga	ctcagggaca	gtaattgccc
129961	gctattttgcc	aaacgtttgt	attcaatatc	aattttgttca	tattcccctg	cctgtggaga
130021	aaatgaattc	aattctttta	gttgatattg	taataactct	tggcgggcag	ttcgttccag
130081	cgactgttgt	tgggtgaagt	ccagatcacg	gcaactttga	tgccaaattt	gataggctgc
130141	cttcattttct	gccaacagag	atgattgatt	tgcgtaggca	tccaataatt	gtttttgatg
130201	atcgggtttg	agcagcagtt	gatgagcgtg	ttggccgtgg	atctgaatta	gatgttggcc
130261	caactctctt	aattgggata	cgggtacagg	cgtaccatta	ataaagcctc	tgaaacggcc
130321	atcagcgcca	atagcgcgcc	gcaacaggca	ttcattattg	tcacgcagat	ggttggtttc
130381	cagccattgg	cgggcagatg	gtgtatccgc	cagtgagaag	cgggcgcaaa	tgtcagcgcg
130441	tgttgccctt	aagcgcacca	tgttgccatc	tgagcgatc	ccgaggcata	accctagtgc
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135541	ċggġcatgċg	ttgttaċācā	ċċċġttatċā	gāāāāċcgtg	āāāāācċacā	ccāctaġttt
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137281	āātāāāāāāā	ttacċtċgttċg	āatgacgċgā	agātċċċacċ	agċacgtgag	ċacċtācagġ
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137881	gātāagggtċċ	ātāacgāgāā	gtgċattgag	ċacgtċgagt	gaaccgtttt	tāċggċāāāā
137941	ċgttċgātāt	āċgggtātā	tgttāāāāāā	ggċgāāāāāā	gaagċttċāā	aggċtāāaggċg
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138121	gātāgttggċ	gttċāātttt	tċāācāgċtā	ċāāāāāāāā	gtgāāāāāāā	tċatċagċtċ
138181	ċactċċāāā	ċgċgtgagātā	tttċċgtċgċ	ċtggċgāagg	ātċċāāċtċg	ttātāāāāāā
138241	tċtātċātātċg	ātċċtċgātāt	tċatgċāāāg	ċāagttāāgg	tātċgāgtt	ātātāāāāāā
138301	ttċċgttċċ	gtggċċātċā	gātċgāāāā	ċttgāāāāāā	tċggtttċgtċ	ggāāāāāāāā
138361	tċtċgttċcāg	āċċtċgātċċ	ttċċtāāāāā	āātċtċgāāā	āagċtċgāāā	ċāāāāāāāā
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150661	ġġcagġcāāā	ġġġġtġċct	caāġġġatġt	tġatġatttġ	tttġġtġġtt	tġġāāāāġċ
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150841	ġatāāāāāgġt	āāatttttatġ	atġcagatċt	ttāāāāāġġc	ġġtāāāāāgġ	atttġġāāt
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150961	ġtġġcāġġct	ġctatġġctġ	āġġāāāāāā	āġġāāāāāā	ċctāāāāāāā	caāāāāāāā
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151261	attġāġattā	ċċāāāġġġt	āġactāġāā	ġtġġġattġ	ġġġttġttċċ	tttāāāāāāā
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L3 ANSWER 101 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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GenBank VERSION (VER): AF276872.2 GI:13162669  
CAS REGISTRY NO. (RN): 306927-06-0  
SEQUENCE LENGTH (SQL): 1743  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Rodents  
DATE (DATE): 28 Feb 2001  
DEFINITION (DEF): Mus musculus sodium and chloride-dependent \*\*\*high\*\*\*  
- \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
\*\*\*transporter\*\*\* mRNA, complete cds.

SOURCE: house mouse.  
ORGANISM (ORGN): Mus musculus  
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On Feb 28, 2001 this sequence version replaced gi:11527247.  
REFERENCE: 1 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Molecular cloning and characterization of \*\*\*human\*\*\*  
and murine high-affinity choline transporters  
JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (09-JUN-2000) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA  
REFERENCE: 3 (bases 1 to 1743)  
AUTHOR (AU): Apparsundaram,S.; Ferguson,S.M.; Blakely,R.D.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (28-FEB-2001) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA

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L3 ANSWER 102 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): AB043997 GenBank (R)  
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 GenBank VERSION (VER): AB043997.1 GI:11231080  
 CAS REGISTRY NO. (RN): 304428-43-1  
 SEQUENCE LENGTH (SQL): 5158  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 19 Nov 2000  
 DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* CHT1, complete  
 cds.  
 SOURCE: Homo sapiens spinal cord cDNA to mRNA.  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo

REFERENCE: 1 (sites)  
 AUTHOR (AU): Okuda,T.; Haga,T.  
 TITLE (TI): Functional characterization of the \*\*\*human\*\*\*  
 \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\*  
 JOURNAL (SO): FEBS Lett., 484 (2), 92-97 (2000)  
 REFERENCE: 2 (bases 1 to 5158)  
 AUTHOR (AU): Okuda,T.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (30-MAY-2000) Takashi Okuda, University of  
 Tokyo, Faculty of Medicine, Department of  
 Neurochemistry; 7-3-1 Hongo, Bunkyo-ku, Tokyo 1130033,  
 Japan (E-mail:okuda@m.u-tokyo.ac.jp,  
 URL:http://park.ecc.u-tokyo.ac.jp/neurochemistry,  
 Tel:81-3-5841-3560, Fax:81-3-6814-8154)

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4741 ttcaatcagt agctctgatt ttcaaaatct gccctcagat gaaaataaaa taaacgaaac
4801 atttagacaa tggctatatt aatctgggaa ggcaacacct gtggataaaa cattagaaga
4861 aaacatatat tttattttca tacttttgat atgattgtaa catatttctt gagtaattta
4921 aatgctttgt tttccacac atattcaaat cagcaagctt gtagctggac tgcaatatca
4981 acaacaagtt gtttcaaaac gcatcaaaat acaacttcat tgctacactt acaagtaatg
5041 aattttatgt gactatgaaa cgaatataag cttaaaataa gtgaatctaa taaaatggct
5101 attcctcttt ttacttgtaa ataataaatt aacattatat tctaaaaaaa aaaaaaaa

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L3 ANSWER 103 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

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LOCUS (LOC): AF276871 GenBank (R)
GenBank ACC. NO. (GBN): AF276871
GenBank VERSION (VER): AF276871.1 GI:10998441
CAS REGISTRY NO. (RN): 392136-26-4
SEQUENCE LENGTH (SQL): 1743
MOLECULE TYPE (CI): mRNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 27 Nov 2000
DEFINITION (DEF): Homo sapiens ***high*** ***affinity***
***choline*** ***transporter*** (SLC5A7) mRNA,
complete cds.
SOURCE: ***human***

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
Hominidae; Homo

NUCLEIC ACID COUNT (NA): 412 a 393 c 406 g 532 t

REFERENCE: 1 (bases 1 to 1743)

AUTHOR (AU): Apparsundaram, S.; Ferguson, S.M.; George, A.L. Jr.;  
Blakely, R.D.

TITLE (TI): Molecular cloning of a \*\*\*human\*\*\*  
hemicholinium-3-sensitive choline transporter  
JOURNAL (SO): Biochem. Biophys. Res. Commun., 276 (3), 862-867 (2000)  
OTHER SOURCE (OS): CA 134:52827

REFERENCE: 2 (bases 1 to 1743)

AUTHOR (AU): Apparsundaram, S.; Ferguson, S.M.; Blakely, R.D.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (09-JUN-2000) Department of Pharmacology and  
Center for Molecular Neuroscience, Vanderbilt  
University, 23rd Avenue South at Pierce, Nashville, TN  
37232-6420, USA

#### FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="2" /map="2q12"
gene	1..1743	/gene="SLC5A7"
CDS	1..1743	/gene="SLC5A7" /note="hCT; solute carrier family 5 member 7" /codon-start=1 /product="high affinity choline transporter" /protein-id="AAG25940.1" /db-xref="GI:10998442" /translation="MAFHVEGLIAIIVFYLLILL VGIWAAWRTKNSGSAEERSEAIIV GGRDIGLLVGGFTMTATWVGGGYINGTAEAVYVP GYGLAWAQAPIGYSLSLILGGLFF AKPMRSKGYVTMLDPFQOIYKRMGGLLFIPALM GEMFWAAAIIFSALGATISVIIDVD MHISVIIISALIATLYTLVGGLYSVAYTDVVQLFC IFVGLWISVPFALSHPAVADIGFT AVHAKYQKPWLGTVDSSSEVYSWLDSFLLMLGGI PWQAYFQVRLSSSSATYAQVLSFL AAFGCLVMAIPAILIGAIGASTDWNQTAYGLPDP KTTEEADMILPIVLQYLCPVYISF FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF RQNASDKEIVWVMRITVFVFGASA TAMALLTKTVYGLWYLSSDLVIYVIFPQLLCVLF VKGTNTYGAVAGYVSGFLFRITGG EPYLYLQPLIFYPGYYPDDNGIYNQKFPFKTLAM VTSFLTNICISYLAHYLFESGTLF PKLDVFDVAVARHSEENMDKTILVKNENIKLDEL ALVKPRQSMTLSSFTNKEAFLDV DSSPEGSGTEDNLQ"

#### SEQUENCE (SEQ):

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1 atggctttcc atgtggaagg actgatatgt atcatcgtgt tctaccttct aattttgctg
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121 gccatcatag ttggtggccg agatattggt ttattgggtg gtggatttac catgacagct
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301 ttctttgcaa aacctatgcg ttcaaagggg tatgtgacca tgtagaccc gtttcagcaa
361 atctatggaa aacgcatggg cggactcctg tttattcctg cactgatggg agaatgttc
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601 atcagcgtcc cttttgcatt gtcacatcct gcagtcgcag acatcgggtt cactgctgtg
661 catgccaaat accaaaagcc gtggctggga actggtgact catctgaagt ctactcttgg
721 cttgatagtt ttctgttggt gatgctgggt ggaatcccat ggcaagcata ctttcagagg
781 gttctctctt cttcctcagc cacctatgct caagtgcgtg ccttctggc agctttcggg
841 tgcctggtga tggccatccc agccatactc attggggcca ttggagcatc aacagactgg
901 aaccagactg catatgggct tccagatccc aagactacag aagaggcaga catgatttta
961 ccaattgttc tgcagtatct ctgccctgtg tatatttctt tctttggtct tgggtgcagtt
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1081 cggāacātcē accaḡctttc cētāgacaa aatgcttcḡg acāaagāaat cgttḡgḡtt
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1201 actgtgtatg ggctctggta cctcagttct gaccttgttt acatcgttat cttccccag
1261 ctgctttgtg tactctttgt taagggaaacc aacacctatg gggccgtggc aggttatgtt
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1441 acacttgcca tggttacatc attcttaacc aacatttgca tctcctatct agccaagtat
1501 ctatttgaaa gtggaacctt gccacctaaa ttagatgtat ttgatgctgt tḡttgcaaga
1561 cacagtgaag aaaacatgga taagacaatt cttḡtcaaaa atgaaaatat taaattagat
1621 gaacttgcac ttḡtgaagcc acgacagagc atgaccctca gctcaacttt caccaataaa
1681 gaggccttcc ttgatgttga ttccagtcca gaagggtctg ggactgaaga taatttacag
1741 tga

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L3 ANSWER 104 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): MMU401467 GenBank (R)  
GenBank ACC. NO. (GBN): AJ401467  
GenBank VERSION (VER): AJ401467.1 GI:9843808  
CAS REGISTRY NO. (RN): 286924-11-6  
SEQUENCE LENGTH (SQL): 1743  
MOLECULE TYPE (CI): mRNA; linear  
DIVISION CODE (CI): Rodents  
DATE (DATE): 16 Aug 2000  
DEFINITION (DEF): Mus musculus mRNA for \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
\*\*\*choline\*\*\* \*\*\*transporter\*\*\* (CHT1 gene).  
SOURCE: house mouse.  
ORGANISM (ORGN): Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi; Mammalia; Eutheria; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus  
NUCLEIC ACID COUNT (NA): 407 a 410 c 410 g 516 t  
REFERENCE: 1 (bases 1 to 1743)  
AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
high affinity choline transporters and characterization  
of the \*\*\*human\*\*\* gene-structure  
JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 1743)  
AUTHOR (AU): Bruess,M.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (14-AUG-2000) Bruess M., University of Bonn,  
Pharmacology and Toxicology, Reuter str. 2b, D-53113  
Bonn, GERMANY

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1743	/organism="Mus musculus" /strain="BALB/cJ" /db-xref="taxon:10090" /tissue-type="brainstem"
gene	1..1743	/gene="CHT1"
CDS	1..1743	/gene="CHT1" /function="sodium- and chloride-dependent reuptake of choline" /codon-start=1 /evidence=experimental /product="high affinity choline transporter" /protein-id="CAC03719.1" /db-xref="GI:9843809" /translation="MSFHVEGLVAILFYLLIFL VGIWAAWKTKNSGNPEEHSEAIIV GGRDIGLLVGGFTMTATWVG GYINGTAVAVYGP GCGLAWAQAPIGYSLSLILGGLFF AKPMRSKGYVTMLDPFQQIYGKRMGGLLFIPALM GEMFWAAAFSALGATISVIIDVD VNISVIVSALIAILYTLVGGLYSVAYTDVVQLFC IFIGLWISVPFALSHPAVTDIGFT AVHAKYQSPWLGTIESVEVYTWLDNLLLMLGGI PWQAYFQFVLSLSSSATYAQVLSYL AAFGCLVMALPAICIGAIGASTDWNQATAYGYPDP KTKEEADMILPIVLQYLCPVYISF FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF

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SEQUENCE (SEQ):

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1741 tga
  
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L3 ANSWER 105 OF 111 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): HSA401466 GenBank (R)  
 GenBank ACC. NO. (GBN): AJ401466  
 GenBank VERSION (VER): AJ401466.1 GI:9843753  
 CAS REGISTRY NO. (RN): 286923-93-1  
 SEQUENCE LENGTH (SQL): 1813  
 MOLECULE TYPE (CI): mRNA; linear  
 DIVISION CODE (CI): Primates  
 DATE (DATE): 16 Aug 2000  
 DEFINITION (DEF): Homo sapiens mRNA for \*\*\*high\*\*\* \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\* (CHT1 gene).  
 SOURCE: \*\*\*human\*\*\*  
 ORGANISM (ORGN): Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;  
 Hominidae; Homo  
 NUCLEIC ACID COUNT (NA): 440 a 406 c 417 g 550 t  
 REFERENCE:  
 1 (bases 1 to 1813)  
 AUTHOR (AU): Wieland,A.; Bonisch,H.; Bruss,M.  
 TITLE (TI): Molecular cloning of the \*\*\*human\*\*\* and murine  
 high affinity choline transporters and characterization  
 of the \*\*\*human\*\*\* gene-structure  
 JOURNAL (SO): Unpublished  
 REFERENCE:  
 2 (bases 1 to 1813)  
 AUTHOR (AU): Bruess,M.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (14-AUG-2000) Bruess M., University of Bonn,  
 Pharmacology and Toxicology, Reuter str. 2b, D-53113  
 Bonn, GERMANY

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1813	/organism="Homo sapiens"

gene 19..1761  
CDS 19..1761

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/tissue-type="hypothalamus"  
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/gene="CHT1"  
/function="sodium- and  
chloride-dependent reuptake of  
choline"  
/codon-start=1  
/evidence=experimental  
/product="high affinity choline  
transporter"  
/protein-id="CAC03717.1"  
/db-xref="GI:9843754"  
/translation="MAFHVEGLIAIIVFYLLILL  
VGIWAAWRTKNSGSAEERSEAIIV  
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GYGLAWAQAPIGYSLSLILGGLFF  
AKPMRSKGYVTMLDPFQQIYGKRMGGLLFIPALM  
GEMFWAAAI FSALGATISVIIDVD  
MHISVIIISALIATLYTLVGGLYSVAYTDVVQLFC  
IFVGLWISVFPALSHPAVADIGFT  
AVHAKYQKPWLGTVDSSSEVYSWLD SFLLLMLGGI  
PWQAYFQRVLSSSSATYAQVLSFL  
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KTTEEADMILPIVLQYLCPVYISF  
FGLGAVSAAVMSSADSSILSASSMFARNIYQLSF  
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VKGTNTYGAVAGYVSGFLFRITGG  
EPYLYLQPLIFYPGYPPDDNGIYNQKFPFKTLAM  
VTSFLTNICISYLA KYLFESGTLF  
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SEQUENCE (SEQ):

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721 tctgaagtct actcttggct tgatagtttt ctggtgttga tgctgggtgg aatcccatgg  
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901 ggagcatcaa cagactggaa ccagactgca tatgggcttc cagatcccaa gactacagaa  
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1261 atcggtattct tccccagct gctttgtgta ctctttgtta agggaaccaa cacctatggg  
1321 gccgtggcag gttatgtttc tggcctcttc ctgagaataa ctggagggga gccatatctg  
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1801 tgtaataggg tag
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L3 ANSWER 106 OF 111 MEDLINE on STN  
AN 2003541411 MEDLINE  
DN PubMed ID: 12827517  
TI Organic cation transporters.  
AU Koepsell H; Schmitt B M; Gorboulev V  
CS Institut fur Anatomie und Zellbiologie, Bayerischen Julius-Maximilians-

SO Hermann@Koepsell.de  
 Reviews of physiology, biochemistry and pharmacology, (2003) 150 36-90.  
 Ref: 390  
 Journal code: 0434624. ISSN: 0303-4240.  
 CY Germany: Germany, Federal Republic of  
 DT Journal; Article; (JOURNAL ARTICLE)  
 General Review; (REVIEW)  
 (REVIEW, ACADEMIC)  
 LA English  
 FS Priority Journals  
 EM 200404  
 ED Entered STN: 20031119  
 Last Updated on STN: 20040501  
 Entered Medline: 20040430

L3 ANSWER 107 OF 111 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN  
 AN 2004:343483 SCISEARCH  
 GA The Genuine Article (R) Number: 802CT  
 TI Expression of \*\*\*high\*\*\* - \*\*\*affinity\*\*\* \*\*\*choline\*\*\*  
 \*\*\*transporter\*\*\* CHT1 in the \*\*\*human\*\*\* leukemic T cell line  
 MOLT-3  
 AU Fujii T (Reprint); Okuda T; Haga T; Kawashima K  
 CS Kyoritsu Coll Pharmaceut Sci, Dept Pharmacol, Tokyo 1058512, Japan; Univ  
 Tokyo, Fac Med, Dept Neurochem, Tokyo 1170033, Japan; Gakushuin Univ, Fac  
 Sci, Inst Biomol Sci, Tokyo 1718588, Japan  
 CYA Japan  
 SO JOURNAL OF PHARMACOLOGICAL SCIENCES, (10 MAR 2004) Vol. 94, Supp. [1], pp.  
 202P-202P.  
 Publisher: JAPANESE PHARMACOLOGICAL SOC, EDITORIAL OFF, KANTOHYA BLDG  
 GOKOMACHI-EBISUGAWA NAKAGYO-KU, KYOTO, 604, JAPAN.  
 ISSN: 1347-8613.  
 DT Conference; Journal  
 LA English  
 REC Reference Count: 0

L3 ANSWER 108 OF 111 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN  
 AN 2004:105139 SCISEARCH  
 GA The Genuine Article (R) Number: 753PR  
 TI Characterization of the \*\*\*human\*\*\* \*\*\*high\*\*\* - \*\*\*affinity\*\*\*  
 \*\*\*choline\*\*\* \*\*\*transporter\*\*\*  
 AU Haga T (Reprint); Okuda T; Kaitsuka C; Okamura M; Osawa C; Nishiyama N;  
 Yamada H; Nakamura T; Kobayashi Y  
 CS Gakushuin Univ, Inst Biomol Sci, Tokyo 171, Japan; Univ Tokyo, Fac Med,  
 Tokyo 113, Japan; Kyorin Univ, Fac Med, Tokyo, Japan  
 CYA Japan  
 SO JOURNAL OF NEUROCHEMISTRY, (DEC 2003) Vol. 87, Supp. [1], pp. 43-43.  
 Publisher: BLACKWELL PUBLISHING LTD, 9600 GARSINGTON RD, OXFORD OX4 2DG,  
 OXON, ENGLAND.  
 ISSN: 0022-3042.  
 DT Conference; Journal  
 LA English  
 REC Reference Count: 0

L3 ANSWER 109 OF 111 USPATFULL on STN  
 AN 2004:63743 USPATFULL  
 TI Invertebrate choline transporter nucleic acids, polypeptides and uses  
 thereof  
 IN Raming, Klaus, Leverkusen, GERMANY, FEDERAL REPUBLIC OF  
 PI US 2004048261 A1 20040311  
 AI US 2002-241784 A1 20020911 (10)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 2653  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/320.100; 435/348.000; 530/350.000; 536/023.500;  
 800/008.000  
 NCL NCLM: 435/006.000  
 NCLS: 435/069.100; 435/320.100; 435/348.000; 530/350.000; 536/023.500;  
 800/008.000  
 IC [7]  
 ICM: C12Q001-68  
 ICS: A01K067-033; C07H021-04; C07K014-705  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 110 OF 111 USPATFULL on STN

TI 18F-labeled choline analogs  
IN DeGrado, Timothy R., Durham, NC, UNITED STATES  
Coleman, R. Edward, Durham, NC, UNITED STATES  
Baldwin, Steven W., Durham, NC, UNITED STATES  
Price, David T., Greenwood, LA, UNITED STATES  
Orr, Matthew D., Durham, NC, UNITED STATES  
Wang, Shuyan, Durham, NC, UNITED STATES

PI US 2002061279 A1 20020523  
US 6630125 B2 20031007  
AI US 2001-844674 A1 20010430 (9)  
PRAI US 2000-200347P 20000428 (60)  
US 2000-231303P 20000908 (60)

DT Utility  
FS APPLICATION

LN.CNT 1576

INCL INCLM: 424/001.890

NCL NCLM: 424/001.890

IC [7]

ICM: A61K051-00

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 111 OF 111 USPATFULL on STN

AN 1999:85438 USPATFULL

TI Decahydroquinoline-based anti-cholinergic agents

IN Efange, S. Mbua Ngale, Plymouth, MN, United States

Parsons, Stanley M., Santa Barbara, CA, United States

PA Regents of the University of Minnesota, Minneapolis, MN, United States  
(U.S. corporation)

PI US 5929087 19990727

AI US 1997-826830 19970408 (8)

DT Utility

FS Granted

LN.CNT 857

INCL INCLM: 514/314.000

INCLS: 514/278.000; 546/017.000; 546/154.000; 546/158.000; 546/164.000

NCL NCLM: 514/314.000

NCLS: 514/278.000; 546/017.000; 546/154.000; 546/158.000; 546/164.000

IC [6]

ICM: A61K031-47

ICS: C07D401-04

EXF 546/164; 546/154; 546/158; 546/17; 514/314; 514/312

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

STN INTERNATIONAL LOGOFF AT 10:22:35 ON 21 MAY 2004